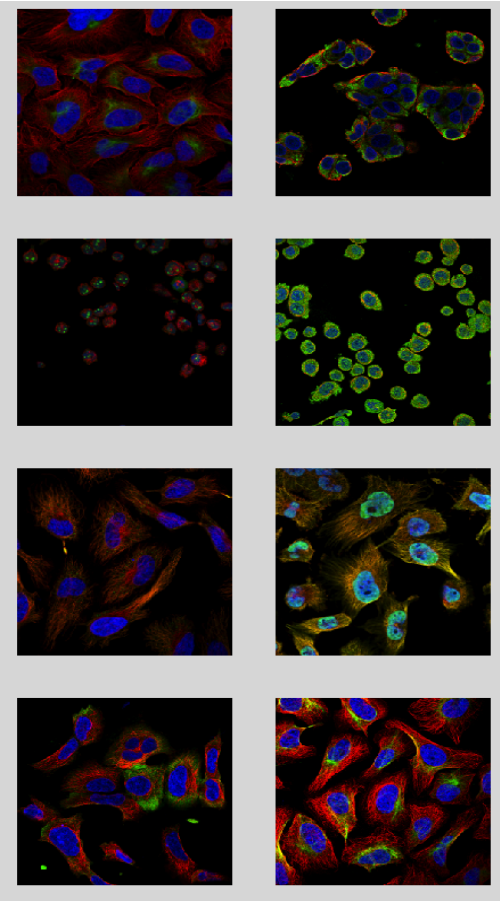
Human Protein Image Classification

Songyang Zhang, Shipeng Yan,
Yongfei Liu, Bo Wan

School of Information Science and Technology
ShanghaiTech University

DIP Course Project, 2019

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.

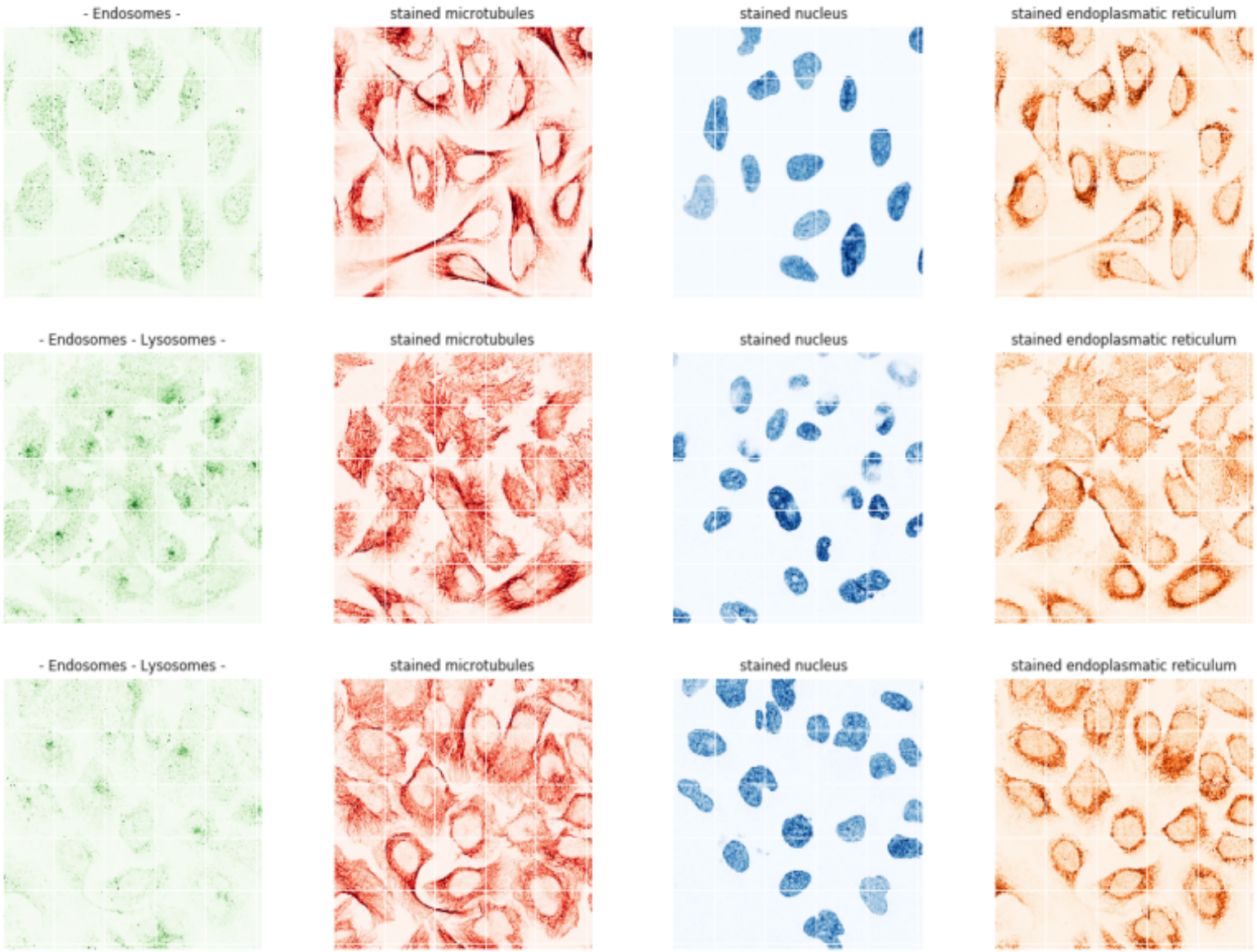
Terminology

Problem Definition

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

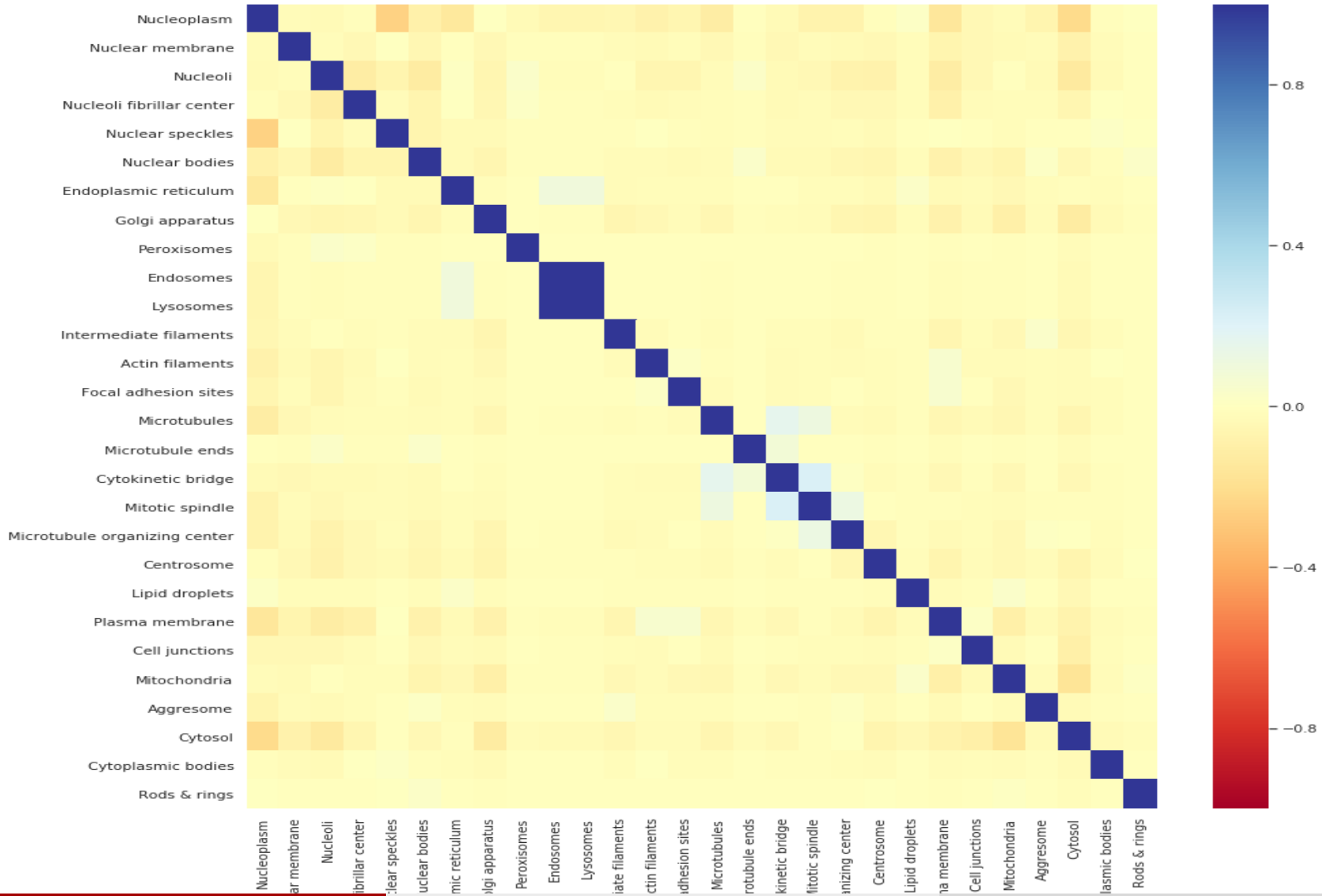
- Input: A 4-channel image $\mathcal{X} \in \mathbb{R}^{4*H*W}$, where H and W is the height and width of the image.
- Output: A subset of the label set $L \in Y$, $Y = \{y_1, y_2, \ldots, y_n\}$, where n is the number of category over the whole dataset.
- $0 \leq |L| \leq n$, $n = 28$ in this task.

Data Analysis(1/3)



Data Analysis(2/3)

Target Correlation

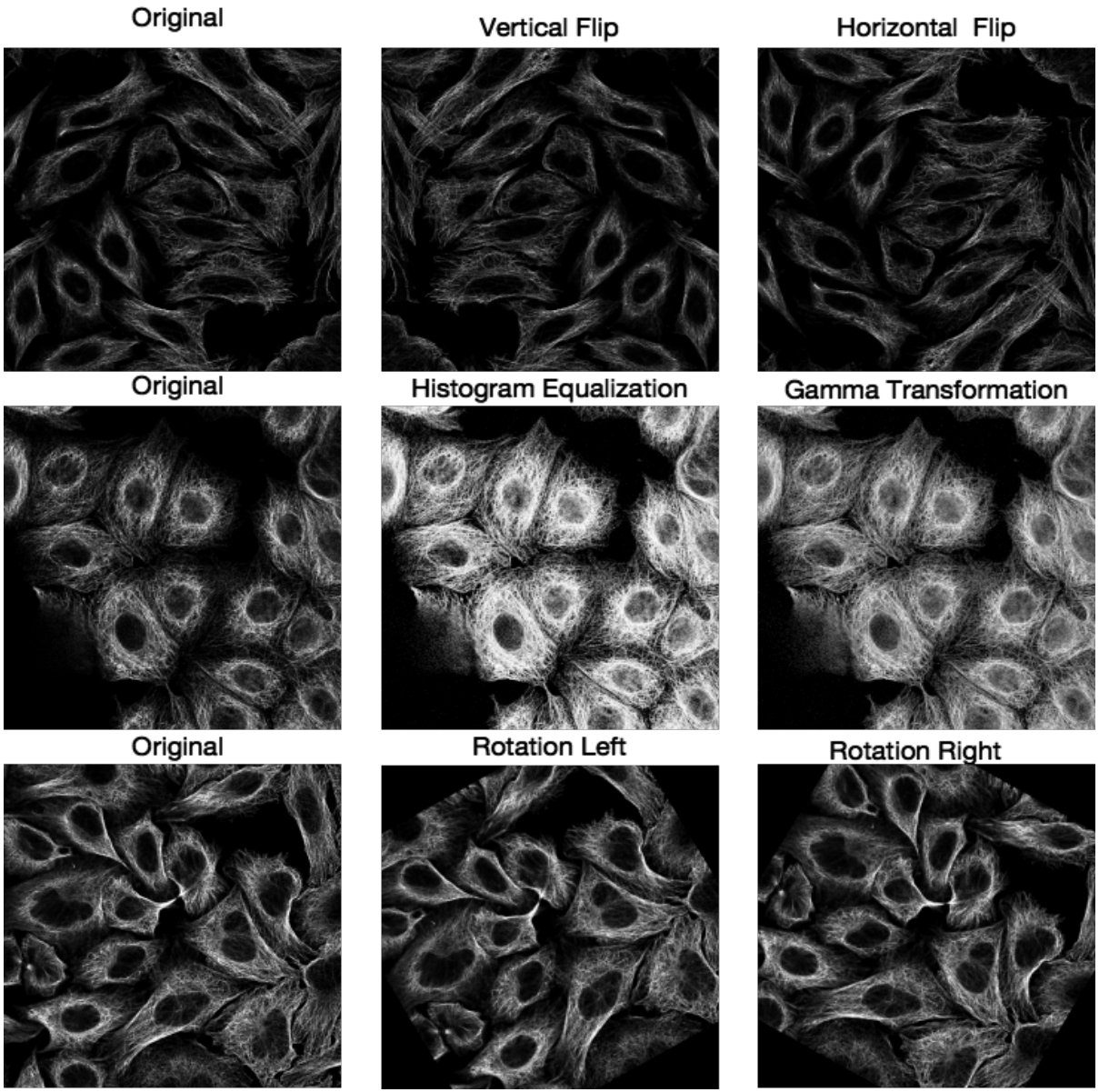


Data Analysis(3/3)

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.

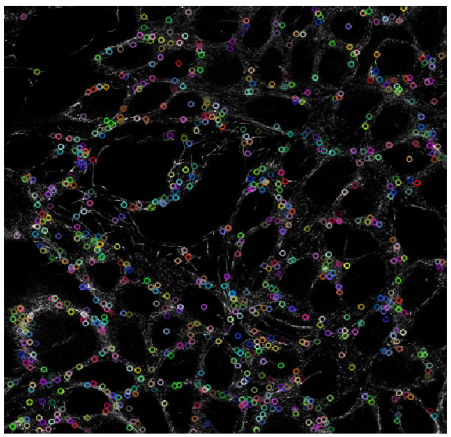
Affine Transfomation/Histogram Equalization/γ Transformation

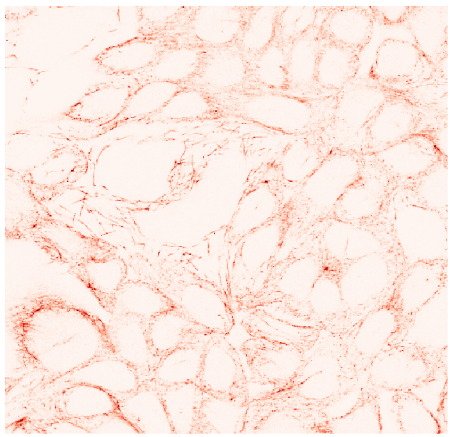


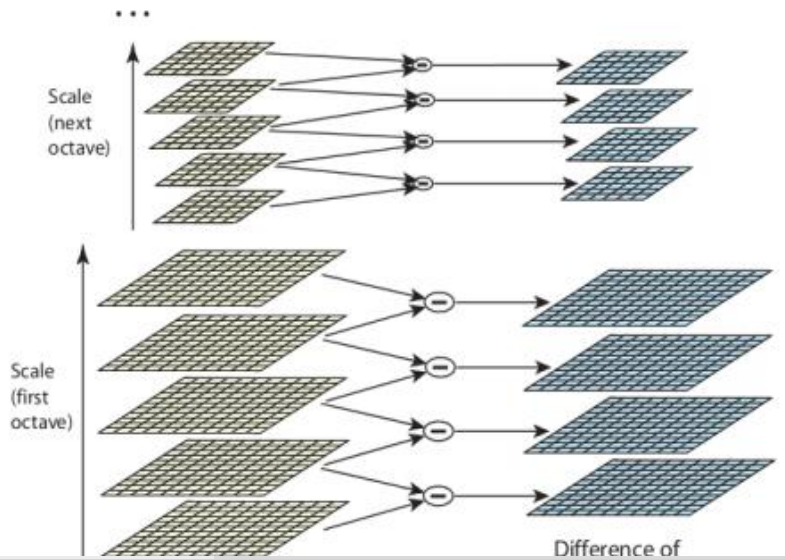
SIFT Operator[6]

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

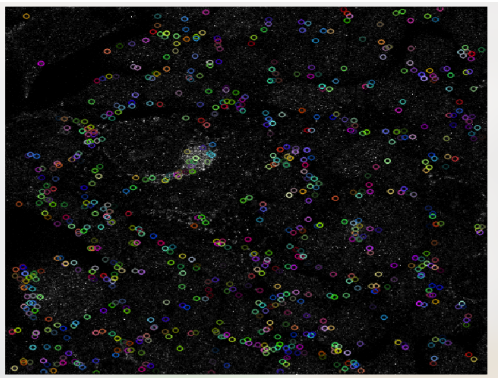




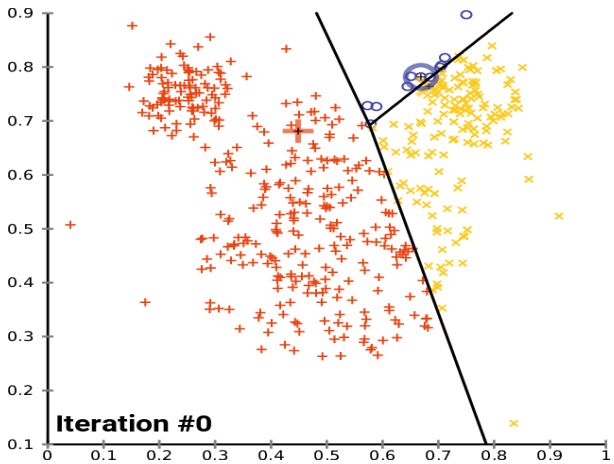


SIFT+Bag-of-Words[1, 5]

Step-1: SIFT Keypoint



Step-2: Kmeans to get Dict[2]



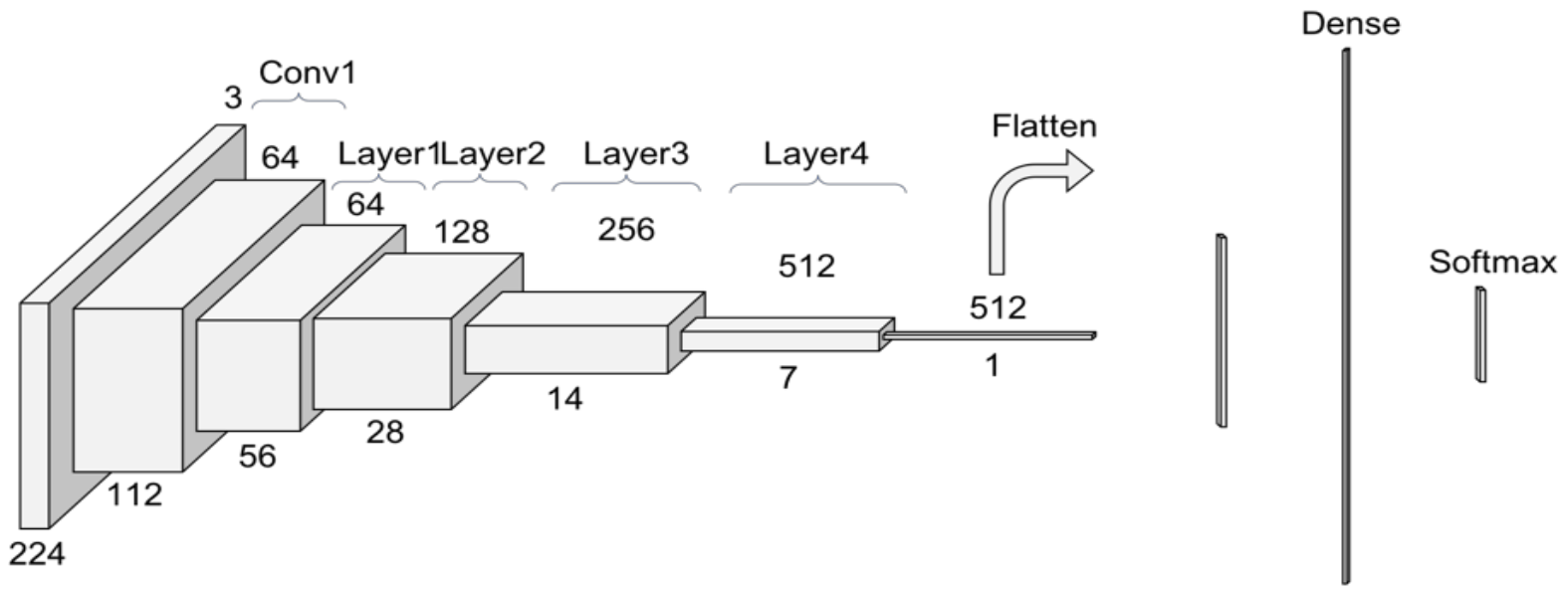
Step-3: Get Feature Vector

$$X = \begin{bmatrix} x_1 \\ x_2 \\ \\ x_d \end{bmatrix}$$

Feature vector

Step-4: Classification

ResNet34[4]


Conv1
3
64
Layer1
64
Layer2
128
Layer3
256
Layer4
512
Flatten
512
Dense
Softmax
224
112
56
28
14
7
1

CNN-SIFT Method

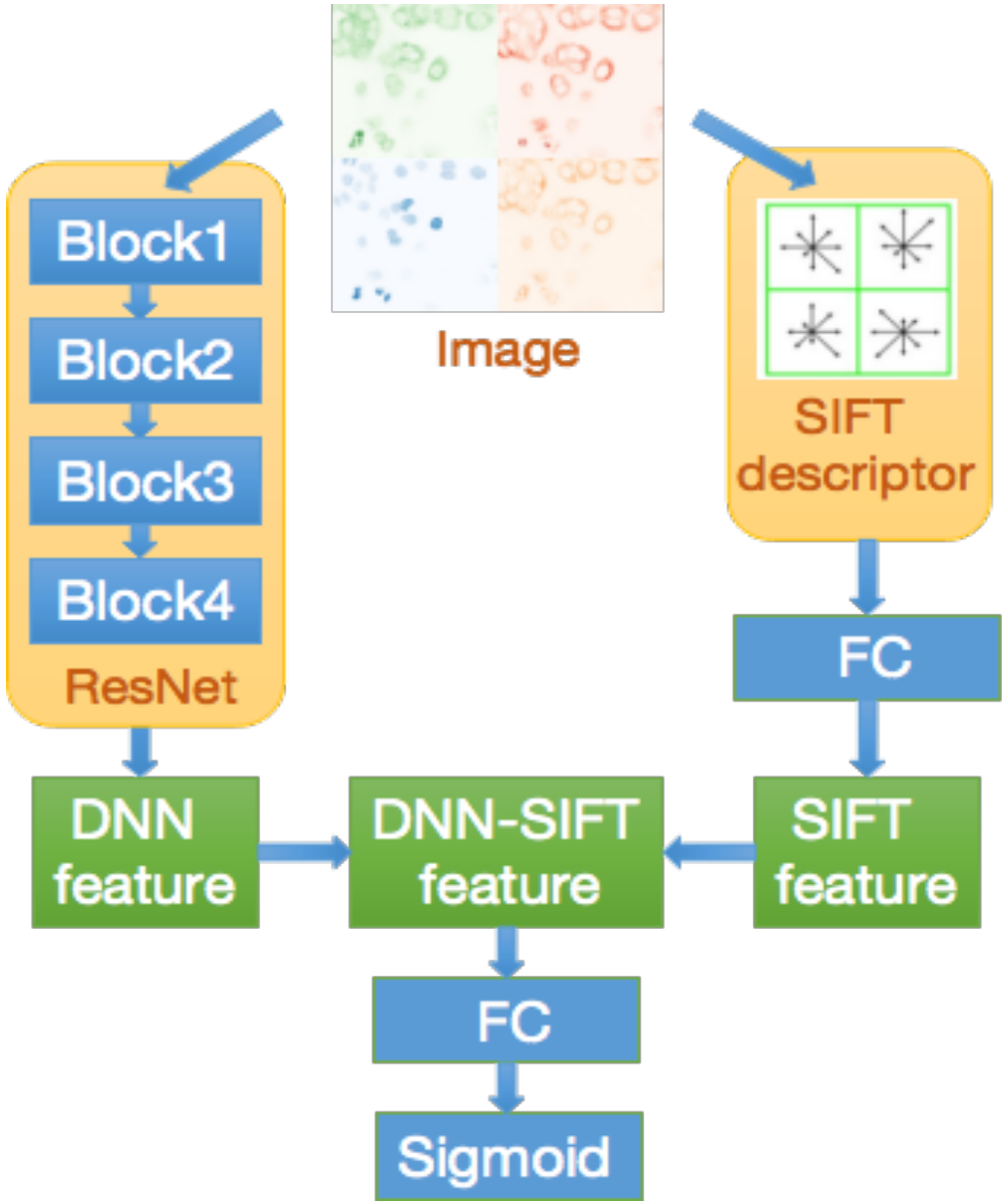


Table: Results on Human Protein Dataset

		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.