On the feasibility of classification-based product package authentication

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***Abstract*—Depending on the product category the authenticity of a consumer good concerns economic, social and/or environmental issues. Counterfeited drugs are a threat to patient safety and cause significant economic losses. Different from physical-marking based approaches this work investigates authentication of drugs based on intrinsic texture features of the packaging material. Therefore, it is assumed that the packaging material of a certain drug shows constant but discriminative textural features which enable authentication, i.e. to prove if the packaging material is genuine or not. This objective requires considering a binary classification problem with an open set of negative classes, i.e. unknown and unseen counterfeits. In order to investigate the feasibility a novel drug packaging texture databases was acquired. The experimental evaluation of two basic requirements in texture classification serves as an evidence on the basic feasibility.**

I. Introduction

Counterfeiting is an economic issue affecting all industries. The OECD [1] reports that in 2013 2.5% of the worldwide traded products were counterfeited ones. For the European Union (EU) a remarkably higher value of 5% for counterfeited and imported products is reported. In case of medicals, counterfeits cause an economic loss and are moreover a potential threat to the consumer and patient health. On the European level, the Falsified Medicines Directive (FMD) 2011/62/EU should be implemented until 2018. The overall aim is to improve patient safety stipulating an efficient anti-counterfeiting system. The actual solution is based on product serialization, i.e. each package is assigned a unique identifier (e.g. 2D barcode) which enables to track and identify each medical package along the supply chain. Hence a central database is required to enable authentication of each package. Such a system will not be available in developing countries. Furthermore, it suffers costs and is exposed to getting compromised by forgers. For example, packages will have to be equipped with safety features in order to avoid tampering. Summarizing, serialization-based product authentication requires to adapt the production, shows significant risks & costs and cannot be implemented in a set of countries.

For this reason, we move from serialization to classification. This means that a product is authenticated based on constant but discriminative intrinsic features of the product or packaging material. Therefore, we target at pill drugs which are packaged in blisters and housed in a cardboard packaging. In [2] we showed that 9 different drugs from 3 manufacturers and some forged ones can be classified based on their cardboard packaging material, in a closed-set multi-class scenario. Results were promising and showed a classification accuracy of 100% for all 8 drugs. However, the testset is fairly small and drug package material authentication is a simplistic two-class (binary classification) problem, i.e. a drug is classified as being genuine or not. Contrasting to the setup in [2], package authentication has to be considered as an open set binary classification problem. In the training stage, the authentication system can capture only a limited subspace of other (known) drugs and forged packagings. It is a basic requirement that the authentication system is able to reject unseen counterfeited packages not known or available at the time of training. For a drug packaging authentication system this requires that a specific drug is distinguished from other known and unknown forgeries and drugs which is referred to as open set recognition. The general open set recognition problem has recently been addressed in the works of [3], [4], [5] which are outlined in Section II. Furthermore, in [6], [7], [8] the authors investigate the performances of the invented open set classification approaches in different applications.

In this work, we investigate the feasibility of a classification-based drug authentication system based on images of the cardboard packaging and top & bottom blister surface textures. Within this work the cardboard packaging texture and the blister top & bottom textures are referred to as modalities. A substantial drug packaging texture database, consisting of images from 45 drugs (multiple instances, i.e. multiple packages in the range of 1 and 15 per drug are acquired). Due to security concerns, strategic purposes and legal issues (toll, pharma industry) no forged packages were available.

So far, packaging or paper authentication refers to identification or serialization of each instance. These are based on the concept of physically unclonable functions (PUFs) which rely on the mapping between a challenge and response function depending on the physical nature of the object. PUFs are unclonable and unpredictable and thus ideally suited to implement identification-based anti-counterfeiting approaches. These either rely on extrinsic or intrinsic PUFs, i.e. which are attached to the product or can be derived from a part of the product itself. The encrypted PUF signature can be attached to the product enabling off-line authentication. [9], [10], [11] showed that the microstructure in a certain region of a paper or package material is discriminative enough to identify it (Paper PUFs). Detailed investigations on paper identification, using a publicly available microstructure dataset [12], are presented

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in [13], [14]. In [13] publicly availablethe authors explore the applicability of two approaches to overcome geometric distortions. The same approaches and a hybrid one are used to investigate package identification using mobile phones in [14]. Furthermore, in [15] a new feature descriptor for microstructure identification using mobile phones is introduced. By comparing the performances for different PUFs the results in [16] indicate that the approach by [11] outperforms the approaches by [12], [13], [14] but it requires a commodity scanner. Thus, in [17] the authors showed that mobile devices and the camera built-in flashlights can also be used to capture images as required for [11].

As identified in previous literature the fibre structure of paper or packaging material is positional highly unique and enables to identify single instances. The move from identification to classification, as done in this work, raises two fundamental research questions:

Positional invariance: Paper PUFs rely on the local uniqueness of the paper fibre texture. Thus, for the paper or cardboard packaging fibre structure it is not clear if (i) the fibre structure shows constant features across different regions and (ii) if those features are discriminative enough to distinguish between different types of paper or cardboard packaging.

Instance generalisation: The second question is a specialisation of the first for which the positional invariance is considered across different instances (i.e. packages) of a modality. Instance generalisation is a pre-requirement for a real-world application. For paper and packaging material it is not clear how the texture and the computed features vary between different instances, i.e. if a classifier which is trained with features from one instance is able to authenticate unseen features from another package instance and to distinguish them from other types of paper or cardboard packaging.

In this work, positional invariance and instance generalisation of the corresponding textural features are investigated for all three modalities. By considering these pre-requirements for classification-based drug packaging authentication, this work enables to draw fundamental conclusions. Based on the new insights the feasibility of a novel serialization-less anti-counterfeiting approach can be considered.

Section II introduces into open set drug package authentication: (i) Section II-A describes a possible scheme for an package authentication system and (ii) in Section II-B the open set recognition problem is considered in more detail. Section III introduces the acquired database. The classification pipeline is outlined in Section IV. Experiments and results are presented in Section V and Section VI concludes this paper.

II. Open-set drug package authentication

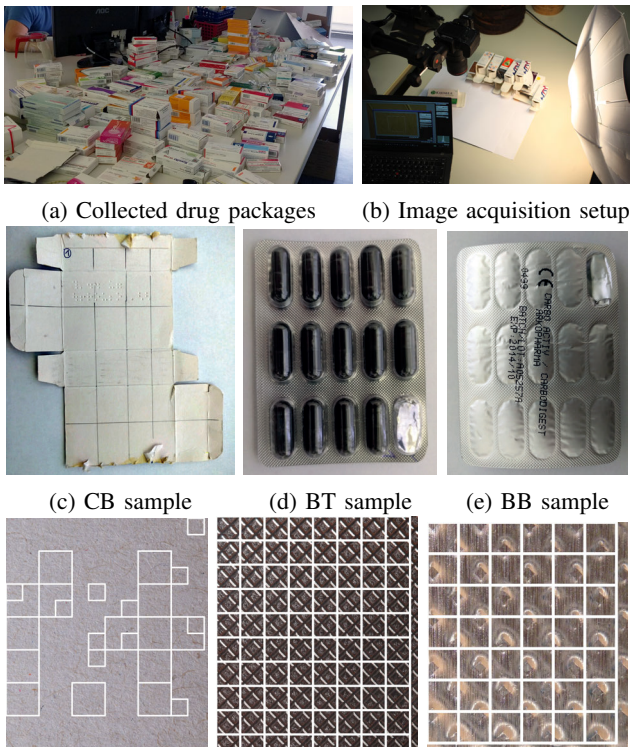
A. Drug package authentication system

For a given drug sample a mobile application guides the user to open/disassemble the drug packaging and to capture images of three different packaging modalities: The cardboard packaging texture I_{CB} as well as the textures visible on the top and bottom blister sides (I_{BT}, I_{BB}). Furthermore, the user is guided to capture the product code I_{PC} (e.g. EAN which is the European article number). All four images compose the authentication vector $\hat{AV} = (I_{CB}, I_{BT}, I_{BB}, I_{PC})$. I_{PC} is processed in order to determine the product code specifying the target product. I_{CB}, I_{BT}, I_{BB} are preprocessed (segmentation, image enhancement). For the resulting texture images T_{CB}, T_{BT}, T_{BB} a set of feature vectors $FV_{CB} = \{\hat{cb}_1, ..., \hat{cb}_i\}$, $FV_{BT} = \{\hat{bt}_1, ..., \hat{bt}_j\}$ and $FV_{BB} = \{\hat{bb}_1, ..., \hat{bb}_k\}$ are computed, where the number of feature vectors per modality i, j, k depends on the size of the preprocessed images and on the utilized feature extraction strategy. Based on the product code, the authentication system selects the corresponding precomputed classification models M_{CB}, M_{BT}, M_{BB} from a model repository. If the required models are not available on the device they could be requested from a remote repository. For each model M and a given feature vector $\hat{v}$ the prediction function $pF(M, v) = 1$ in case the vector is labelled as being genuine and -1 if not. For each model M_{CB}, M_{BT}, M_{BB} and the corresponding feature vector sets $FV_{CB}, FV_{BT}, FV_{BB}$ the prediction function is applied to all feature vectors which leads to the predictions for each modality of the packaging instance $P_{CB} = \{p_1, ..., p_i\}$, $P_{BT} = \{p_1, ..., p_j\}$ and $P_{BB} = \{p_1, ..., p_k\}$. Finally, a decision function $f(P_{CB}, P_{BT}, P_{BB}) = (v, p)$ needs to be defined, where $v \in \{1, -1\}$ gives the final authenticity vote of the authentication system and $p \in [0, 1]$ specifies a probability score for the final vote which are then presented to the user.

Such an authentication system relies on the assumption that different modalities of the packaging material of all instances from the same product show constant but discriminative features which enable to detect and distinguish the product from a known and unknown set (=open set) of other as well as from counterfeited products. For training of a classifier, only a limited subset of other drugs and available counterfeits is utilized. As a precondition for authentication, the classifier must be able to reject unseen data. This is a typical binary classification problem, either a given sample is labelled as genuine or not. The undefined set of unknown other classes leads to an open set recognition problem. This differs from closed-set classification where only known classes are separated from each other. Substantial efforts in the field of open set recognition were made in [3], [4], [5]. In [3] the authors introduce and formalize the open set recognition problem. Furthermore, in [3], [4], [5] the authors propose different SVM extensions which specifically address the open set recognition problem. In order to investigate the two research questions and as a consequence to prove the principal feasibility of an authentication system we base our experiments on the formalization of the open set recognition problem provided in [3], [4].

B. Formalization of the open set recognition problem

In [3] the authors define the *Open Space Risk* as $R_O(f) = \frac{\int_O f(x)dx}{\int_{S_O} f(x)dx}$. S_O needs to be considered as a large ball which is a subspace of the open space including all training samples. O is the open space. $f(x)$ is a recognition function where $f(x) = 1$ if x is recognized as the class of interest y and $f(x) = 0$ if



(a) Collected drug packages (b) Image acquisition setup

(c) CB sample (d) BT sample (e) BB sample

(f) CB image (g) BT image (h) BB image

Fig. 1: Image Acquisition Overview: 3rd Row: exemplary images showing the selected 128×128 and 256×256 image patches.

not. Consequently, the open set risk R_O is the fraction of the positively labelled open space in S_O compared to the positive labelled samples in O. The goal in open set recognition is to minimize the open space risk R_O whilst balancing it against the empirical (known) risk R_E computed over the available training data. Therefore, $\hat{P} = \{p_1, ..., p_n\}$ are samples from the positive training class P and $\hat{N} = \{n_1, ..., n_m\}$ are samples from a set of other known classes N. $\hat{N}$ is defined as the negative training data. U is the larger universe of negative unknown classes only utilized for evaluation and $E = \{e_1, ..., e_z\}, e_i \in P \cup N \cup U$ specifies all evaluation data. For a given training data $\hat{P} \cup \hat{N}$ and the open space and empirical risk functions R_O, R_E the open set recognition problem is to find a function f, where $f(x) > 0$ for positive recognitions, which minimizes the open set risk:

$$\underset{f}{arg\,min}\{R_O(f) + \lambda_r R_E(f(\hat{P} \cup \hat{N}))\} \quad (1)$$

where λ_r is a regularization constant.

Hence, open set recognition is a minimization problem which combines the open set and the empirical risk over the space of allowable recognition functions. Further, the empirical risk (i.e. the training error) can be optimized using predefined constraints. The stated minimization problem requires a set of known classes which are utilized for training and a set of known unknown classes in U which are only used for evaluation.

III. Drug Packagings Texture Database (DPT-DB)

For image acquisition, a large variety of drug packages were collected from different pharmacies (1st row in Fig. 1). From each drug package (=instance) the CB fibre texture on the inner raw side of the packaging, the BT texture (blister top side) and the BB texture (blister bottom side) were captured. For image acquisition a Canon 70D (100mm lens and flashlight), mounted on a tripod, was utilized (see Fig. 1b). From each CB,BT&BB instance images from different and non-overlapping sections were captured (e.g. Fig. 1c)). In total images for 45 drugs from 28 different producers were taken. For each drug between 1 and 15 package instances are available. All captured images were manually cropped ensuring that just texture remains.

IV. Classification Pipeline

Two different classification scenarios are considered: (i) CLASS to investigate the positional invariance of the CB,BT&BB texture. (ii) PACKAGE to prove instance invariance which is a step towards a real-world setup. In order to train and evaluate SVM-based classifiers data needs to be sampled and then partitioned into training (T) and evaluation (E) data. The amount of data (k) to be sampled is predefined for both scenarios. In this work, data relates to image texture patches of CB,BT&BB. For patch sampling, each CB,BT&BB image is subdivided into a grid which is specified by the size of the feature descriptor (e.g. 128×128 or 256×256 pixels). The 3rd row in Fig. 1 depicts sample images for CB,BT&BB for which the image patch grids are shown.

In case of CLASS k patches are sampled from all instances of each drug and modality. Contrary, for PACKAGE k patches are selected from each instance of each drug and modality. This is important in that for cross-validation the partitioning into T and E differs in principle as illustrated in Fig. 2. For CLASS the k patches of a drug and modality are partitioned so that different patches of each instance are included in T & E. On the other hand for PACKAGE the patches are partitioned instance-wise into T and E.

A. Feature vector computation

For each selected patch in CLASS or PACKAGE a set of discriminative features is computed. Prior to feature extraction Contrast Limited Adaptive Histogram Equalization (CLAHE) [18] is applied to each patch (parameters: block radius=50, bins=256, slope=40). Exemplary CLAHE enhanced patches are shown in the 1st and 2nd row of Fig. 3.

a) Feature Extraction: For the experiments feature extraction approaches producing low dimensional feature-vectors are utilized, mainly due to the fact that high dimensional features and feature encoding cause computational and memory issues when computing all classification configurations (CCs) for different SVMs, i.e. RAM & I/O limitations. We already did small-scale experiments on a subset of the CCs with SIFT,

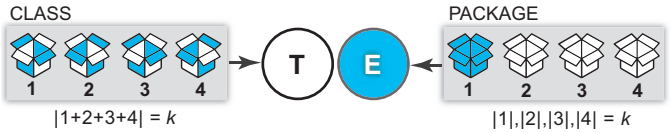


Fig. 2: Training (T) and evaluation (E) data sampling and partitioning strategies applied for CLASS and PACKAGE

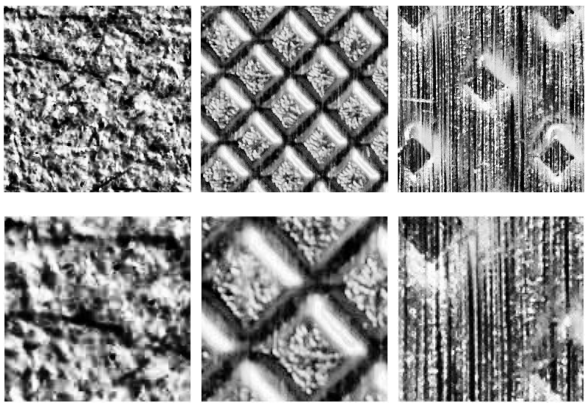


Fig. 3: Preprocessed patches of the CB,BT&BB images in Fig.1 - 1st Row: 256×256 pixels, 2nd Row: 128×128 pixels

SURF & feature encoding and the results indicate that the classification performance even increases.

The following features are utilized: Local Binary Pattern (LBP) [19], Local Ternary Pattern (LTP) [20], LiLBP (LiLBP) [21], Histogram of Gradients (HOG) [22], Dual Tree Complex Wavelet Transform (DTCWT) [23], Multifractal Spectrum (MFS) [24], Edge Co-Occurence Matrix (ECM) [25].

For each selected patch of CLASS & PACKAGE a feature vector for each listed feature extraction approach is computed.

B. Classification Approaches

For classification LIBSVM [26] and the open set extensions provided by [27] are utilized. From LIBSVM we use the ONE-CLASS and the C-SVC SVM (BINARY C-SVC)for one-class and binary classification, respectively. Additionally, as an approach specifically addressing open set recognition, the WSVM [4] is applied for binary classification. As the ONE-CLASS SVM uses a radial basis function (RBF) kernel, the same is chosen for BINARY C-SVC and WSVM.

In the experiments, the classification approaches are utilized to investigate a large set of different CCs. $D = \{d_1, ...d_{45}\}$ is the set of drugs and $DM = \{dm_1, ..., dm_{28}\}$ is the set of drug manufacturers in the testset where $fdm(d_i) : D \rightarrow DM$ specifies the drug manufacturer for each drug. $M = \{CB, BT, BB\}$ specifies the packaging modalities. $FE = \{fe_1, ..., fe_n\}$ is the set of feature extraction methods and $CS = \{CLASS, PACKAGE\}$ gives the classification scenarios. The feature vector sets for a certain drug $d \in D$ & modality $m \in M$, for the k-patches defined for the cla ssification scenario $cs \in CS$ computed with feature extraction method $fe \in F$, are given by $FV_{(d,m,f,cs)} = \{fv_1, ..., fv_k\}$. Following, a specific CC is defined by the tuple

$$CC = (d \in D, m \in M, fe \in FE, cs \in CS) \quad (2)$$

where d specifies the target drug which should be authenticated. The respective set of feature vector sets for CC is given by $FV_{CC} = \{FV_{(d_1,m,f,cs)}, ..., FV_{(d_{45},m,f,cs)}\}$ which is composed by the CC specific feature vector sets from each drug. The positive training data $P_{CC} = FV_{(d,m,f,cs)}$ is specified by the target drug d in CC. The negative training data $N_{CC} = \{FV_{CC}\} \setminus \{FV_{(d,m,f,cs)}\}$ is composed by all feature vector sets of all other drugs. The positive and negative training data P_{CC}, N_{CC} are then used for nested cross-validation using a specific classification approach.

C. Cross-fold validation

Optimization is crucial as the standard LIBSVM parameters did not succeed in our experiments. Therefore, cross-validation (CV) strategies have been carefully designed and employed in order to optimize the SVM parameters and to strictly avoid that training data is used for evaluation.

Therefore, the negative training data is split into known negatives KN_{CC} and unknown negatives $UN_{CC} = N_{CC}/KN_{CC}$. Therefore, for KN_{CC} the feature vector sets from a fixed number of drugs (e.g. 6) are selected, where the manufacturers are different to the target drug manufacturer of d in CC. Now, a set of positive training data P_{CC}, a set of known negatives KN_{CC} and unknown negatives UN_{CC} is available. Based on P_{CC}, KN_{CC}, UN_{CC} nested CV procedures for CLASS and PACKAGE are defined as illustrated in Fig.4.

For CLASS, we apply a k-fold data split strategy, i.e. P_{CC}, KN_{CC} are class-wise split into k-folds $\{P_1, ..., P_k\}$ and $\{KN_1, ..., KN_k\}$, i.e. all drug classes are distributed equally in the k folds. In the outer loop, we iterate over the k positive and k negative known data folds. Thereby, the ith positive and jth negative was selected for evaluation. The evaluation set is given by $E_{i,j} = P_i \cup KN_j \cup UN_{CC}$ and the training set by $Ti, j = \{P_1, ..., P_k\} \setminus \{P_i\} \cup \{KN_1, ..., KN_k\} \setminus \{KN_j\}$. Thus a large set of known unknown drugs UN_{CC} are used only for evaluation. Note that $|\{KN_1, ..., KN_k\} \setminus \{KN_j\}|$ is reduced to the same size of the positive training data $|P_i|$ in a classwise manner. For each $T_{i,j}$ in the inner CV loop the best hyperparameters are determined in a grid search. Same as in the outer loop, k-fold validation is performed repeatedly in order to test a set of SVM parameters. For the ONE-CLASS SVM just the positive samples in $T_{i,j}$ are split into k-folds and the known negative training samples are only used for validation. As a measure for the performance the F-Measure is utilized which is well suited to balance between specialisation and generalisation in binary classification tasks. For the binary SVM approaches, each prediction is assigned a probability. In the inner loop, the probabilities are used to determine a threshold which maximizes the F-Measure. The SVM parameters delivering the highest F-Measure (and the probability threshold in case of binary SVMs) are selected for

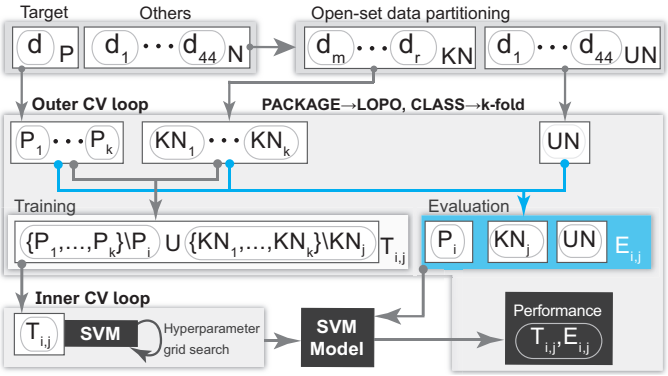


Fig. 4: Cross-validation scheme for CLASS and PACKAGE

CC	CLASS						PACKAGE					
	128×128			256×256			128×128			256×256		
	CB	BT	BB	CB	BT	BB	CB	BT	BB	CB	BT	BB
ONE-CLASS	LTP 0.83 ±7.9	LTP 0.9 ±6.2	LTP 0.92 ±5.8	LTP 0.91 ±4.4	LTP 0.85 ±13.6	LBP 0.87 ±13.5	LBP 0.81 ±8.7	LBP 0.86 ±6.3	LTP 0.84 ±11.3	LTP 0.85 ±9.1	LBP 0.88 ±5.0	LBP 0.85 ±7.1
BINARY	LTP 0.88 ±6.9	$LiLBP$ 0.94 ±3.2	LTP 0.93 ±4.1	LTP 0.91 ±5.2	$LiLBP$ 0.92 ±9.0	LTP 0.93 ±5.0	LTP 0.82 ±9.5	LTP 0.92 ±3.7	LTP 0.87 ±8.9	LTP 0.85 ±5.5	LTP 0.94 ±5.7	$LiLBP$ 0.87 ±10.0
WSVM	LTP 0.86 ±7.6	LTP 0.93 ±4.1	LTP 0.93 ±4.3	$LiLBP$ 0.88 ±6.0	LTP 0.88 ±7.6	MFS 0.88 ±9.1	LTP 0.85 ±8.2	LTP 0.91 ±4.2	$LiLBP$ 0.85 ±9.2	$LiLBP$ 0.83 ±8.5	LTP 0.89 ±8.7	$LiLBP$ 0.84 ±10.1

TABLE I: Classification performances: For each configuration the mean F-Measure (CLASS=45 & PACKAGE=8 target drugs) and the StDev for the best feature are presented. BEST CLASS/ PACKAGE configurations for each modality are layered green.

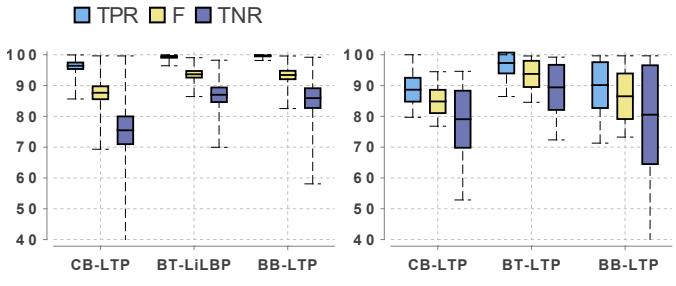
the outer loop. Finally, the SVM approach is trained with $T_{i,j}$ (for ONE-CLASS only the positive data P_i is utilized) and the selected hyper parameters from the inner CV loop. The trained model is evaluated using the evaluation data $E_{i,j}$ and probability threshold in case of binary SVMs.

For PACKAGE, a nested leave-one-package-out (LOPO) CV procedure is applied. Thereby, P_{CC} is split into k-folds in a package-wise manner, where k is given by the number of packages in P_{CC}, i.e. the number of available packages from the target drug. KN_{CC} is reduced to contain a fixed number of feature vectors from each class which are sampled package-wise. Furthermore, for KN_{CC} the features of each drug are split into two folds KN_1, KN_2 package-wise. Same as for CLASS, in the outer CV loop we iterate over the i positive and the $j = 2$ known negative training folds Ti, j and evaluate it with $E_{i,j}$, as done in the CLASS scenario. For ONE-CLASS in the inner CV loop the same procedure as for the outer loop is applied. However, for binary SVMs the inner CV loop has been adopted to better match the open set recognition problem. Therefore, the known negative training data in Ti, j is split classwise into two folds TKN_1 and TKN_2. One fold simulates known negatives and the other one unknown negatives in the inner loop. While the known negatives are further used for training and validation, the unknown negatives are just used for validation. This strategy adapts the inner CV loop and the parameter grid search to the open set recognition problem and is supposed to minimize the difference between the inner CV validation- and the outer CV evaluation-error.

V. Experiments

A. Experimental setup

All classification approaches (Section IV-B) were utilized to cross-validate all CC combinations (Eq.2) using the CS-specific CV strategies (Section IV-C). For both, PACKAGE and CLASS a patch number k of 500 is set. For CLASS the outer and inner CV loops are iterated twice and the data is split into 2-folds. In case of PACKAGE LOPO is performed for all package instances of drugs with at least 5 instances. For each LOPO CV the positive data is split into 2-folds, in the inner and outer CV loop. For both CSs, 5 drugs are selected for the known negative training data KN_{CC}. In order to enable a fair evaluation, all data splits for CLASS & PACKAGE are stored and reused for different features and classification approaches.



(a) CLASS - 128×128 (b) PACKAGE - 256×256

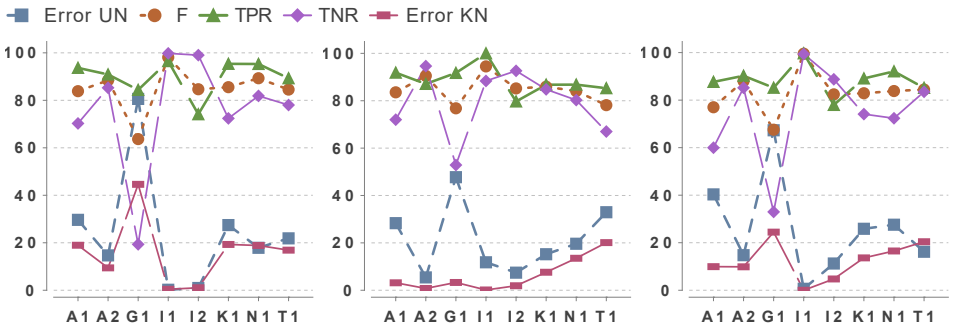
Fig. 5: CLASS vs. PACKAGE (Binary C-SVC): TPR = $\frac{TP}{TP+FN}$, TNR = $\frac{TN}{TN+FP}$ [Y-Axis: Mean accuracies, min, max and variance in %]

B. Results and discussion

Table I provides an overview of the results for each classification scenario, different patch sizes, modalities and SVMs. For CLASS the averaged results over all 45 drugs are shown. In case of PACKAGE, mean values for drugs with at least 5 instances are shown.

Considering positional invariance, the results for the best (green layered) CLASS configurations show high mean F-Measures over 0.9. This indicates that the textures from all three modalities show constant but highly discriminative features which enable to recognize the same drug class and to distinguish it from other classes. Regarding the question of instance invariance, the F-Measures for the best PACKAGE configurations provide an evidence on the feasibility of a drug package authentication system. The PACKAGE results show that the textural features are constant across different instances for all three modalities. This is a basic requirement for a classification-based authentication system. Although only low-level features have been utilized, the achieved F-Measures are very promising. Most of the best results for both scenarios and the different modalities were achieved with the BINARY C-SVC Y SVM. Fig. 5 provides a more detailed view on the BINARY C-SVC CLASS and PACKAGE results for the best features from each modality. Thereby, it is clearly visible that the performance decreases in case of the more difficult PACKAGE scenario. Furthermore, the comparison between the class accuracy (=true positive rate - TPR) and the others accuracy (=true negative rate - TNR) shows that for all results a higher class accuracy is achieved.

Finally, Fig. 6 shows accuracies and errors for PACKAGE,CB and all SVMs for the best features. For each tested drug (=8) and all SVMs, results show that the error for known data (KN=seen in training) is lower than the error for unknown data (UN=open set). Considering the different



(a) ONE-CLASS (b) BINARY C-SVC (c) WSVM

Fig. 6: PACKAGE (256×256) – SVM performance comparison for CB and all target drugs with more than 5 instances (=8 drugs): Accuracies (TPR,TNR) and recognition errors for the unseen data (Error UN) and seen training data (KN) are shown [X-Axis: Target drug (d) ids: e.g. A1 = manufacturer A+drug number].

SVMs, the accuracies and errors for ONE-CLASS and WSVM vary more compared to the per-drug results of the BINARY C-SVC. Furthermore, the WSVM does not outperform the classical BINARY C-SVC in terms of achieving a lower error for recognizing unknown data (UN).

VI. Conclusion

Results showed that textural features of drug packaging material are constant and highly discriminative. Very important, the experiments indicate that a classifier can be trained with a set of known instances and is able to authenticate unseen instances.

In future work, we will use high-level features, feature encoding and fusion techniques and it is planned to employ deep learning techniques. Furthermore, causes for classification errors need to be investigated in detail, e.g. in case of a high false positive rate it can be that other drugs from the same manufacturer have the same packaging material.

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