

Exploring Local Features and the Bag-of-Visual-Words Approach for Bioimage Classification

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ABSTRACT

With recent advances in imaging technologies large numbers of bioimages are currently being acquired. Automated classification of these bio-images is a very important and challenging problem. Here we investigate the capabilities of local features and the Bag-of-Visual-Words (BOV) approach in the area of bioimage classification. We have tested both sparse and dense placement of local features. The local feature that we have tested is Scale-Invariant Feature Transform (SIFT), but we are in the process of testing other local features. The standard BOV approach is based on counting the number of local descriptors assigned to each quantization. In our case we are also using other statistics (mean and covariance of local descriptors). The classifier used for this study is the Support Vector Machine (SVM). We have performed classification experimentation on the well-tested single cell dataset of 2D HeLa from CMU and have achieved performance similar to the state of the art.

Categories and Subject Descriptors

I.4 Image Processing and Computer Vision

General Terms

Algorithms

Keywords

Bioimage, classification, local features, bag-of-visual-words

1. INTRODUCTION

With recent advances in imaging technologies large numbers of bioimages are currently being acquired. Automated classification of these bioimages is a very important and challenging problem.

One of the most widely used benchmark for classification is the fluorescence microscopy images dataset of 2D HeLa cells [2] from the Murphy lab, stained with various organelle-specific fluorescent dyes. The dataset consist of ten classes for intracellular organelles and structures. 2D HeLa cells were stained with dyes (DAPI, MitoTracker, and DiOC6), and/or antibodies (Giantin, GPP130, Lamp2, Nucleolin, TfR, Actin, and Tubulin). The dataset contains roughly 100 images for each of 10

subcellular classes (sample images from each of the classes are shown in Figure 1). Some other popular datasets used for bioimage classification are Locate endogenous and Locate transfected [10], Locate Confocal [11] and IICBU 2008 benchmark [3].

Many researchers have reported results on the 2D HeLa classification benchmark, such as: Boland and Murphy, 2001[2]; Chebira et al., 2007 [6]; Nanni et al., 2010 [5]; Coelho et al., 2013 [4]; Shamir et al., 2008 [3] and Tahir et al., 2012 [7]. The best-published results have been obtained by Tahir et al. [7] and Nanni et al. [5], with classification accuracy of 99.7% and 97.5 % respectively, using a combination of different features.

Besides our study, which is based on local features and BOV approach, Coelho et al. [4] is the only other study based on it. In spite of its simplicity, flexibility, and effectiveness, the BOV method, which originated from the text retrieval field, has not been used in the area of bioimage classification. We investigate the capabilities of local features and the Bag-of-Visual-Words (BOV) method for bioimage classification

2. METHOD DESCRIPTION

The proposed algorithm for bioimage classification is based on using local features with a bag-of-visual-words (BOV) approach. The local feature that we have tested is the Scale-Invariant Feature Transform (SIFT), which is an algorithm to detect salient points and describe local features around these points in images [1]. We have tested both sparse SIFT (Figure 2) and dense SIFT (Figure 2.) placement of local features. The dataset used for this study is the fluorescence microscopy images of 2D HeLa cells [2].

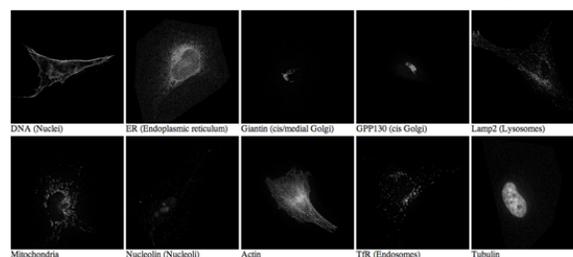


Figure 1. Shows sample images form the 2D HeLa dataset.

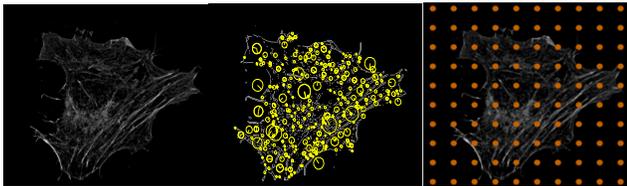
The standard BOV approach is based on counting the number of local descriptors assigned to each quantization [9]. The quantization is based on the standard k-means approach and the size of the codebook is 300. In our case we are also using other statistics (mean and covariance of local descriptors). The Support Vector classifier (SVM) from the Weka software [8] is used in our study with 10-fold cross-validation where 50 % of images are used for training and the rest of the images for testing.

We have developed a baseline approach based on global texture features consisting of co-occurrence features, moments, entropy, smoothness and uniformity [12] (feature length of 44) called SHARP Global.

3. RESULTS

We present the classification accuracy results based on three different methods and compare our approach to other published results.

The baseline SHARP Global reports an accuracy of 85.2 %. We have tested two different local feature implementations with a BOV approaches, one with sparse SIFT salient point placement (SHARP Sparse Local) and the other with dense SIFT (SHARP Dense Local) point placement and the classification results are 87.0 % and 91.8 % respectively. Finally we have combined our dense SIFT implementation with our global texture features and have achieved a classification accuracy of 95.2 % (SHARP Dense Local & Global). The classification accuracy is presented in Table 1 for our methods and different published results. Tahir et al. [7] and have obtained the best results of 99.7 %. Our classification accuracy is slightly lower than those reported in [5], [6] and [7], but we have not yet tried to optimize the different parameters in our implementations. Our results are slightly higher than those reported in [4].



Figures 2. Shows a sample 2D HeLa image and corresponding sparse and dense SIFT salient point locations.

Table 1. Classification accuracy on the 2D HeLa with other published results

Method	Classification Accuracy %
WND-CHARM [3]	84.0
SHARP Global	85.2
SHARP Sparse Local	87.0
SHARP Dense Local	91.8
SHARP Dense Local & Global	95.2
Nanni et al., 2010 [5]	97.5
Chebira et al., 2007 [6]	95.4
Tahir et al., 2012 [7]	99.7
Coelho et al., 2013 [4]	94.4

4. CONCLUSIONS

We have implemented a local feature and bag-of-visual-words approach for bioimage classification and have tested it on a widely used 2D HeLa benchmark and have achieved performance similar to the state of the art. We have shown that combining this approach with the standard global texture features can improve the classification accuracy. In the future we plan to test some other local features and besides using k-means for BOV

quantization, we plan to test both soft coding and sparse coding. In the future we plan to test our method on other bioimage classification datasets: Locate endogenous and Locate transfected [10] and Locate Confocal [11].

5. DISCLAIMER

Any mention of commercial products or reference to commercial organizations is for information only; it does not imply recommendation or endorsement by NIST nor does it imply that the products mentioned are necessarily the best available for the purpose.

6. REFERENCES

- [1] Lowe, D. G. (2004). Distinctive image features from scale-invariant keypoints. *International journal of computer vision*, 60(2), 91-110.
- [2] Boland, M. V. and Murphy, R. F. (2001). A neural network classifier capable of recognizing the patterns of all major subcellular structures in fluorescence microscope images of HeLa cells. *Bioinformatics (Oxford, England)*, 17(12).
- [3] Shamir, L., Orlov, N., Eckley, D. M., Macura, T. J., & Goldberg, I. G. (2008). IICBU 2008: a proposed benchmark suite for biological image analysis. *Medical & biological engineering & computing*, 46(9), 943-947.
- [4] Coelho, L. P., Kangas, J. D., Naik, A. W., Osuna-Highley, E., Glory-Afshar, E., Fuhrman, M., & Murphy, R. F. (2013). Determining the subcellular location of new proteins from microscope images using local features. *Bioinformatics*, 2013.
- [5] Nanni, L., Brahmam, S., and Lumini, A. (2010). Novel features for automated cell phenotype image classification. *Advances in experimental medicine and biology*, 680, 207-13.
- [6] Chebira, A., Barbotin, Y., Jackson, C., Merryman, T., Srinivasa, G., Murphy, R. F., and Kovacevic, J. (2007). A multiresolution approach to automated classification of protein subcellular location images. *BMC bioinformatics*, 8(1), 210
- [7] Tahir, M., Khan, A., & Majid, A. (2012). Protein subcellular localization of fluorescence imagery using spatial and transform domain features. *Bioinformatics*, 28(1), 91-97.
- [8] Hall, M., Frank, E., Holmes, G., Pfahringer, B., Reutemann, P., & Witten, I. H. (2009). The WEKA data mining software: an update. *ACM SIGKDD Explorations Newsletter*, 11(1), 10-18.
- [9] Li, X., Godil, A., & Wagan, A. (2008, August). 3D part identification based on local shape descriptors. In *Proceedings of the 8th Workshop on Performance Metrics for Intelligent Systems* (pp. 162-166). ACM.
- [10] Hamilton, N. A., Pantelic, R. S., Hanson, K., and Teasdale, R. D. (2007). Fast automated cell phenotype image classification. *BMC bioinformatics*, 8, 110.
- [11] Locate endogenous and Locate transfected: <http://locate.imb.uq.edu.au/>
- [12] Gonzalez, R. C., & Richard, E. (2002). *Woods, digital image processing*. ed: Prentice Hall Press, ISBN 0-201-18075-8.