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Acute Lymphoblastic Leukemia Detection Based on Adaptive Unsharpening and Deep Learning

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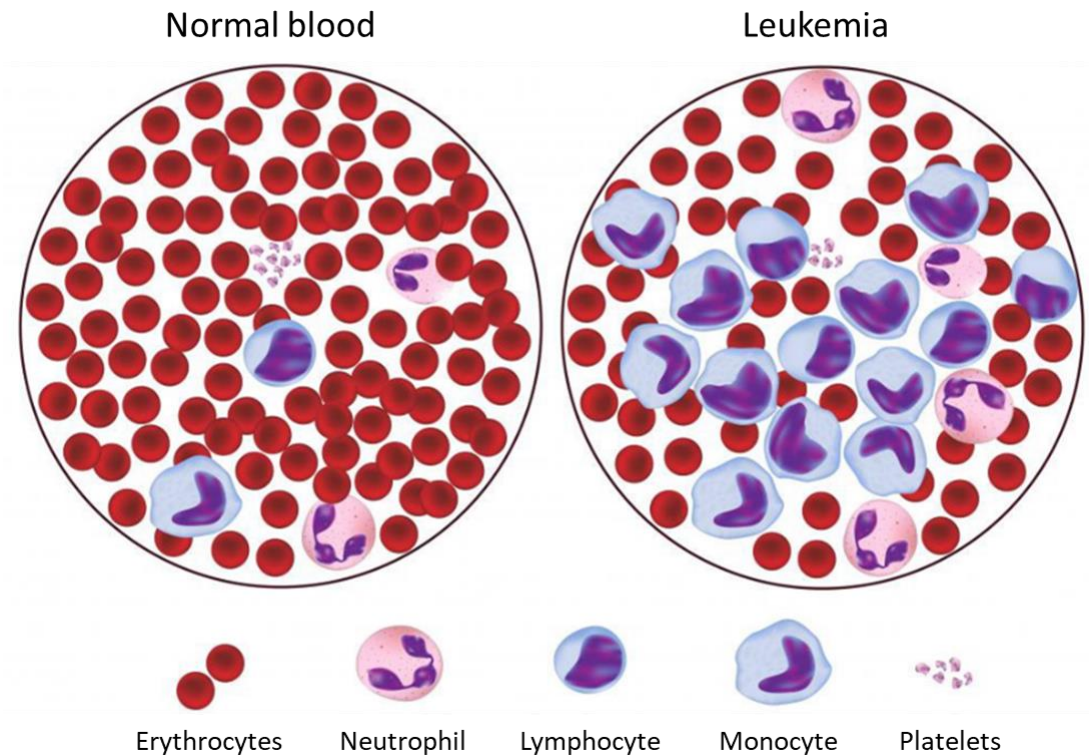
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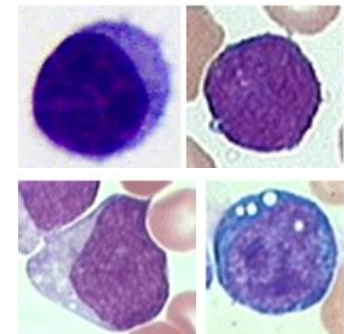
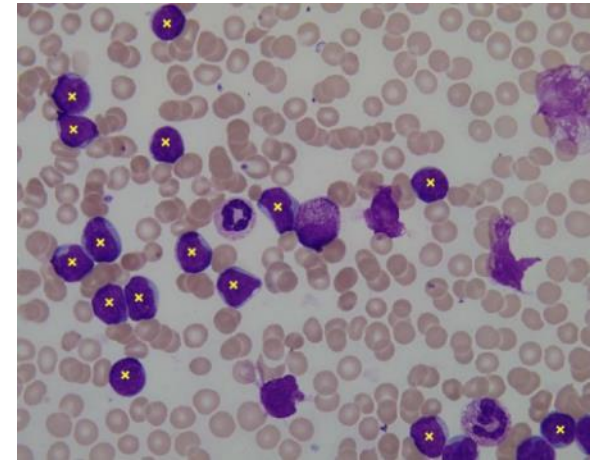
Outline

- Introduction
 - Acute Lymphoblastic Leukemia (ALL)
 - Computer Aided Diagnosis (CAD)
 - Deep Learning (DL) for ALL
- Proposed method
- Experimental results
 - Quantitative analysis
 - Qualitative analysis
- Conclusions



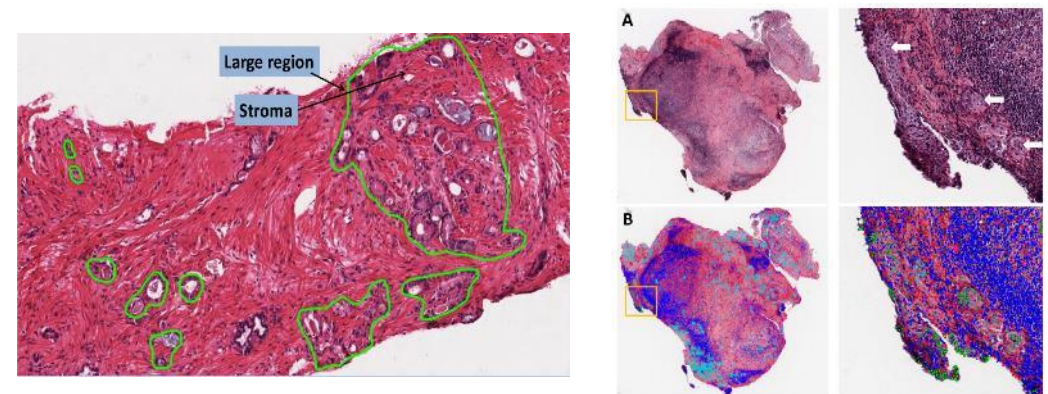
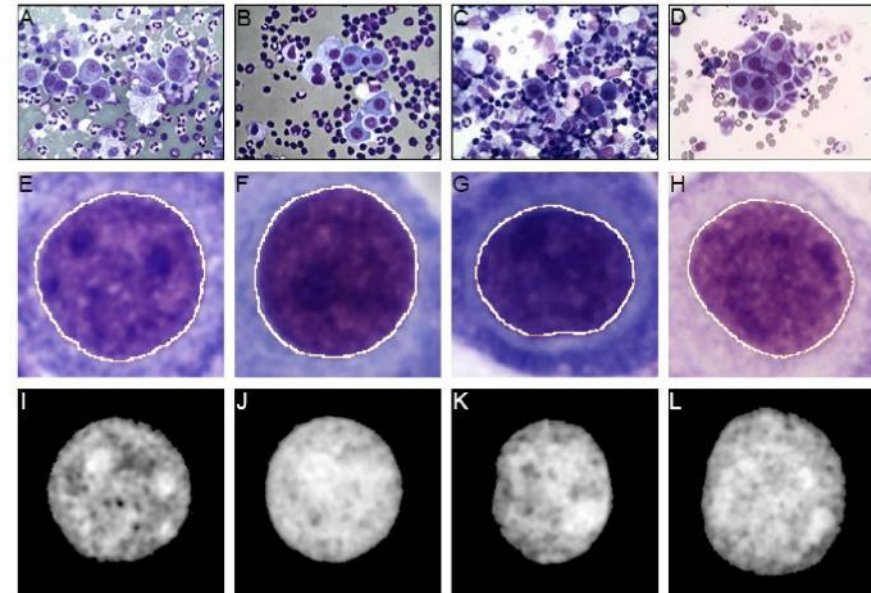
Acute Lymphoblastic Leukemia (ALL)

- Disease
 - Affects the blood cells, rapidly spreads
 - Fatal consequences if left untreated
- Diagnosis
 - Experienced pathologist manually inspects white cells in peripheral blood samples identifying the cells with the typical blast morphology
 - **Lymphoblasts:** white cells with an altered morphology
 - Normally present in the bone marrow
 - *An increased number of lymphoblasts in peripheral blood can be associated with ALL*



Computer Aided Diagnosis (CAD)

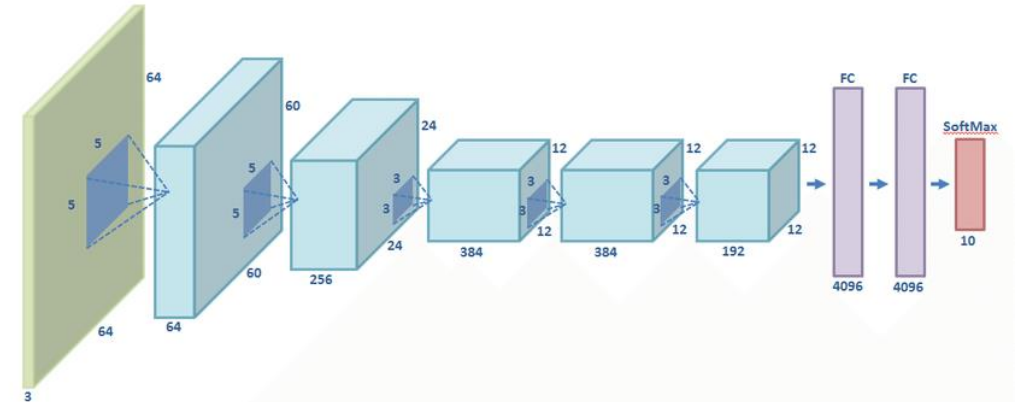
- Partially automate Lymphoblast detection process
 - Image processing
 - Machine Learning (ML)
- Three main categories
 - Handcrafted feature extraction and shallow ML classifier
 - Handcrafted feature extraction and Deep Learning (DL)
 - **Pure DL**



Deep Learning (DL) for ALL

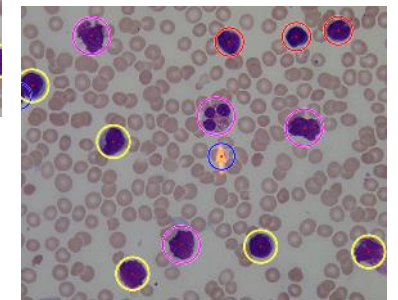
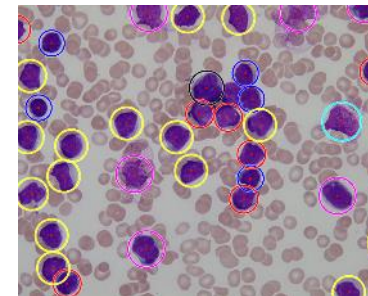
- Deep Learning

- Automatically learns data representations
- No need for handcrafted feature extraction
- *Higher accuracy*



- State of the art of DL for ALL

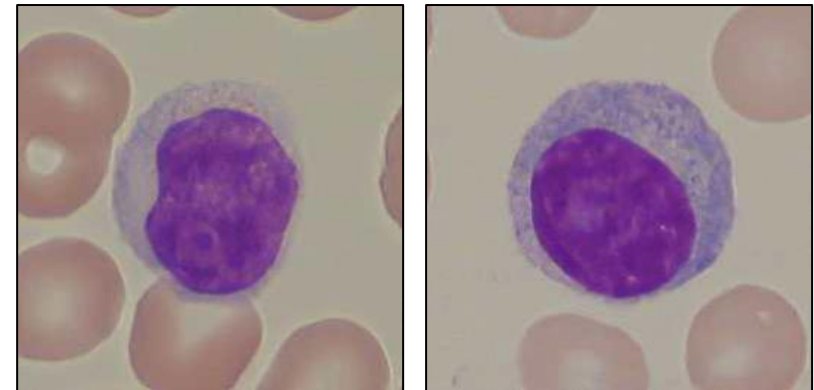
- Strive towards higher classification accuracy
 - More efficient learning procedures
 - Original network architectures
- **However, no method deals with ALL data analysis**
 - No focus or quality analysis
 - No preprocessing algorithm



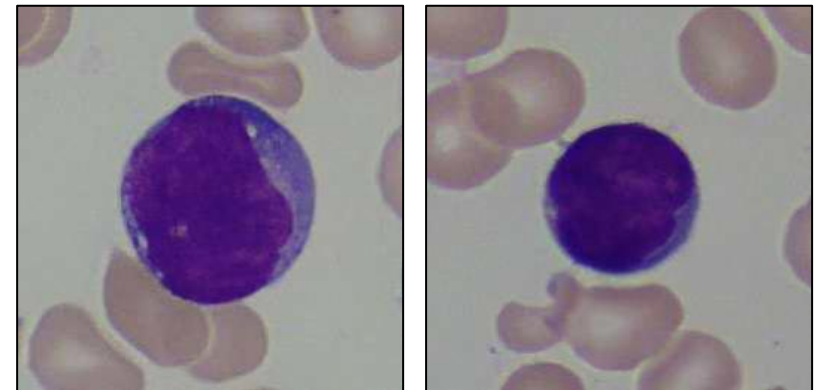
Proposed Method (1/2)

- First DL-based method for lymphoblast detection that analyzes ALL data
 - **Focus** quality estimation
 - Adaptive **unsharpening**
 - White blood cell classification using **CNNs**
 - 0: «normal»
 - 1: «lymphoblast»

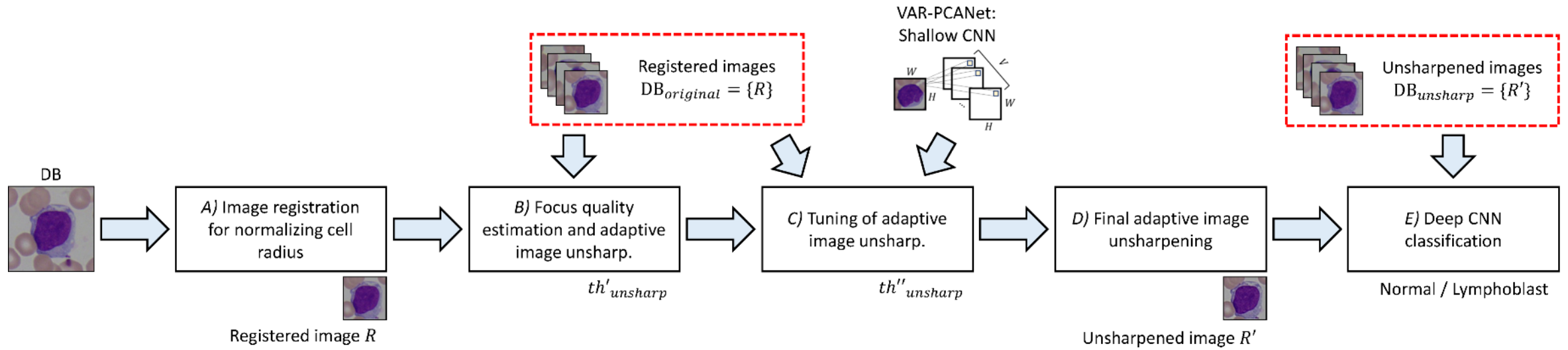
Normal



Lymphoblast



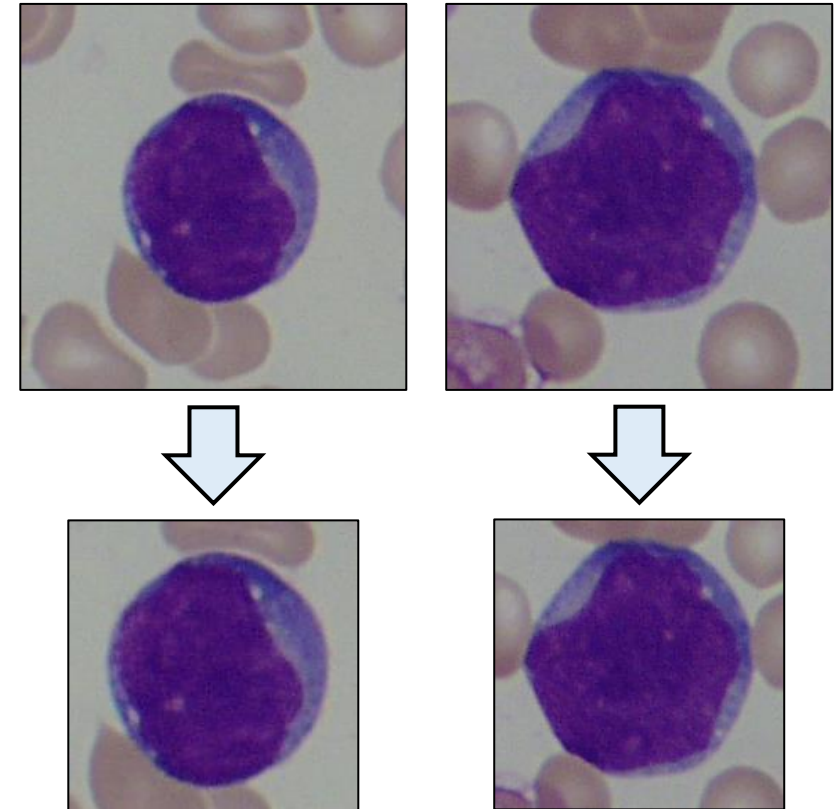
Proposed Method (2/2)



- A) Image registration
- B) Focus quality estimation and adaptive image unsharpening
- C) Shallow CNNs for tuning of adaptive image unsharpening
- D) Final adaptive image unsharpening
- E) Deep CNN classification

Image Registration

- Color normalization and grayscale conversion
- M_{thresh} = Otsu's binarization
- M_{fcm} = Fuzzy C-means clustering
 - Discard largest class (background)
- $M = M_{thresh} + M_{fcm}$
 - Extraction of largest CC
- Active contour refinement
- Ellipse fitting
 - Center of ellipse: c_x, c_y
 - Axes of ellipse: a_{max}, a_{min}
- Extraction of ROI centered on c_x, c_y , with size $1.5 \cdot a_{min}$



Focus Quality Estimation and Adaptive Image Unsharpening (1/2)

- Estimation of focus quality

- FQPath method

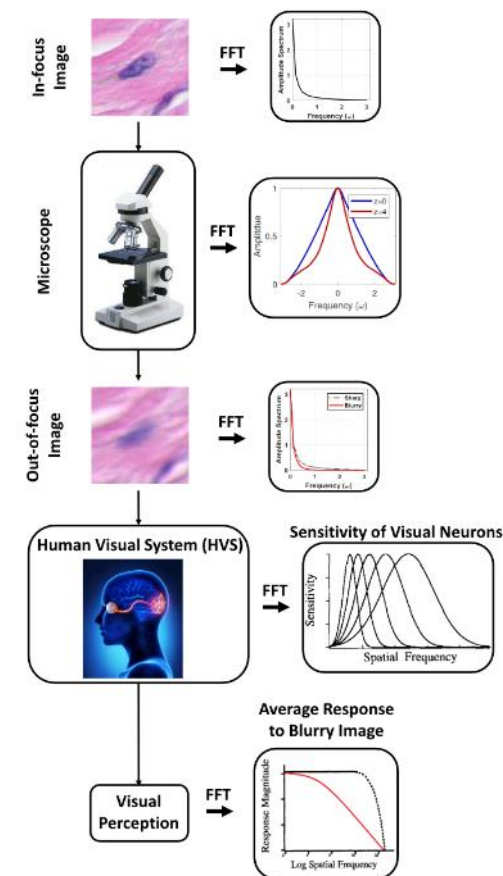
- Decomposes the input image using a visual sensitivity-like FIR filter corresponding to the out-of-focus lens
 - Extracts high order statistical moment features to quantize the image sharpness level
 - Vector of focus qualities $\mathbf{f} = [f_1, f_2, \dots, f_N]$

- Estimation of data bias

- Correlation coefficient between \mathbf{f} and vector of labels \mathbf{l} :

$$b = \text{corrcoeff}(\mathbf{f}, \mathbf{l})$$

- **Significant data bias: $|b| > 50\%$**



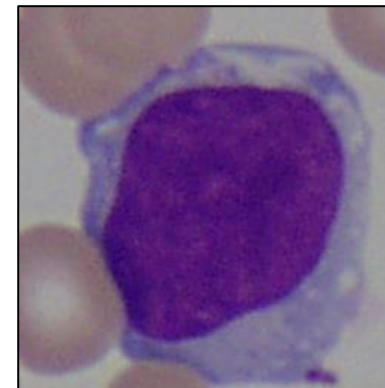
M. S. Hosseini, J. A. Z. Brawley-Hayes, Y. Zhang, L. Chan, K. N. Plataniotis and S. Damaskinos, "Focus Quality Assessment of High-Throughput Whole Slide Imaging in Digital Pathology," in IEEE Transactions on Medical Imaging, vol. 39, no. 1, pp. 62-74, Jan. 2020, doi: 10.1109/TMI.2019.2919722.

Focus Quality Estimation and Adaptive Image Unsharpening (2/2)

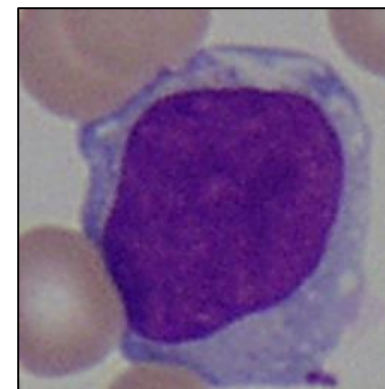
- **Adaptive unsharpening**

- Improving focus quality for each image until it reaches the threshold $th_{unsharp}$
 - The threshold is uniquely computed *for each training subset*
 - Determines which focus the images should have
- Unsharp masking
 - Gaussian kernel with standard deviation σ_i
 - σ_i is adaptively estimated *for each image* to reach the focus quality $th_{unsharp}$
 - $\sigma_i = \arg \min_{\sigma} (f_i - th_{unsharp})$
- Threshold is computed to minimize the data bias:
 - $th_{unsharp} = \arg \min(|b|)$

Original

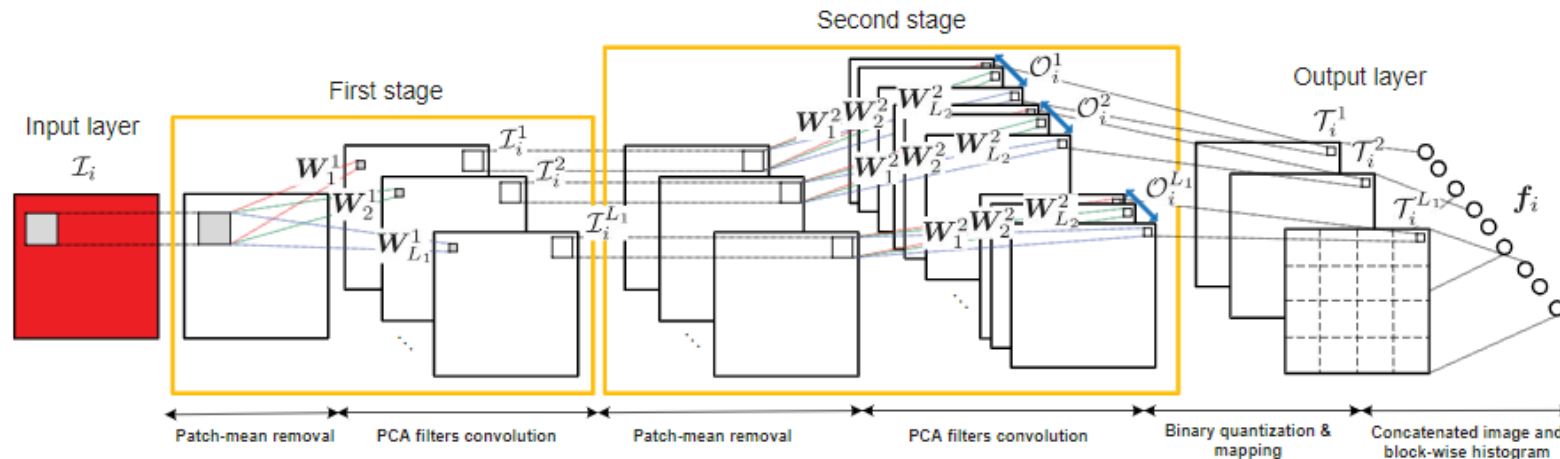


Unsharpened



Shallow CNNs for Tuning of Adaptive Image Unsharpening (1/2)

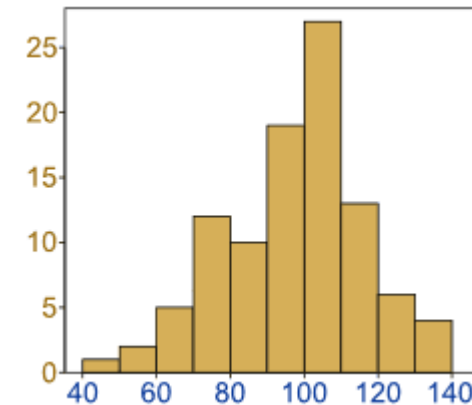
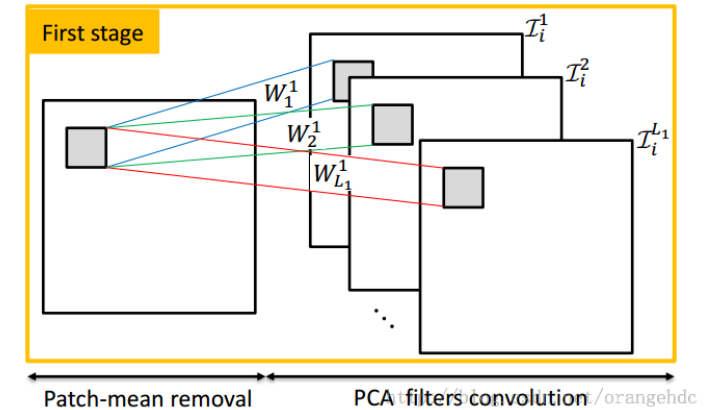
- Tuning of $th_{unsharp}$ using a *shallow CNN*
 - Train a CNN on the unsharpened samples
 - Varying $th_{unsharp} \pm 10\%$
 - Considering the value for which the CNN obtains the best classification accuracy



Shallow CNNs for Tuning of Adaptive Image Unsharpening (2/2)

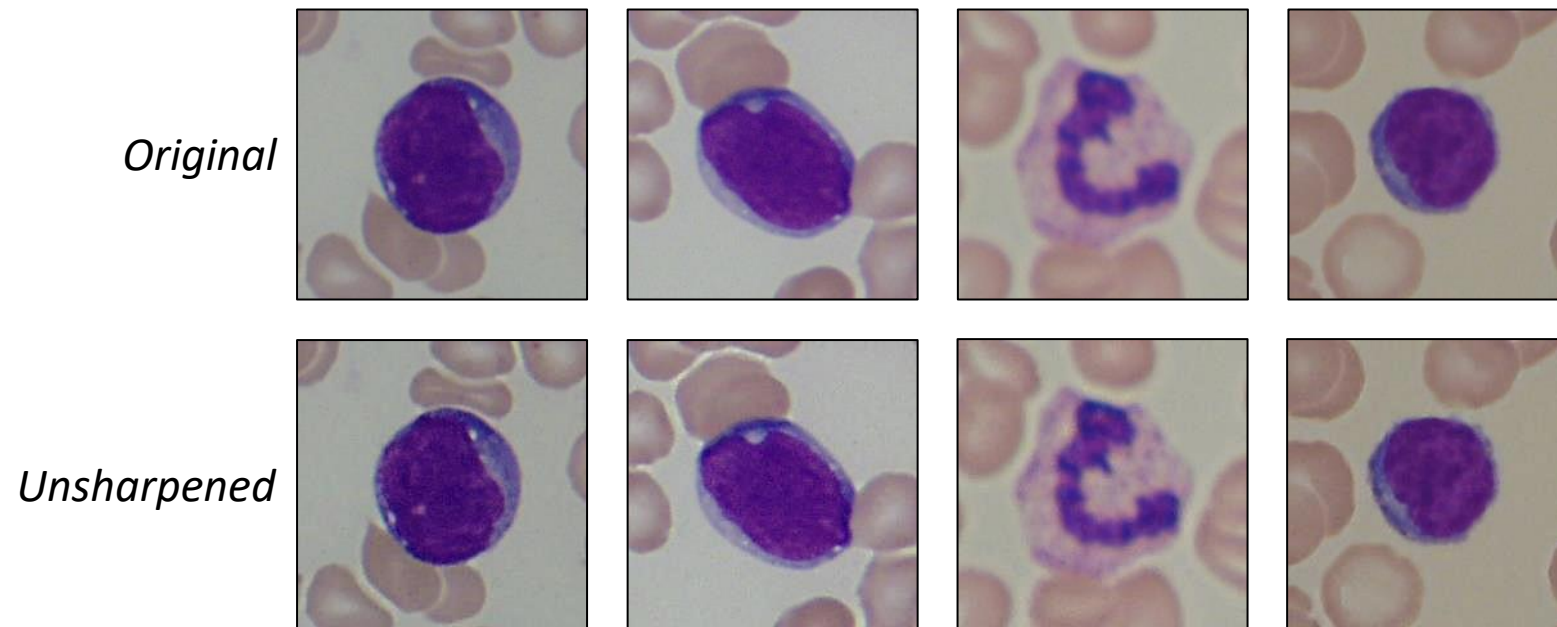
- Shallow CNN: **VAR-PCANet**

- High-accuracy baseline in several fields
- 1 layer
- Filters are computed as eigenvectors of input data
 - Number of filters V adaptively estimated to preserve a percentage th_{var} of variance of input data
 - $V = \arg \min_V ((\sum_{v=1}^V \lambda_v) - th_{var})$
- Feed-forward design
- Extracts a feature vector
 - Compare samples in the feature space
 - Classification with Nearest Neighbor (1-NN) classifier
 - No training
 - Output only depends on the feature vector



Final Adaptive Image Unsharpening

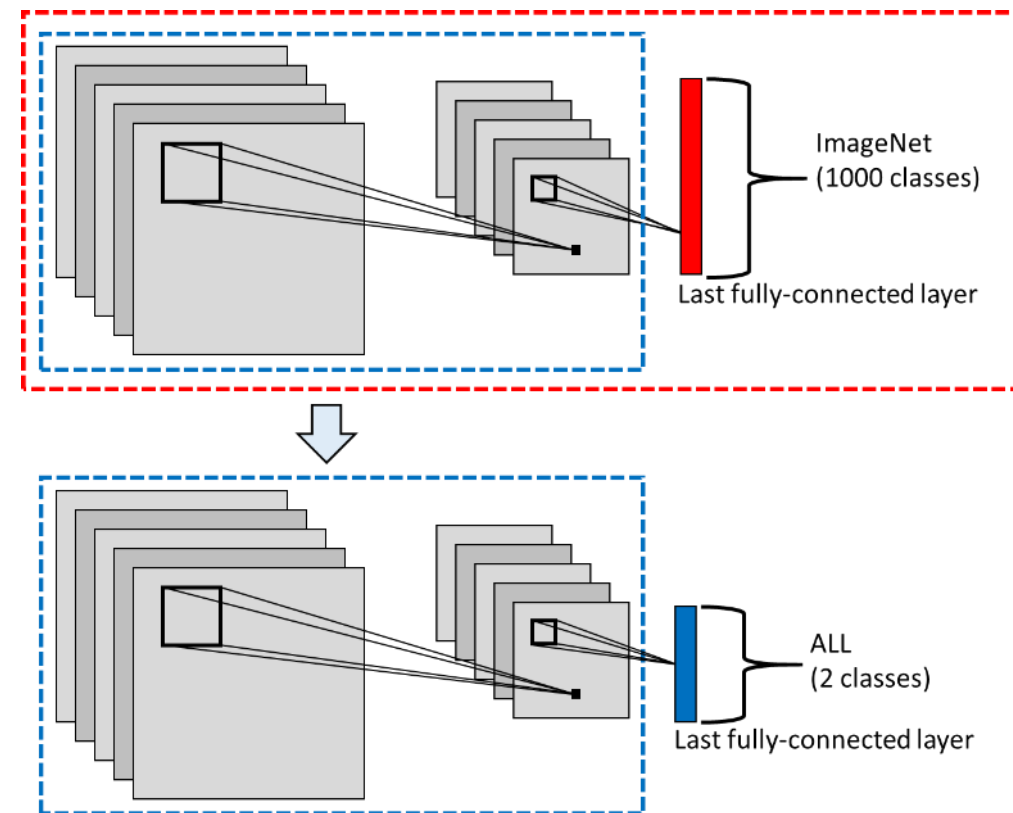
- Application of tuned threshold $th_{unsharp}$
 - Both training and testing subsets
 - Set of unsharpened images $DB_{unsharp}$



Deep CNN Classification

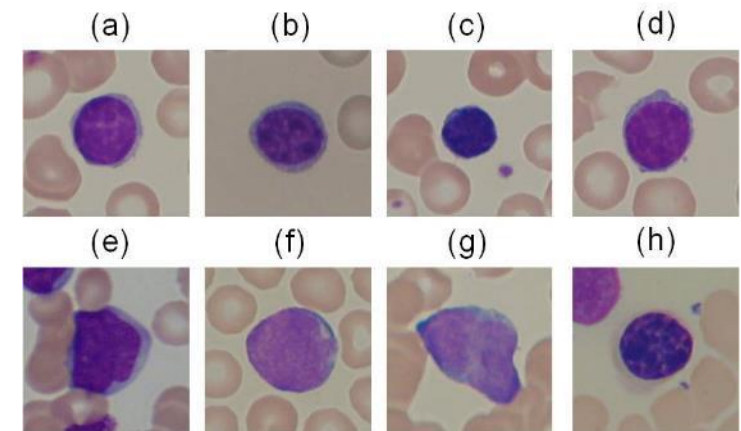
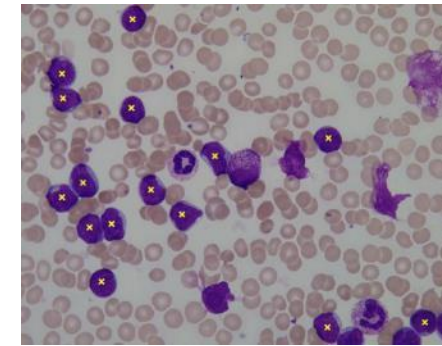
- Pre-trained CNN

- Limited number of samples
- Substitute last layer
 - 1000 classes (ImageNet) → 2 classes (ALL)
 - (0: “normal”; 1: “lymphoblast”)
- Fine tuning on the ALL database
 - Train on the training subset
 - Inference on the testing subset



Experimental Results

- Database
 - ALL-IDB2 dataset
 - 260 images of white cells, each with binary label
 - (0: “normal”; 1: “lymphoblast”)
 - Cropped to show only region around the cell
- Evaluation procedure
 - N -fold validation ($N = 2$) repeated 10 times, results averaged
 - Apply the proposed methodology on the training subset
 - Estimate $th_{unsharp}$, perform the final unsharpening, train the Deep CNN on $DB_{unsharp}$
 - Apply Deep CNN to perform the classification on the testing subset of $DB_{unsharp}$

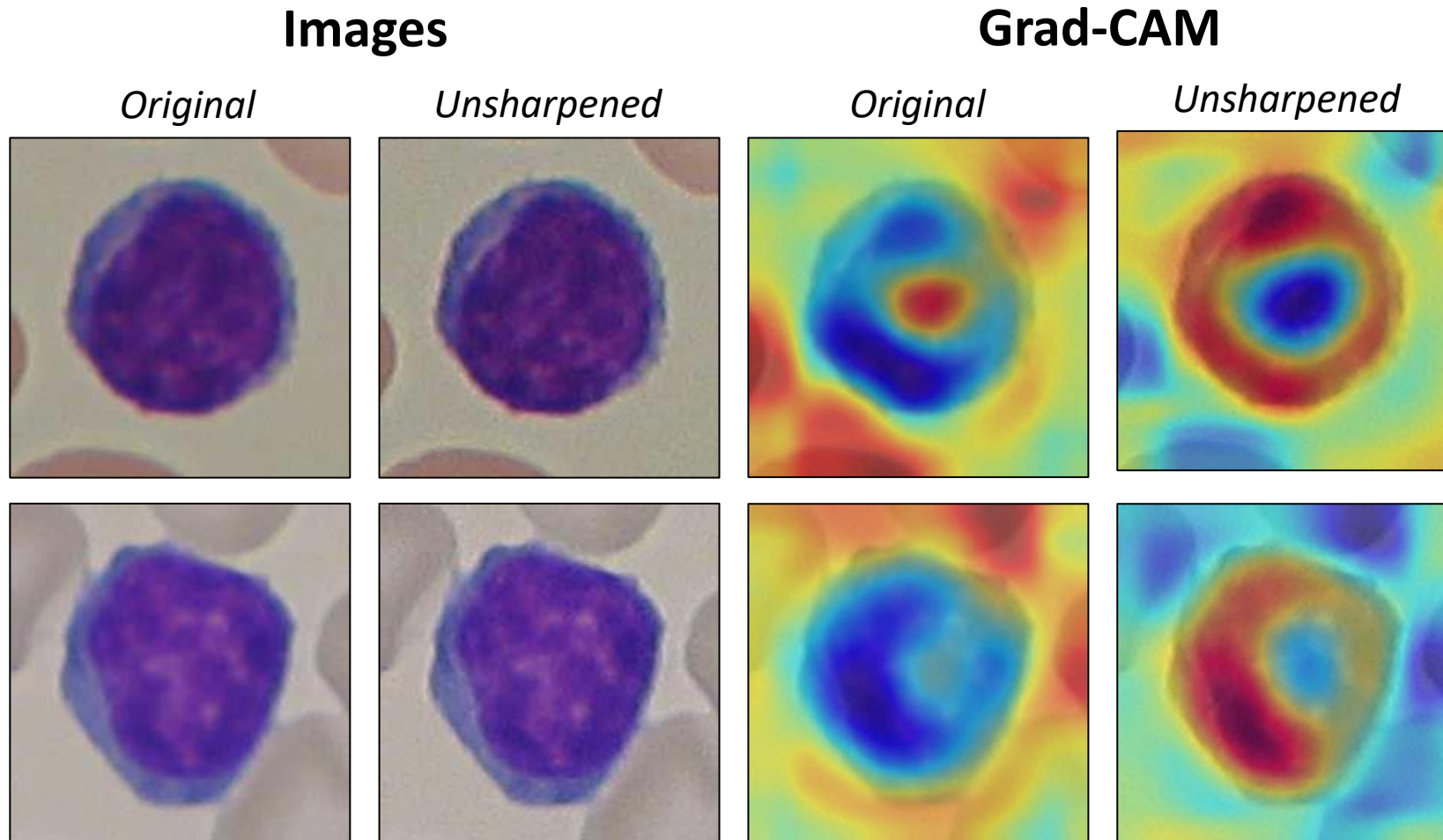


R. D. Labati, V. Piuri and F. Scotti, "All-IDB: The acute lymphoblastic leukemia image database for image processing," 2011 18th IEEE International Conference on Image Processing, Brussels, Belgium, 2011, pp. 2045-2048, doi: 10.1109/ICIP.2011.6115881. <https://homes.di.unimi.it/scotti/all/>

Quantitative Analysis

Original		Unsharp	
Deep CNN	Accuracy (%) (<i>Mean</i> _{Std})	Deep CNN	Accuracy (%) (<i>Mean</i> _{Std})
AlexNet	93.76 _{2.06}	AlexNet	95.07 _{1.85}
VGG16	95.30 _{2.52}	VGG16	96.84_{1.27}
VGG19	95.38 _{2.05}	VGG19	95.53 _{1.57}
ResNet18	96.00 _{1.01}	ResNet18	96.00 _{1.13}
ResNet50	96.00 _{1.48}	ResNet50	96.69 _{1.49}
ResNet101	95.53 _{1.97}	ResNet101	96.00 _{1.87}
DenseNet201	96.76 _{1.48}	DenseNet201	96.69 _{1.14}

Qualitative Analysis

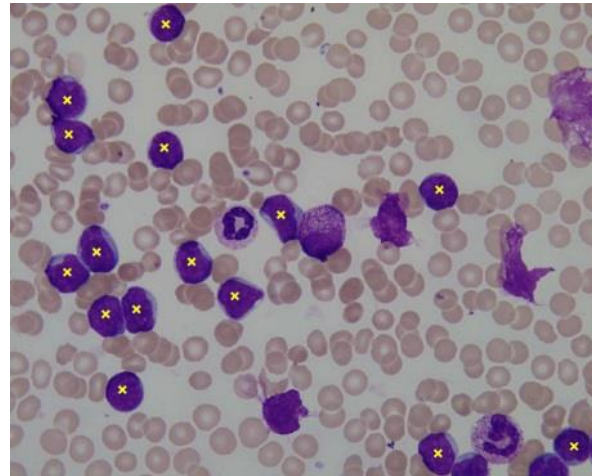


Conclusions

- First ML-based for focus quality estimation, adaptive unsharpening, and classification of ALL blood samples
 - Improve sharpness of images prior to classification
 - Shallow CNN to tune the unsharpening parameters
 - Adaptively reducing bias between quality and label
- Experiments show increase in classification accuracy using state-of-the-art pretrained CNNs
- Future works
 - Databases with more samples
 - Different DL architectures



Thank you for your kind attention!



<https://iebil.di.unimi.it/cnnALL/index.htm>

<https://homes.di.unimi.it/scotti/all/>