

Human Protein Image Classification

Songyang Zhang, Shipeng Yan,
Yongfei Liu, Bo Wan

School of Information Science and Technology
ShanghaiTech University

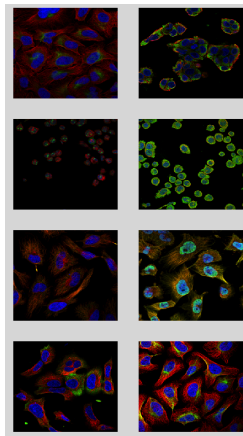
DIP Course Project, 2019



- 1 Problem
 - Background
 - Terminology
- 2 Method
 - Data Analysis
 - Data Pre-Processing
 - Low-level Method
 - DNN-based Method
 - SIFT-CNN Method
- 3 Experiment
 - Quantitive Results
- 4 Conclusion
 - Summary
 - Future Research
 - Reference



Background



- Human protein classification can help us understand the human cells and disease.
- Classify mixed patterns across a range of different human cells is challenging
- High-throughput microscopy could generate high-resolution cell images.
- Human cells hold the key for the next breakthrough in medicine.



Terminology

Problem Definition

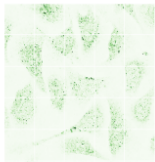
Multi-label classification task requires the model give each input data multiple labels

- Input: A 4-channel image $\mathcal{X} \in \mathbb{R}^{4 \times H \times W}$, where H and W is the height and width of the image.
- Output: A subset of the label set $L \in Y$, $Y = \{y_1, y_2, \dots, y_n\}$, where n is the number of category over the whole dataset.
- $0 \leq |L| \leq n$, $n = 28$ in this task.

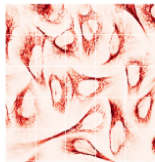


Data Analysis(1/3)

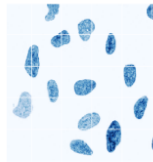
- Endosomes -



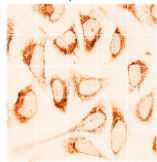
stained microtubules



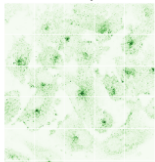
stained nucleus



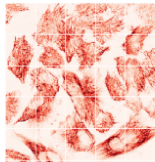
stained endoplasmic reticulum



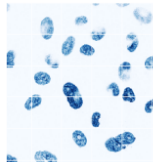
- Endosomes - Lysosomes -



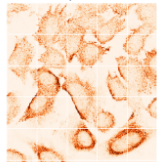
stained microtubules



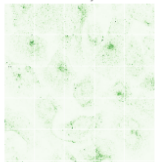
stained nucleus



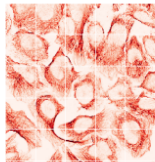
stained endoplasmic reticulum



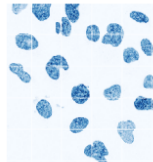
- Endosomes - Lysosomes -



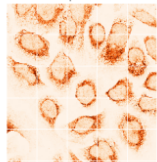
stained microtubules



stained nucleus

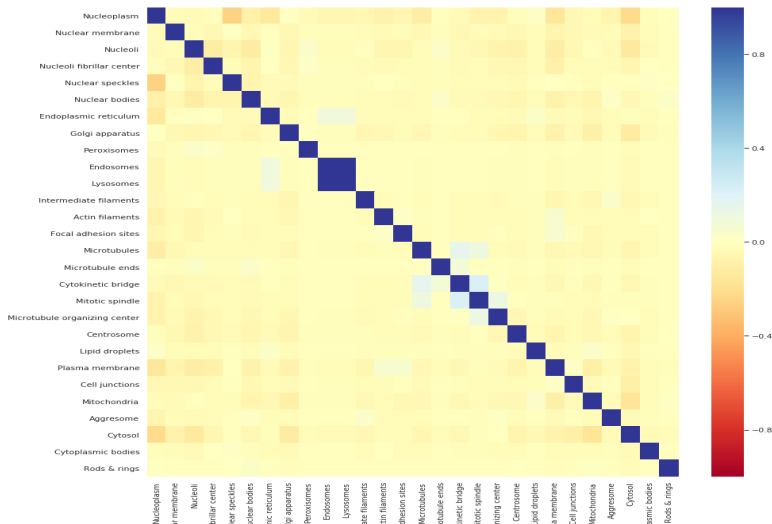


stained endoplasmic reticulum



Data Analysis(2/3)

Target Correlation



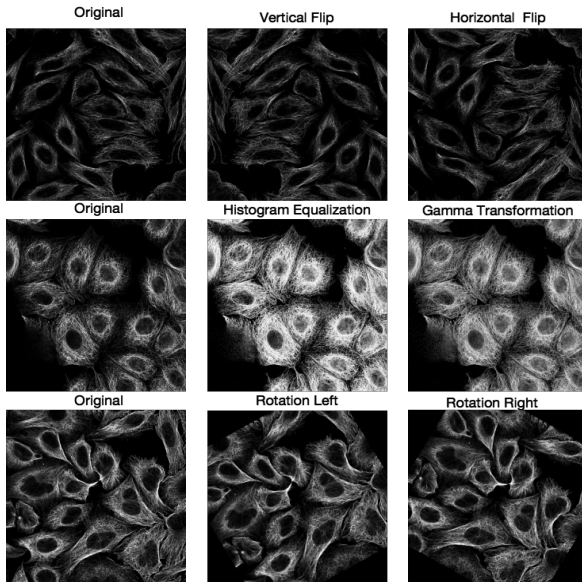
Data Analysis(3/3)

Highlight Points

- Data is different from the traditional RGB image.
- Data imbalance exists in this dataset.
- Some targets are correlated.
- Classification results may depend on one or two channels.



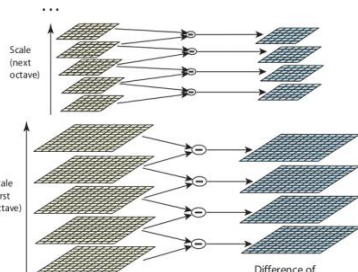
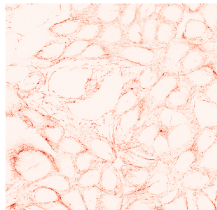
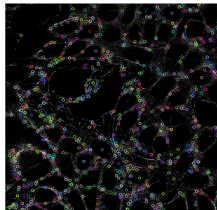
Affine Transformation/Histogram Equalization/ γ Transformation



SIFT Operator[6]

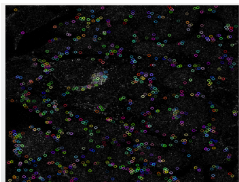
Scale Invariant Feature Transform(SIFT) for extracting the keypoints and computing its descriptors.

- 1 Scale-space Extrema Detection(DoG)
- 2 Keypoint Localization
- 3 Orientation Assignment
- 4 Keypoint Descriptor
- 5 Keypoint Matching

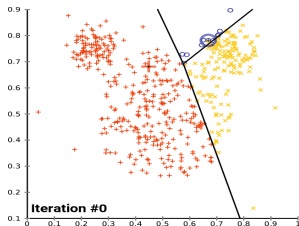


SIFT+Bag-of-Words[1, 5]

Step-1: SIFT Keypoint



Step-2: Kmeans to get Dict[2]



Step-3: Get Feature Vector

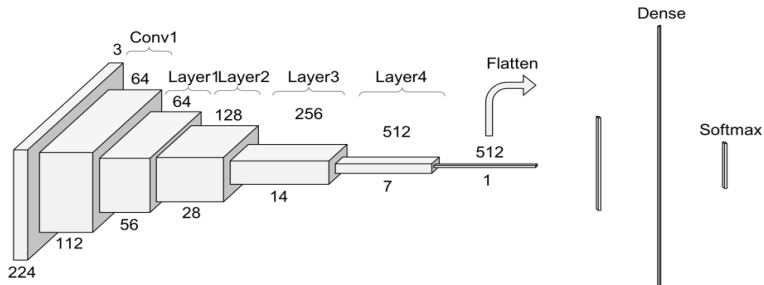
$$\mathbf{x} = \begin{bmatrix} x_1 \\ x_2 \\ \vdots \\ x_d \end{bmatrix}$$

Feature vector

Step-4: Classification



ResNet34[4]



CNN-SIFT Method

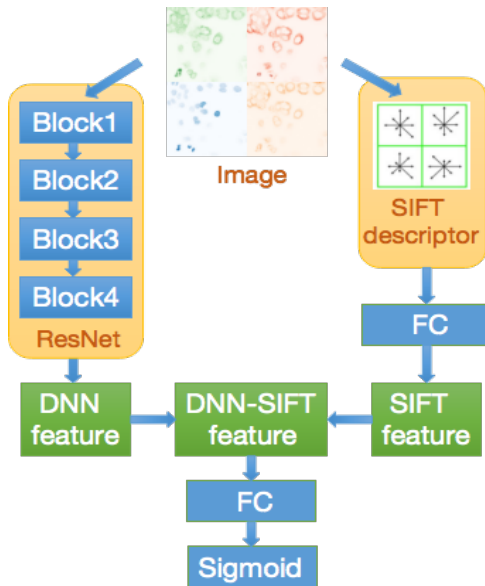


Table: Results on Human Protein Dataset

		Test F1-Score
Low-level Method	SIFT+Bag-of-Words	14.3
DNN Method	ResNet-34	37.6
	ResNet-34+PreProcessing	42.8
SIFT-CNN Method	ResNet-34+SIFT	40.8
	ResNet-34+SIFT+PreProcessing	44.5



Summary

- Pre-Processing is essential for image classification.
- SIFT operator is not as well as DNN-based method.
- SIFT and DNN feature are complementary, we can use this strategy to achieve better performance.
- F1-Score is good measurement for multi-label classification problem.
- Over-sampling[3] or weighted loss are helpful for data imbalance.



Feature Work

- Propose new feature descriptor or network architecture for human protein image.
- Explore combining traditional method with learning based method for robust and better performance.



References I



Mundher Al-Shabi, Wooi Ping Cheah, and Tee Connie.
Facial expression recognition using a hybrid cnn-sift aggregator.
arXiv preprint arXiv:1608.02833, 2016.



Sugato Basu, Arindam Banerjee, and Raymond Mooney.
Semi-supervised clustering by seeding.
In *In Proceedings of 19th International Conference on Machine Learning (ICML-2002)*. Citeseer, 2002.



Nitesh V Chawla, Kevin W Bowyer, Lawrence O Hall, and W Philip Kegelmeyer.
Smote: synthetic minority over-sampling technique.
Journal of artificial intelligence research, 16:321–357, 2002.



References II



Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun.

Deep residual learning for image recognition.

In Proceedings of the IEEE conference on computer vision and pattern recognition, pages 770–778, 2016.



David W Hosmer Jr, Stanley Lemeshow, and Rodney X Sturdivant.

Applied logistic regression, volume 398.

John Wiley & Sons, 2013.



Pauline C Ng and Steven Henikoff.

Sift: Predicting amino acid changes that affect protein function.

Nucleic acids research, 31(13):3812–3814, 2003.

