

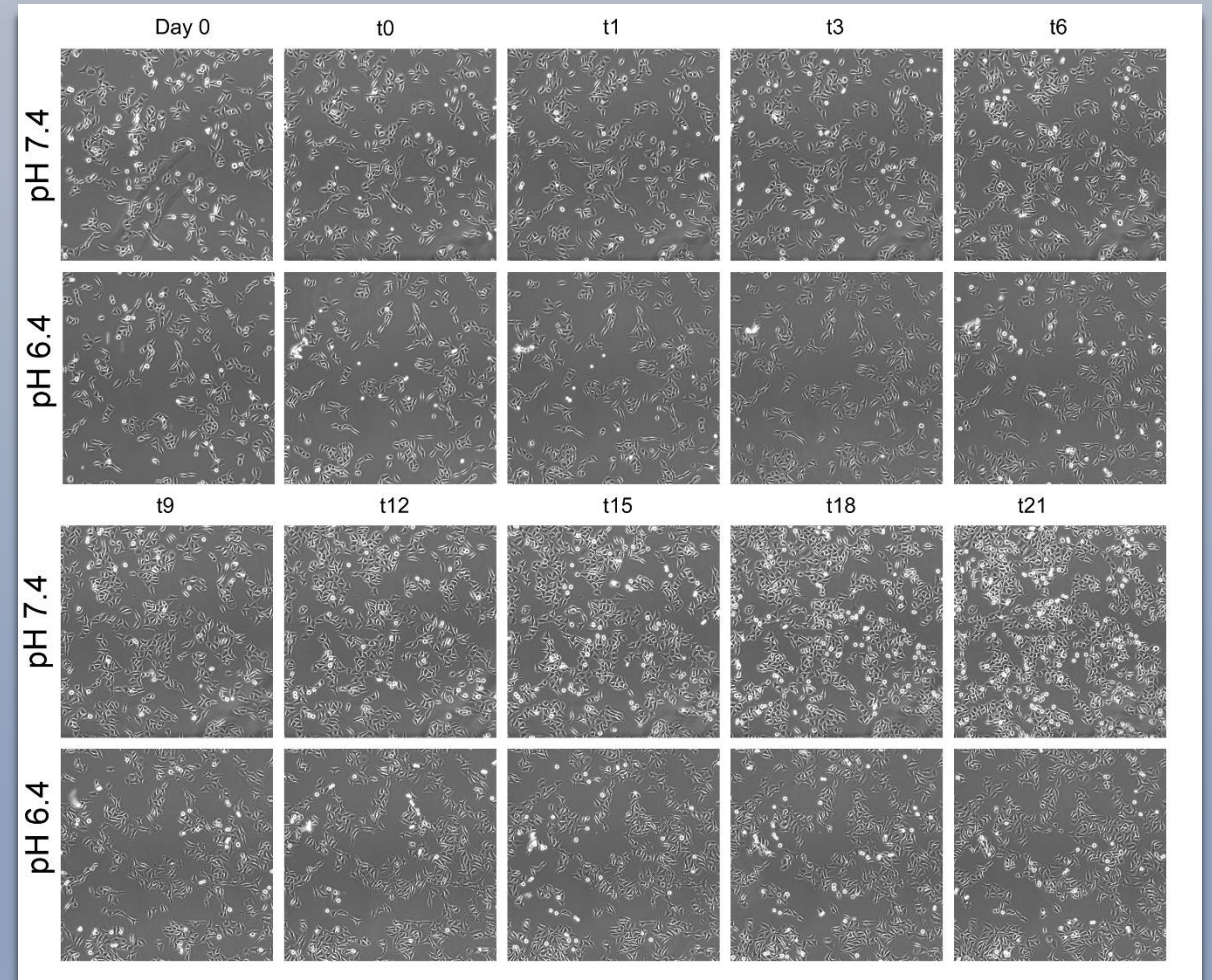
A fluorescence microscopy image showing numerous cells. The cells are stained with two different dyes, resulting in blue and red/purple colors. The blue staining likely represents the nuclei, while the red/purple staining represents the cytoplasm or other cellular components. The cells are of various shapes and sizes, and are distributed across the field of view.

Cell counting by Adaptive Fully Convolutional Redundant Counting

Wang Xinyi, Zhang Daofu, Sun Dajun

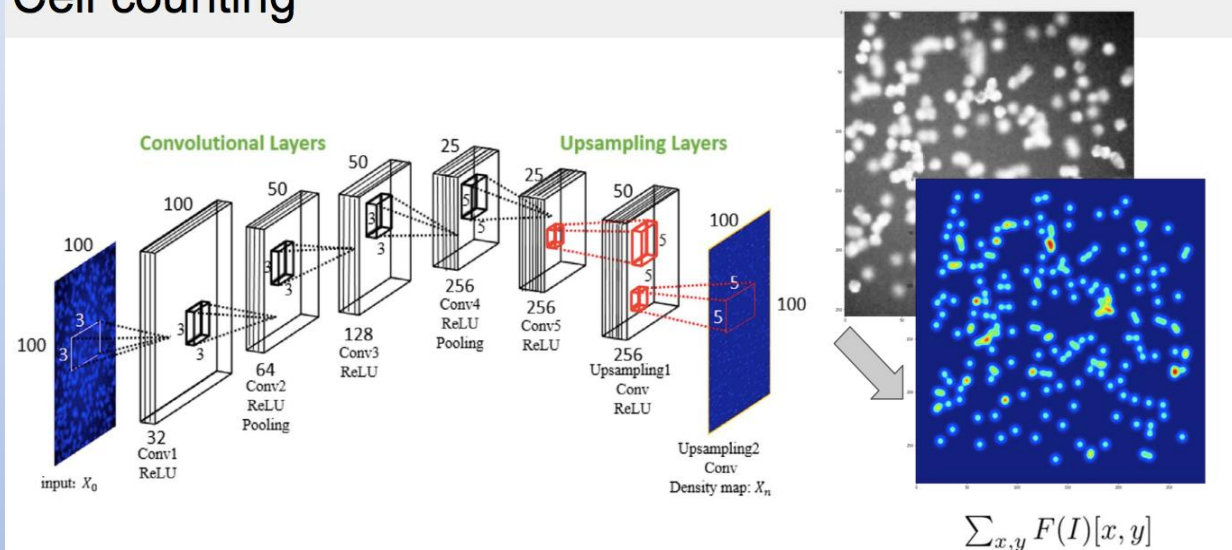
Why counting cells?

- In cancer cell study, we need to treat cancer cells with different drugs and monitor their effect on proliferation
- In hospitals, we use cell counting to determine the health condition of a patient i.e. Full Blood Count(FBC)
- Microbiologists use cell counting in researching the behaviour of infectious viruses and bacteria
- And so on...



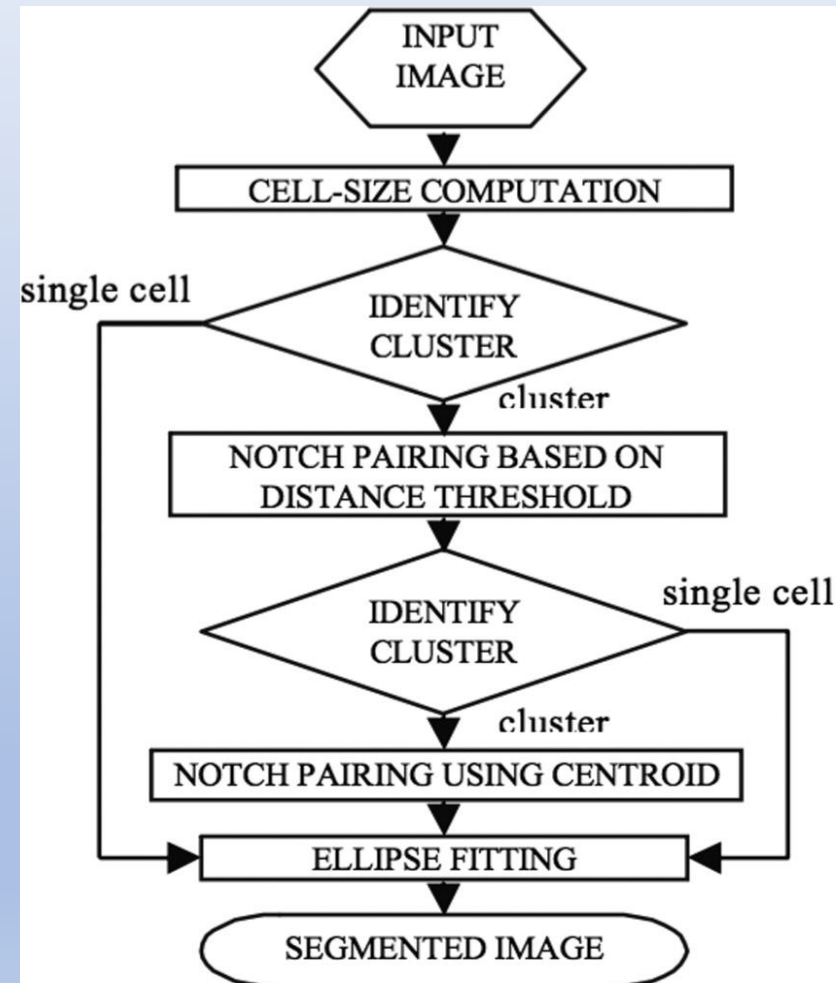
Generally speaking, current counting methods can be divided into two categories: detection based and regression based

Cell counting



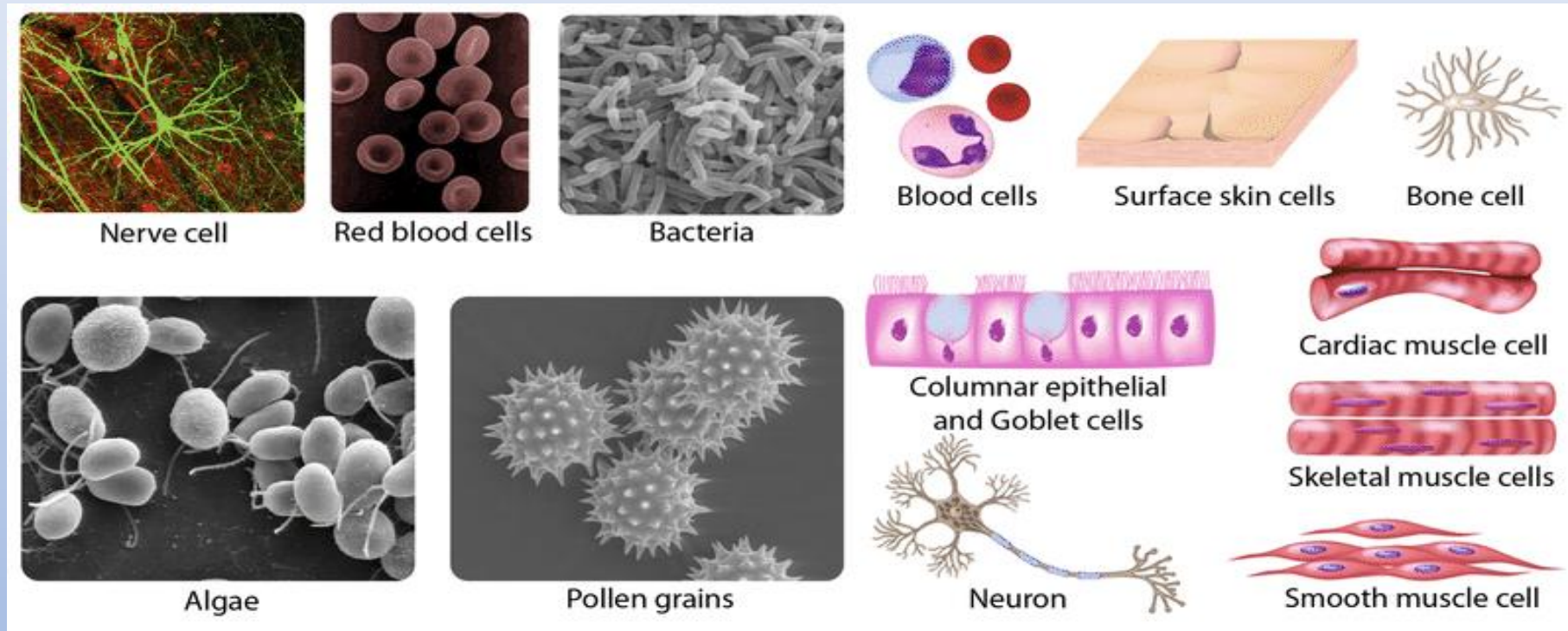
W. Xie, J. A. Noble, and A. Zisserman, "Microscopy cell counting and detection with fully convolutional regression networks," 2016.
V. Lempitsky and A. Zisserman, "Learning To Count Objects in Images," 2010.

Regression based counting by W. Xie et.al.



Segmentation based counting
proposed by May D Wang.et.al.

- However, the above models only work for one specific type of object(cell)
- What if one want to count the number of different types of cells?



You need to train separate networks for many times

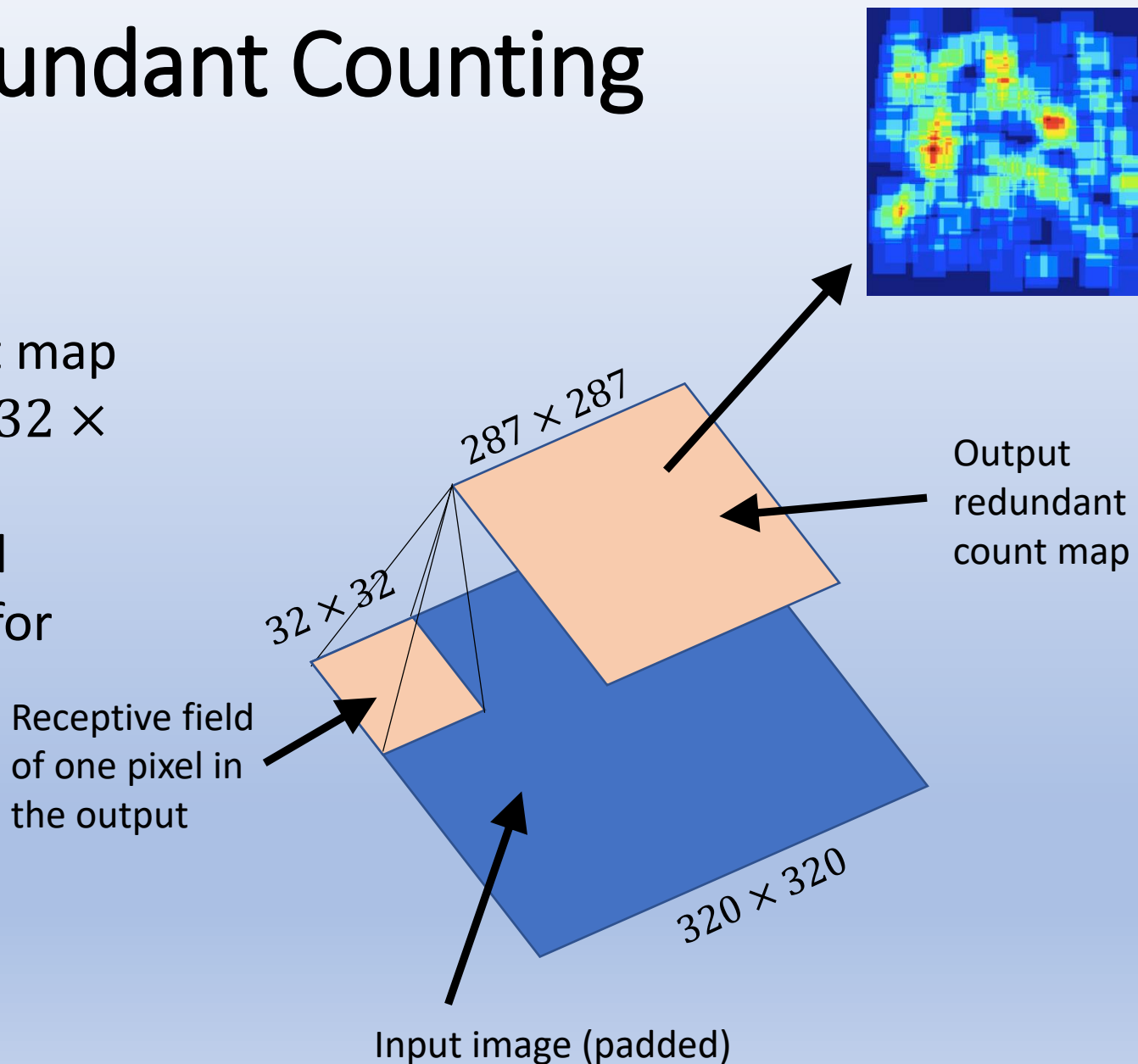
So our problem is to use minimal number of data to transfer a pre-trained network to count different types of cells.

Our Methods

- *Count-ception: [Cohen et al., 2017]
 - Redundant count map (reduce random error)
 - Fully convolutional network
- *Residual Adapter: [Rebuffi et al., 2017]
 - Enable a high degree of parameter sharing
 - Enable our model to adapt to various domains

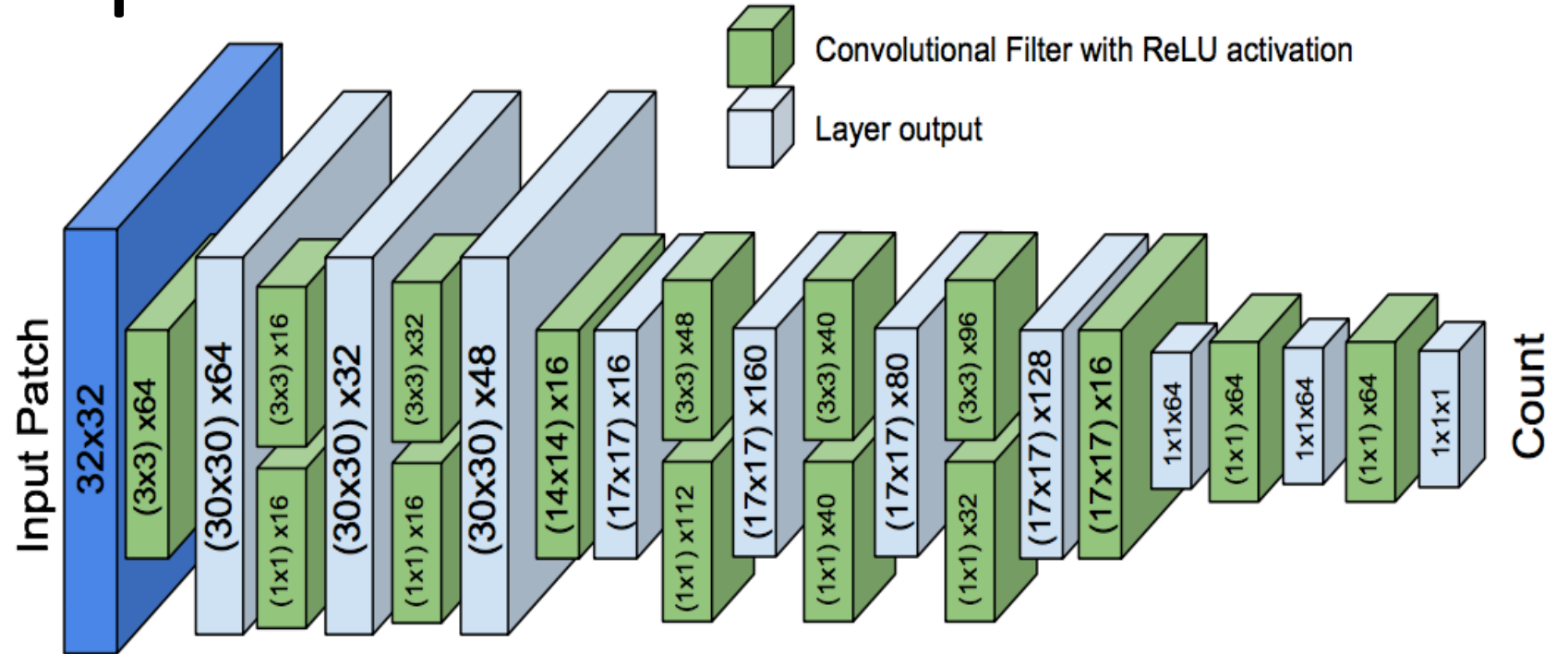
Count-ception: Redundant Counting

- Used as ground truth
- Each pixel in the output map has a receptive field of 32×32
- Square kernels are used
- Each object is counted for 1024 times



Count-ception

Fully
Convolutional
Neural
Network



- This figure shows the receptive of one pixel in the output
- Basically FCN, 3×3 and 1×1 filters are used
- Batch normalization in between each layer
- No pooling or strides

Residual adapter: Intuition

- To enable our model to perform multi-domain counting
- Deep neural networks may share a significant amount of low and mid-level parameters

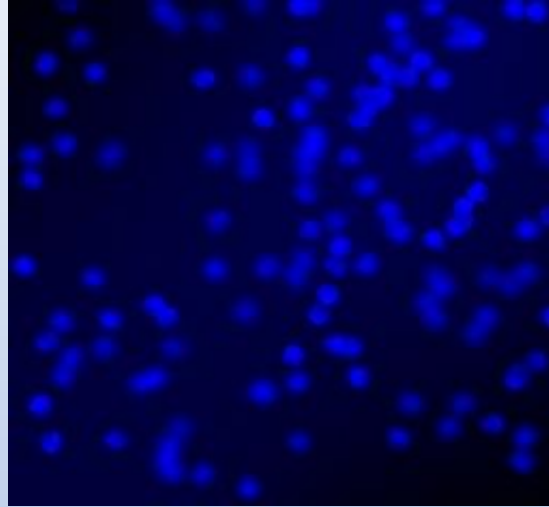
Mathematically, the parameterization process can be interpreted as:

$$G = \alpha * F * x$$

Where G is the final output, α is domain-specific parameters, F is domain-agnostic parameters and x is the input

With the help of adapter modules, we can...

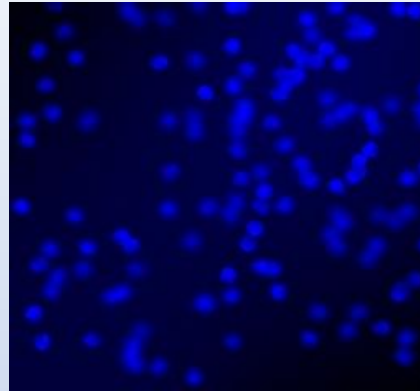
Train on this



VGG
dataset

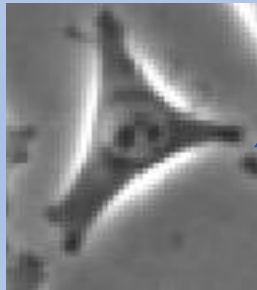
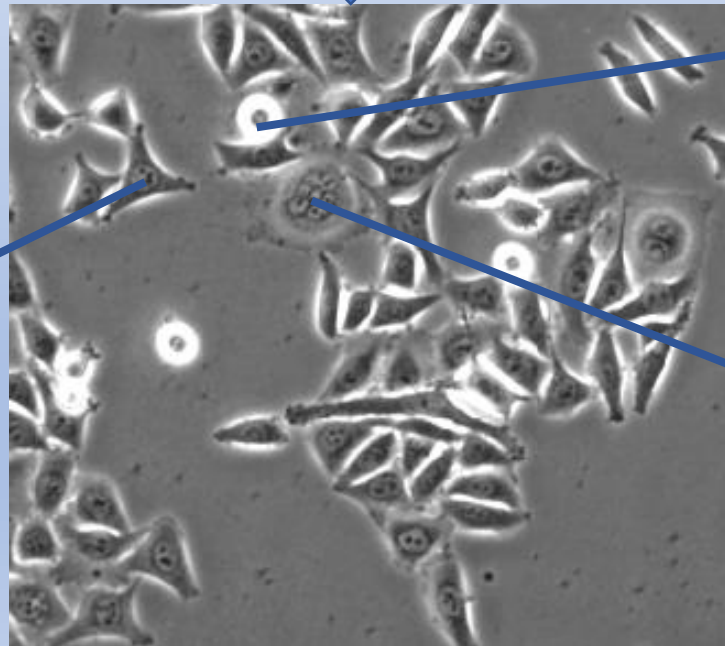
With the help of adapter modules, we can...

Train on this



VGG
dataset

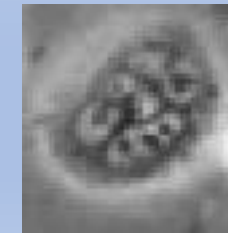
And count these



①. Normal cancer cells

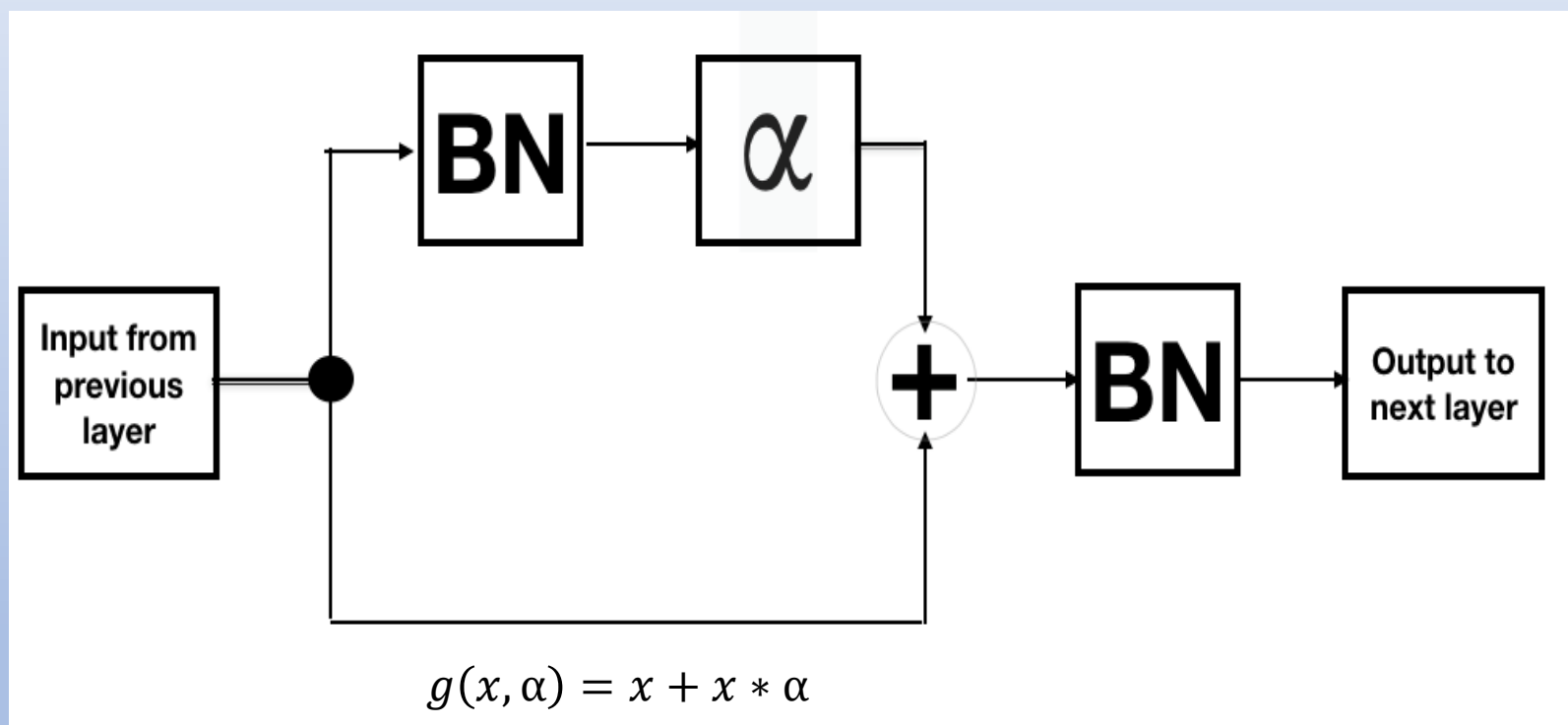


②. Dividing cells



③. Multi-nucleate cells

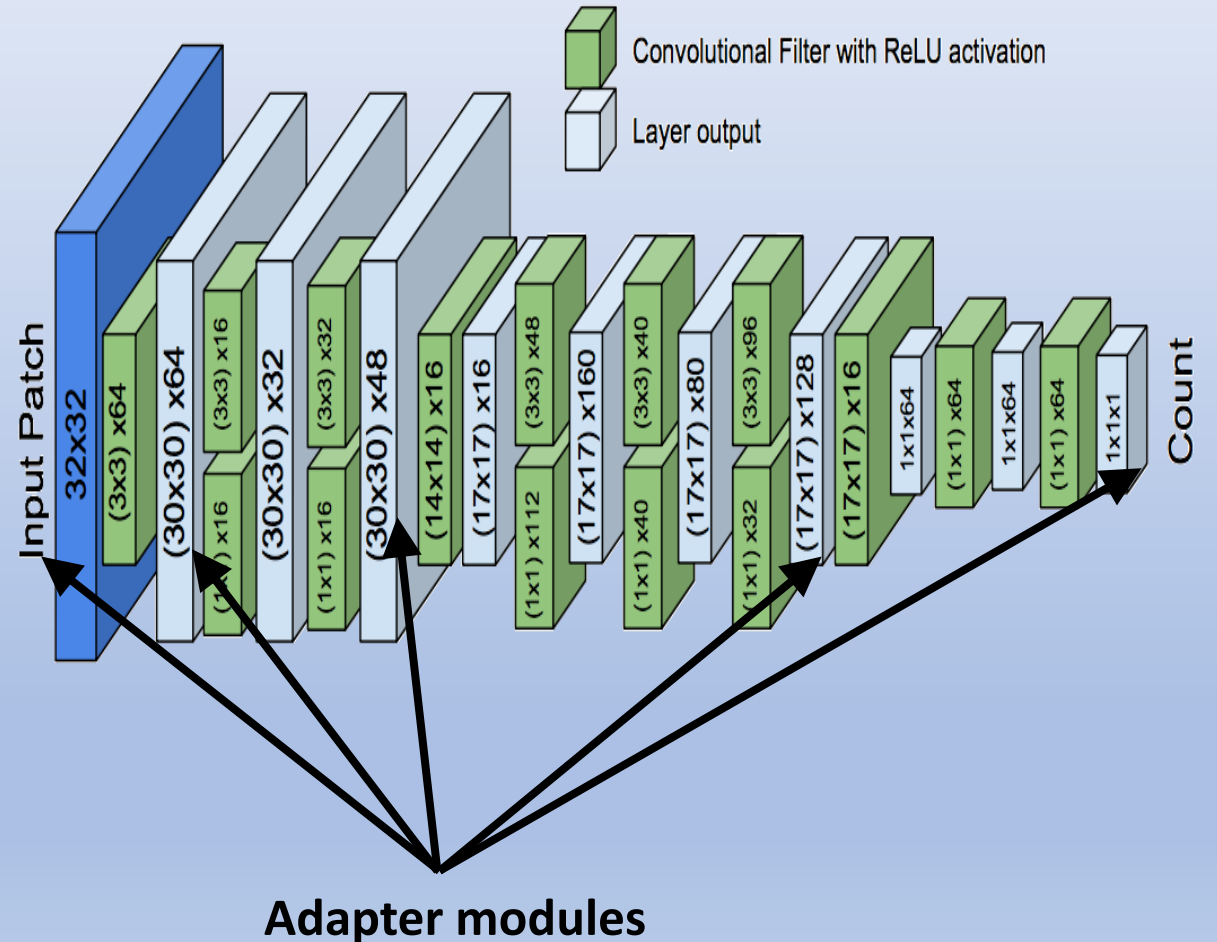
Architecture of an adapter module



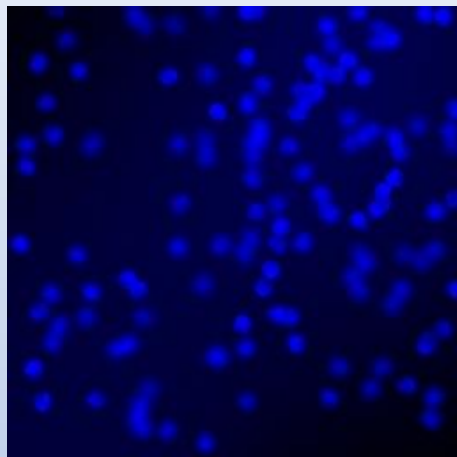
- α is a bank of 1×1 filters to be learned
- Do not change the shape of output and the receptive field

Proposed Architecture

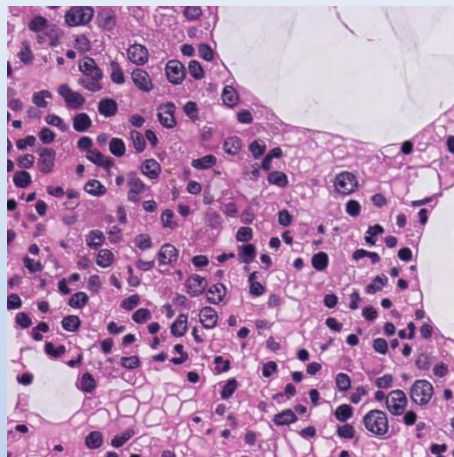
- Pre-train all layers on a large dataset (VGG)
- Domain translation: only train on the adapter layers and BN with minimal amount of new data (less than 2% of all parameters)



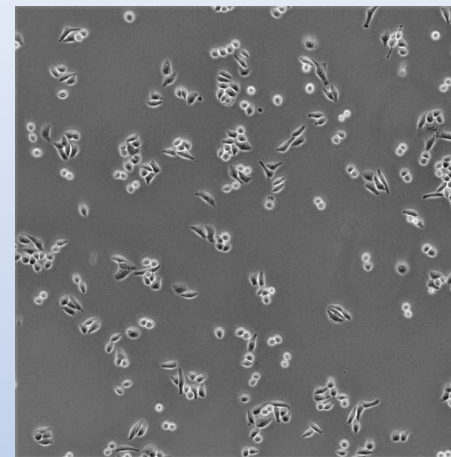
Datasets (modified)



VGG



MBM



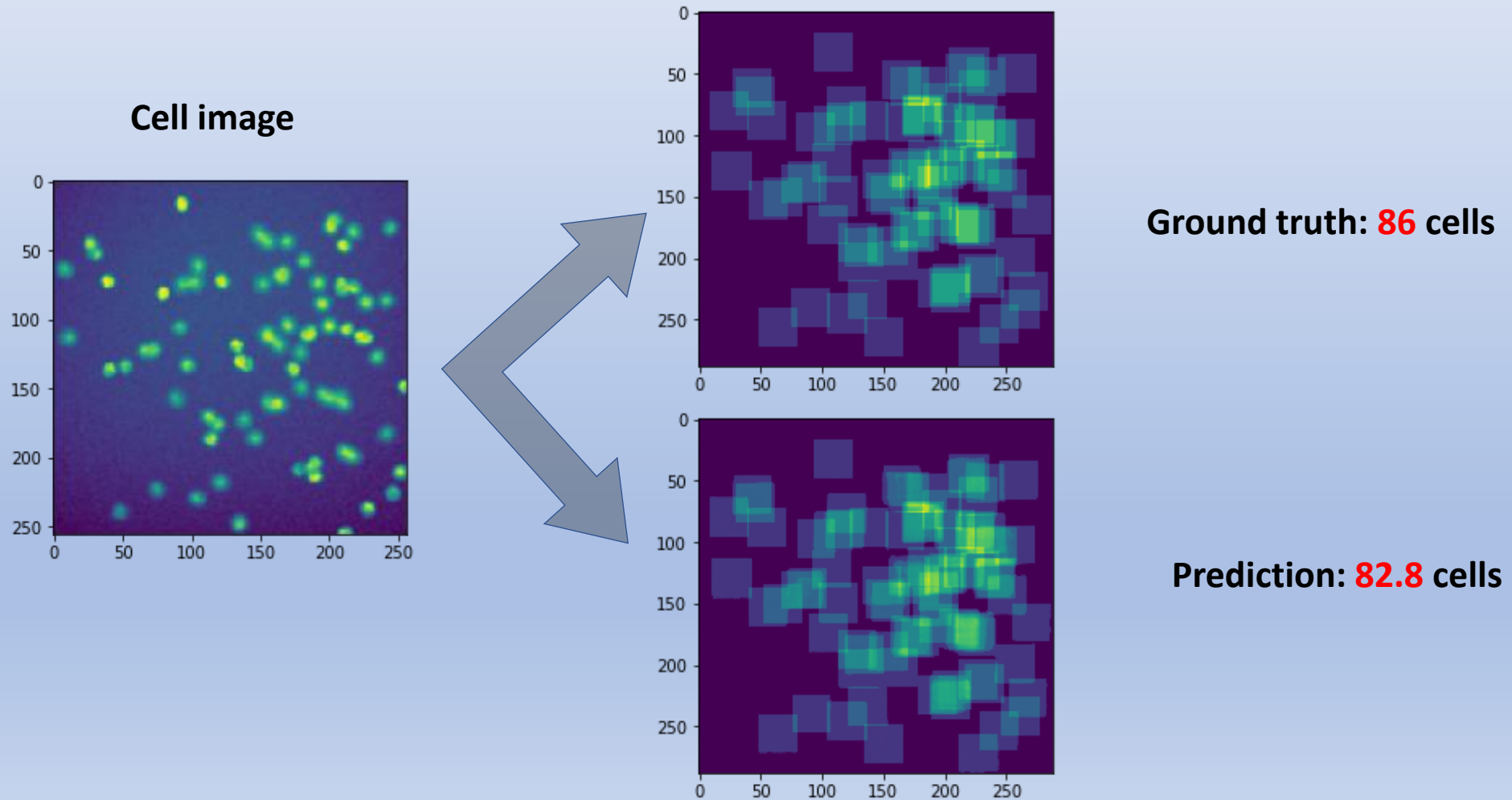
Our Dataset*

Dataset	Number of images	Image size	Average count
VGG [Lempitsky and ZisSerman, 2010]	200	256 × 256	169.1 ± 56.9
MBM [Kainz et al., 2015]	44	256 × 256	94.41 ± 21.10
Ours (count all cells)	79	256 × 256	93.36 ± 18.62
Ours (count dividing cells)	79	256 × 256	19.63 ± 10.00

*Collected from Prof. Hong Xue's biochemistry lab in HKUST.

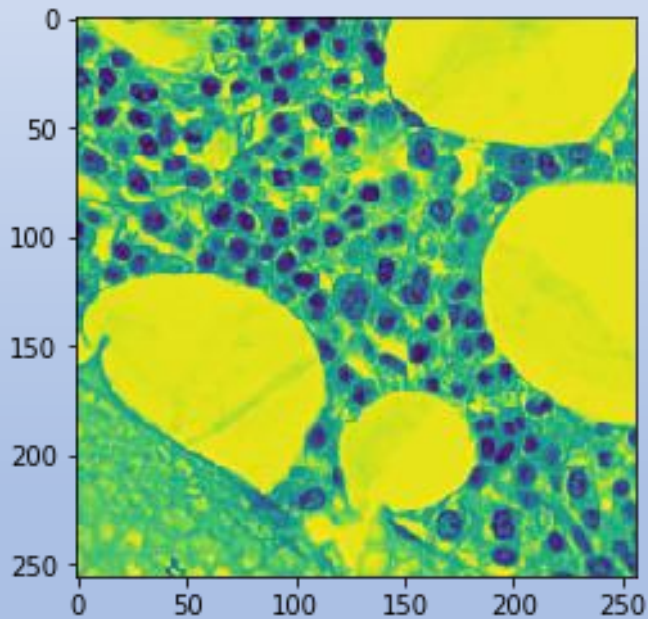
VGG

- 160 for training, 20 for validation and 20 for test.
- The network is trained for 100 epochs and use a batch size of 4.

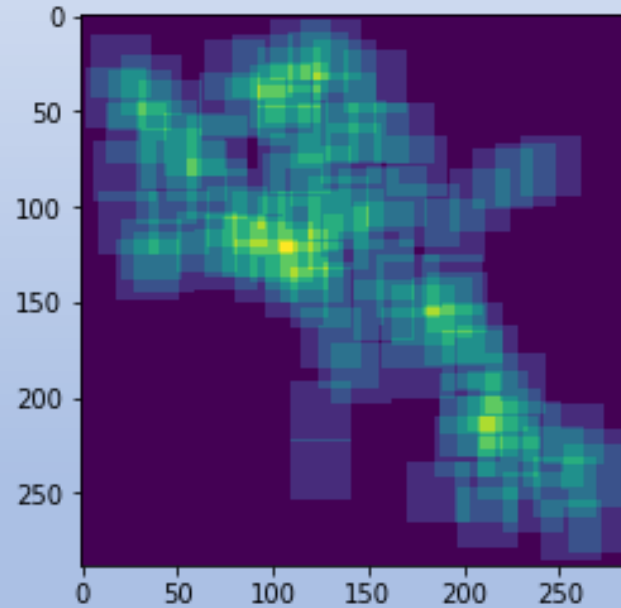


MBM

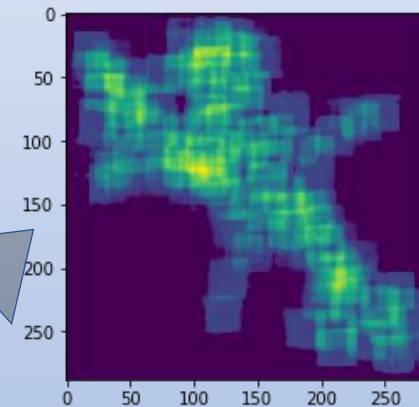
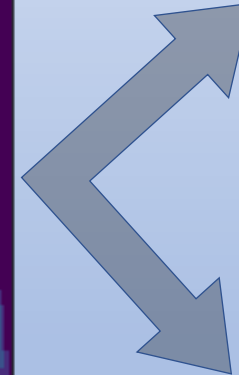
- 35 for training, 5 for validation, 4 for test.
- The network is trained for 100 epochs and batch size is 4.



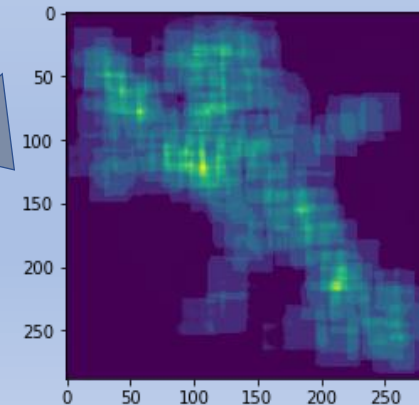
Cell image



Ground truth: **111** cells



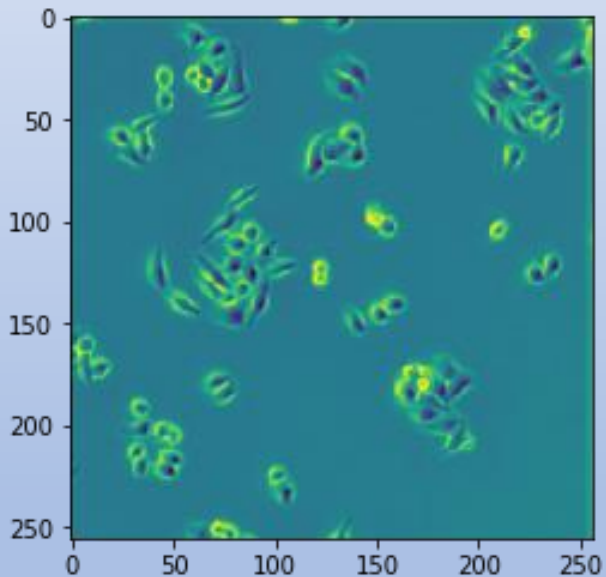
Train from scratch
prediction: **84.6** cells



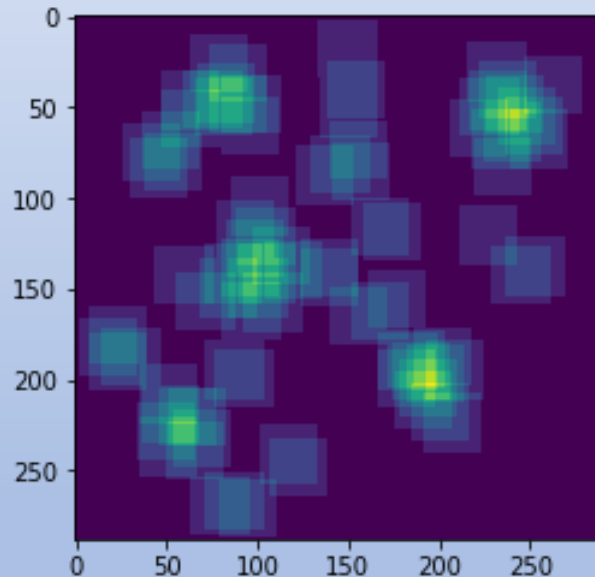
Use adapter
prediction: **107** cells

Our dataset (count all cells)

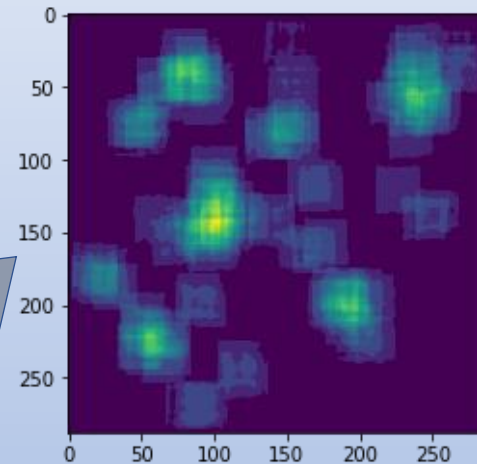
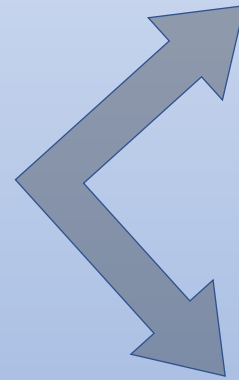
- 67 for training, 8 for validation, 4 for test.
- The network is trained for 100 epochs and batch size is 4.



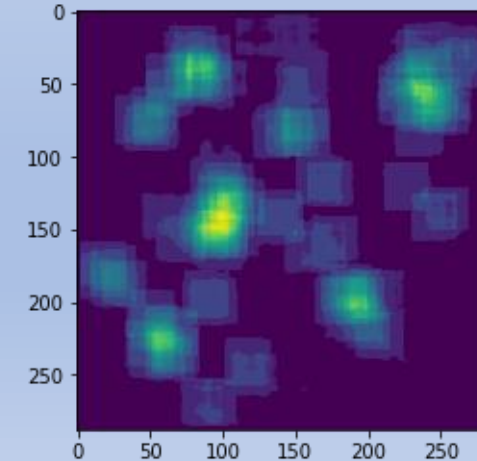
Cell image



Ground truth:
89 cells



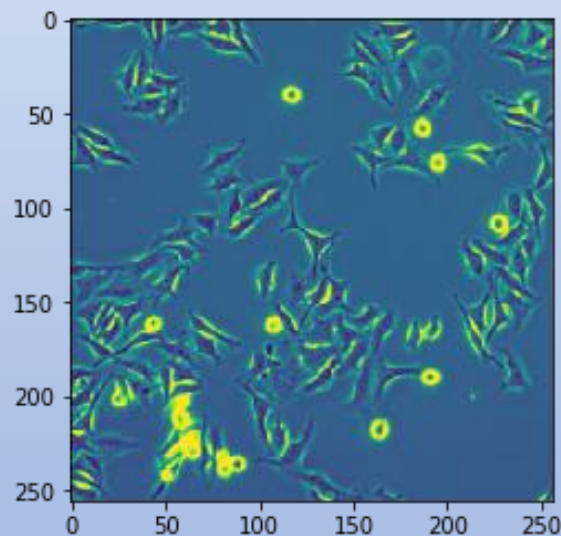
Train from scratch
prediction: **79.9** cells



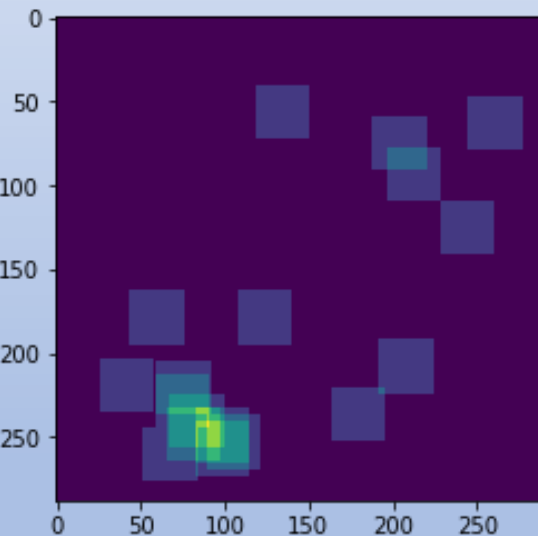
Using adapter
prediction: **84** cells

Our dataset (count dividing cells)

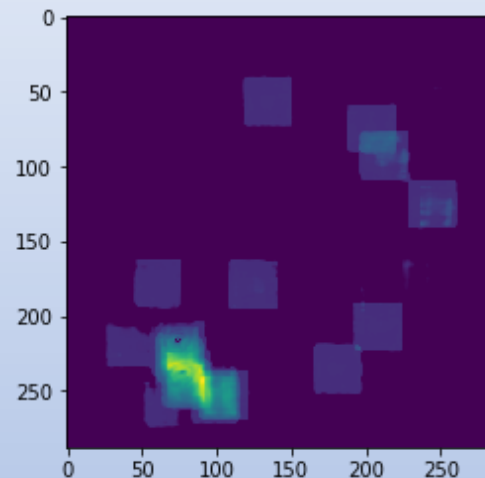
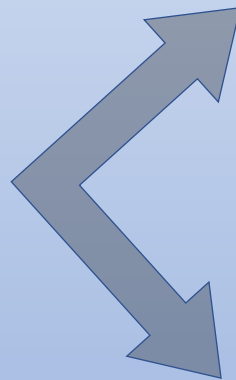
- 67 for training, 8 for validation, 4 for test.
- The network is trained for 100 epochs and batch size is 4.



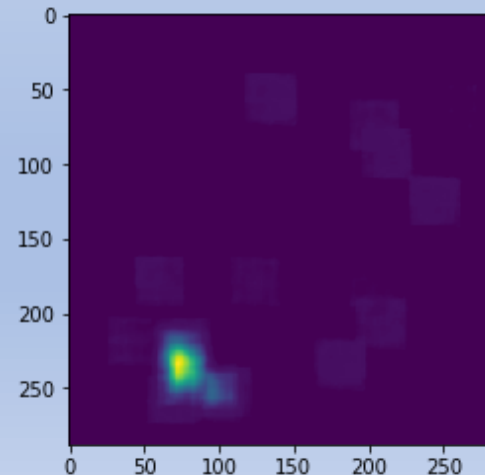
Raw image



Ground truth:
18 cells



Train from scratch
prediction: **19.7** cells



Using adapter
prediction: **43.4** cells

Results and Conclusion

- Pre-train on VGG dataset
- Transfer to MBM and our proposed dataset using adaptive modules.
- Also tried to train from scratch.
- Evaluation metric: Mean Absolute Error (MAE).

Dataset	Ground truth average	MAE (from scratch)	MAE (use adapter)
VGG	169.1	3.25 ± 2.58	<i>Not applicable</i>
MBM	94.41	32.59 ± 5.31	$6.08 \pm 5.98^*$
Ours (count all cells)	93.36	15.15 ± 3.70	$11.86 \pm 4.11^*$
Ours (count dividing cells)	19.63	1.87 ± 1.96	8.34 ± 12.21

References

- J. P. Cohen, G. Boucher, C. A. Glastonbury, H. Z. Lo, and Y. Bengio. Count-ception: Counting by fully convolutional redundant counting. In *International Conference on Computer Vision Workshop on BioImage Computing*, 2017.
- A. Lehmussola, P. Ruusuvuori, J. Selinummi, H. Huttunen, and O. Yli-Harja. Computational framework for simulating fluorescence microscope images with cell populations. *IEEE Transactions on Medical Imaging*, 2007.
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- W. Xie, J. A. Noble, and A. Zisserman. Microscopy cell counting and detection with fully convolutional regression networks. *Computer Methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*, 2016.