Classification of Blood Cells Using DCNN

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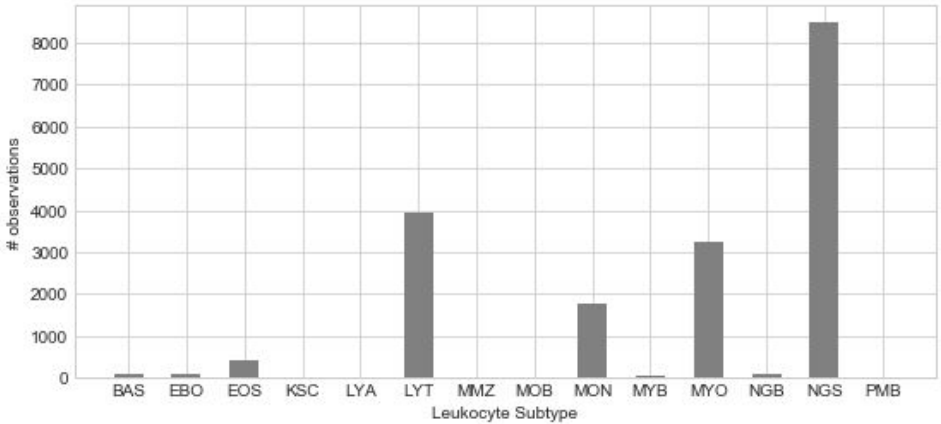
Dataset 1: Acute Myeloid Leukemia recognition

Matek, C., Schwarz, S., Spiekermann, K. et al. *Human-level recognition of blast cells in acute myeloid leukaemia with convolutional neural networks.* Nat Mach Intell 1, 538–544 2019

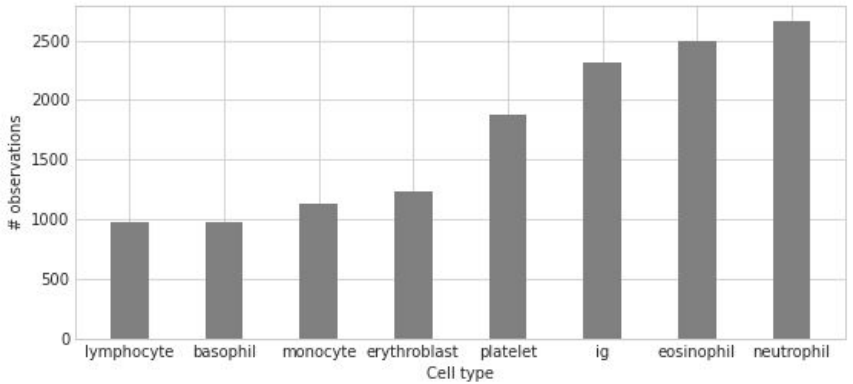
- over 18,000 images of white blood cells (400x400) from 200 individuals (100 healthy, 100 AML)
- 15 classes
- used to feed a ResNeXt model with results:
    - >0.9 precision and sensitivity wih classes with over 100 observations
    - AUC > 0.99 in blast and atypical cell recognition



Dataset 2: microscopic peripheral blood cell images

Acevedo Lipes, Andrea & Alférez, Santiago & Merino, Anna & Puigví, Laura & Rodellar, José. (2019). *Recognition of peripheral blood cell images using convolutional neural networks*. Computer Methods and Programs in Biomedicine. 180.

- over 17,000 images of normal peripheral blood cells (380x363)
- 8 classes
- only from healthy individuals
- available in Mendeley repository



Goals

1. Recreate the results of Matek et al. (2019)
2. Improve training data
   a. other data augmentation techniques (noise introduction, brightness control etc.)
   b. additional data for the infrequent classes
3. Compare with a newer CNN architecture (e.g. EfficientNets, DenseNet)

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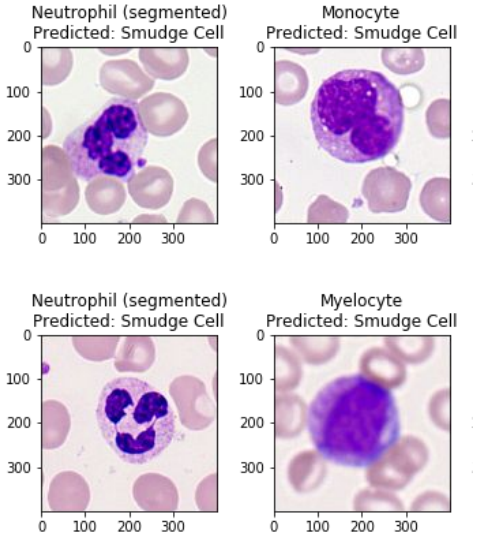
1. Reproduce results from Matek et al. (2019)
2. Transfer learning - use the network trained on 1st dataset to classify data from the 2nd one

Reproducibility issues



- Loss: 12.7114
- Accuracy: 0.0302
- 100% smudge cells on the sample of original images from TCIA and provided test images
- Model architecture with 16 output classes, 15 classes in the original data
- Merged probabilities don’t match the subclasses described in the paper

Model 1: recreate the results

1. Stratified split
   - train: 150021 (~80%)
   - test: 1850 (~10%)
   - val : 1828 (~10%)
2. Data augmentation:
   - horizontal and vertical flips, random rotation (0-359 degrees)
   - ~ 10.000 training images per class
3. Training:
   - ResNeXt architecture provided in CodeOcean
   - no pre-trained weights
   - lr = 0.01
   - 20 epochs
   - 2 days on NVIDIA Tesla P100 (Google Cloud Platform)

Model 2: transfer learning

1. Pre-processing
   1.1. Data augmentation (~ 3.000 per class)
   1.2. Size adjustment (400x400)
   1.3. Stratified split (80%/10%/10%)

2. Adjust the last layer
   2.1. Build a model using the architecture and weights from the original network trained on the TCBI dataset (Matek et al., 2019)
   2.2. Freeze all the layers
   2.3. Remove the top layer of the original network and add a new one, adjusted to the new dataset (8 classes)
   2.4. Compile and train for 10 epochs with lr = 0.01

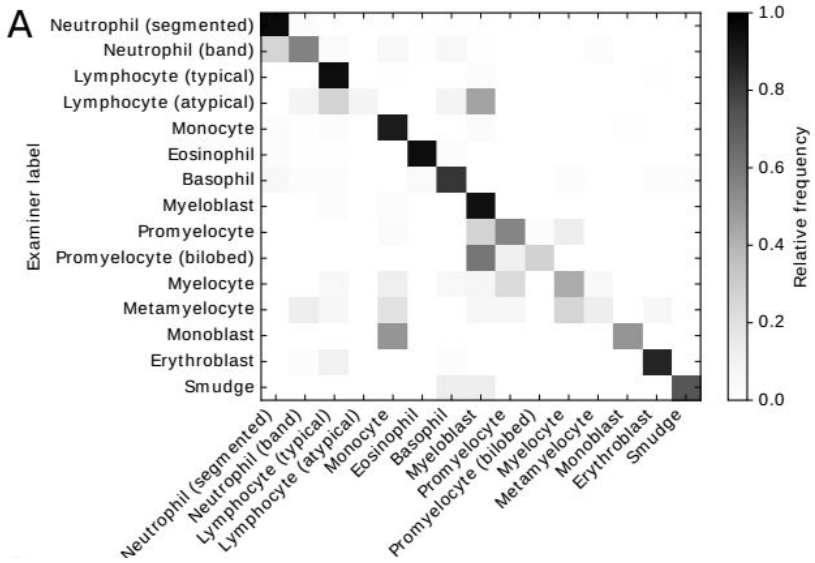
3. Fine-tuning
   3.1. Unfreeze the model, except for batch normalization layers
   3.2. Compile and re-train: for 10 epochs with lr = 0.00001

~10h on NVIDIA Tesla P100 (Google Cloud Platform)

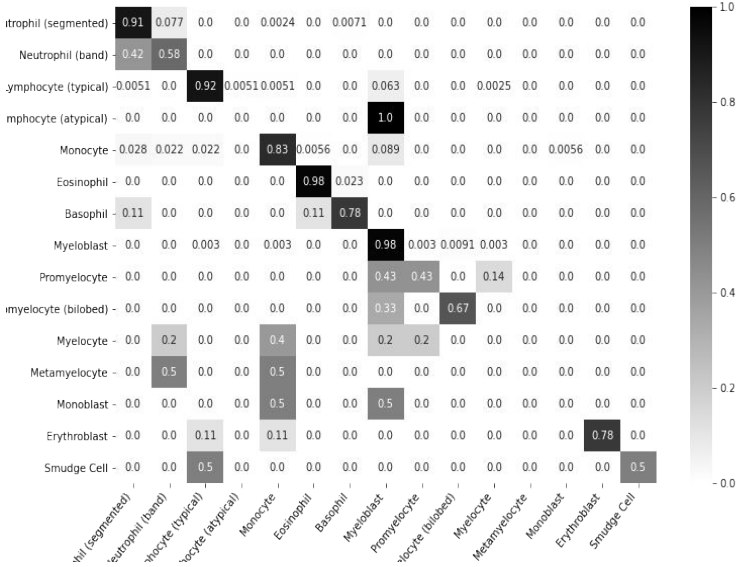
Results: Model 1

Confusion matrix

Original model from Matek et al. (2019)



Model 1



Results: Model 1

Class-wise prediction accuracy

Original model from Matek et al. (2019)

Class	Precision	Sensitivity	Number of images
Neutrophil (segmented)	0.99 ± 0.00	0.96 ± 0.01	8,484
Neutrophil (band)	0.25 ± 0.03	0.59 ± 0.16	109
Lymphocyte (typical)	0.96 ± 0.01	0.95 ± 0.02	3,937
Lymphocyte (atypical)	0.20 ± 0.4	0.07 ± 0.13	11
Monocyte	0.90 ± 0.04	0.90 ± 0.05	1,789
Eosinophil	0.95 ± 0.04	0.95 ± 0.01	424
Basophil	0.48 ± 0.16	0.82 ± 0.07	79
Myeloblast	0.94 ± 0.01	0.94 ± 0.02	3,268
Promyelocyte	0.63 ± 0.16	0.54 ± 0.20	70
Promyelocyte (bilobed)	0.45 ± 0.32	0.41 ± 0.37	18
Myelocyte	0.46 ± 0.19	0.43 ± 0.07	42
Metamyelocyte	0.07 ± 0.13	0.13 ± 0.27	15
Monoblast	0.52 ± 0.30	0.58 ± 0.26	26
Erythroblast	0.75 ± 0.20	0.87 ± 0.09	78
Smudge cell	0.53 ± 0.28	0.77 ± 0.20	15
Total			18,365

Model 1

	Precision	Sensitivity	Support
Basophil	0.50	0.78	9
Erythroblast	1.00	0.78	9
Eosinophil	0.95	0.98	43
Smudge Cell	1.00	0.50	2
Lymphocyte (atypical)	0.00	0.00	2
Lymphocyte (typical)	0.98	0.92	395
Metamyelocyte	NaN	0.00	2
Monoblast	0.00	0.00	4
Monocyte	0.93	0.83	180
Myelocyte	0.00	0.00	5
Myeloblast	0.87	0.98	328
Neutrophil (band)	0.09	0.58	12
Neutrophil (segmented)	0.98	0.91	849
Promyelocyte (bilobed)	0.40	0.67	3
Promyelocyte	0.60	0.43	7

Results: Model 1

Recognition of blasts and atypical cells

Original model:

Atypical cells AUC = 0.992 ± 0:001
Blast cells AUC = 0:991 ± 0:002

Probability that a given cell has blast character

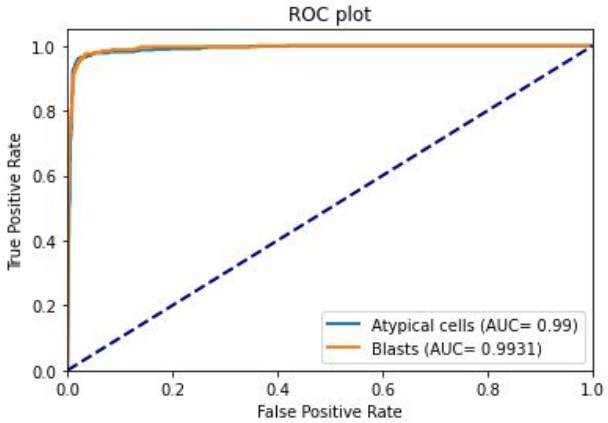
$$P_{blast} = P_{myeloblast} + P_{monoblast}$$

- binary prediction of the network is given by $y = P_{blast} \geq t$

Probability that a cell doesn't belong to the cell types normally present in non-pathological blood smears.

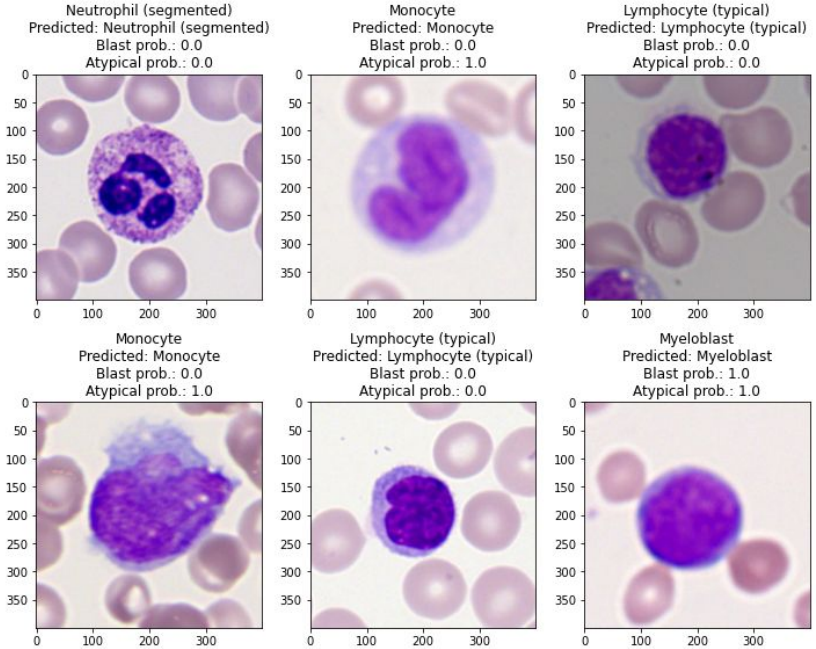
$$P_{atypical} = P_{myeloblasts} + P_{monoblast} + P_{myelocytes} + P_{metamyelocytes,} + P_{promyelocytes} + P_{p\ erythroblasts} + P_{atypical\ lymphocytes}$$

Model 1



Results: Model 1

Examples of predictions



Results: Model 2

Confusion matrix

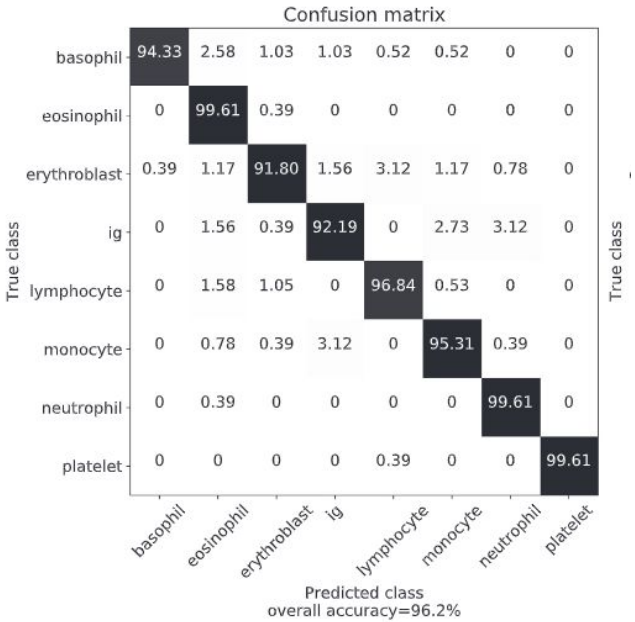
- test accuracy:
- test loss:

	Accuracy	Precision	Sensitivity	Support
basophil	0.99	0.97	0.90	123
eosinophil	1.00	1.00	0.98	313
erythroblast	1.00	0.98	0.97	156
ig	0.96	0.83	0.96	290
lymphocyte	0.99	0.96	0.95	122
monocyte	0.98	0.88	0.90	142
neutrophil	0.98	0.99	0.90	334
platelet	1.00	1.00	1.00	236

Results: Model 2

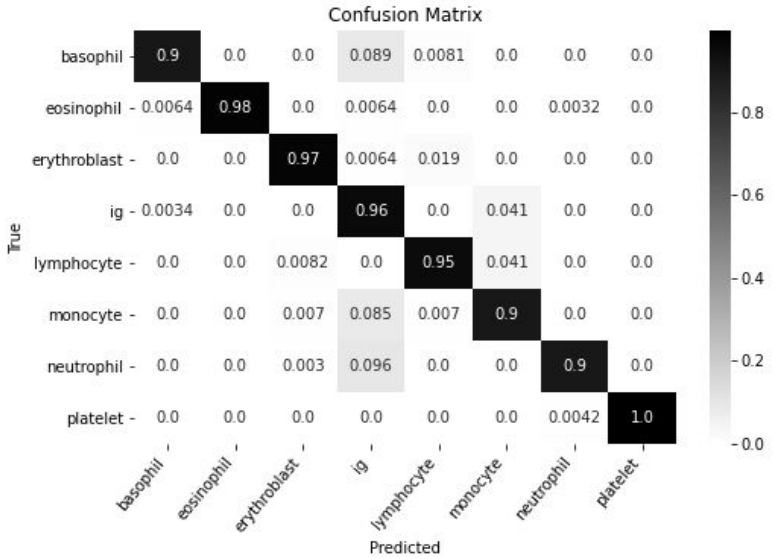
Confusion matrix

Acevedo et al. (2019)



(a) Vgg-16 based model

Model 1



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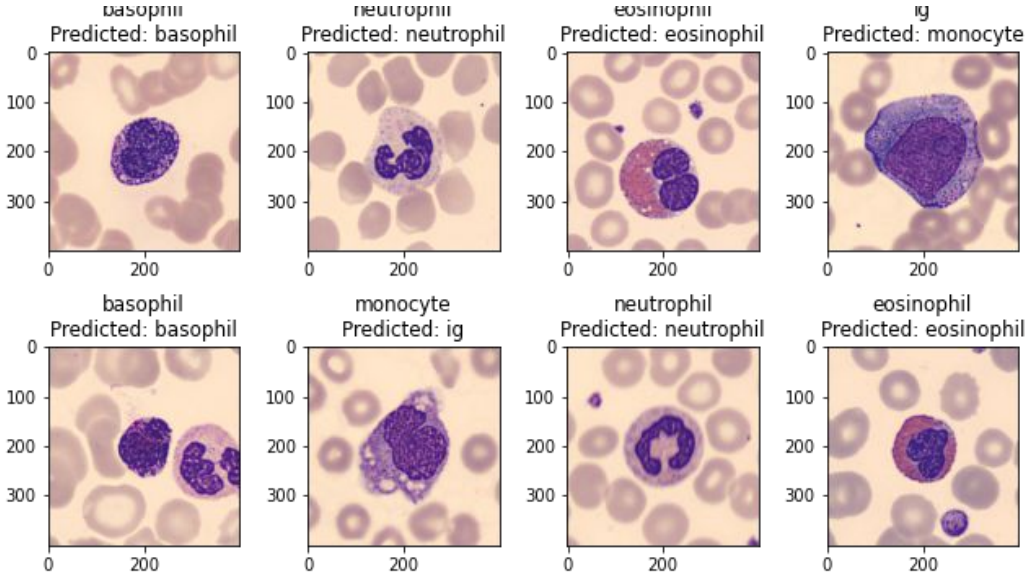

Conclusions

- deep learning can be gratifying but requires time and resources
- what else could be done:
  - cross-validation
  - compare Model 2 vs. ResNeXt trained from scratch
  - visualization of intermediate feature maps

Sources

- Matek, C., Schwarz, S., Marr, C., & Spiekermann, K. (2019). A Single-cell Morphological Dataset of Leukocytes from AML Patients and Non-malignant Controls [Data set]. The Cancer Imaging Archive. https://doi.org/10.7937/tcia.2019.36f5o9ld

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