DEPARTMENT OF COMPUTER SCIENCE
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SEGMENTATION OF HUMAN SEMEN USING CONVOLUTIONAL NEURAL NETWORKS

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Basic measures of sperm quality analysis

- Concentration
- Motility
- Morphology

Accurate identification the basis of all these analyses

Dataset

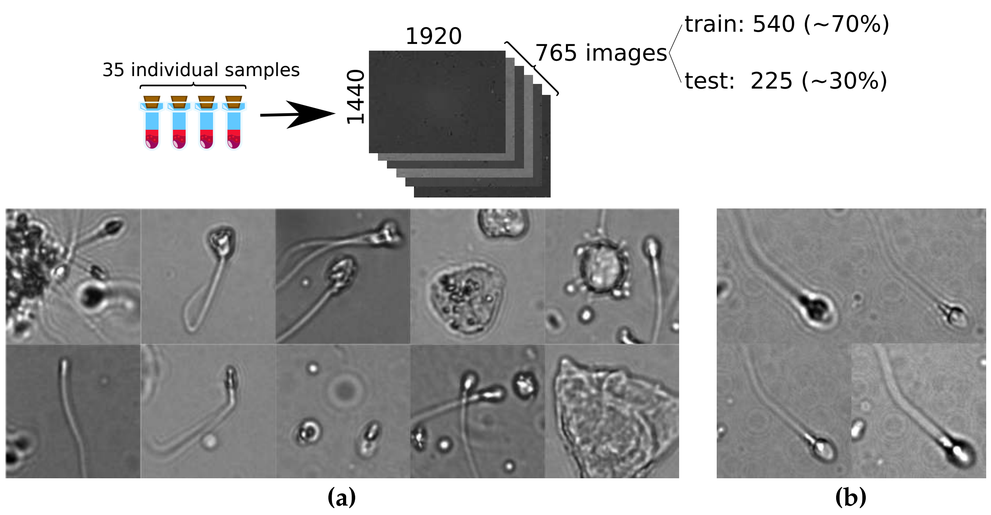
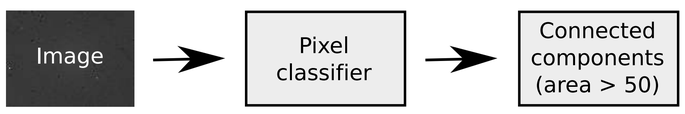


Figure 1: Debris and variations (1a) and sperm cell at different foci (1b)

Pipeline



Convolutional Neural networks (implemented in Caffe [1])

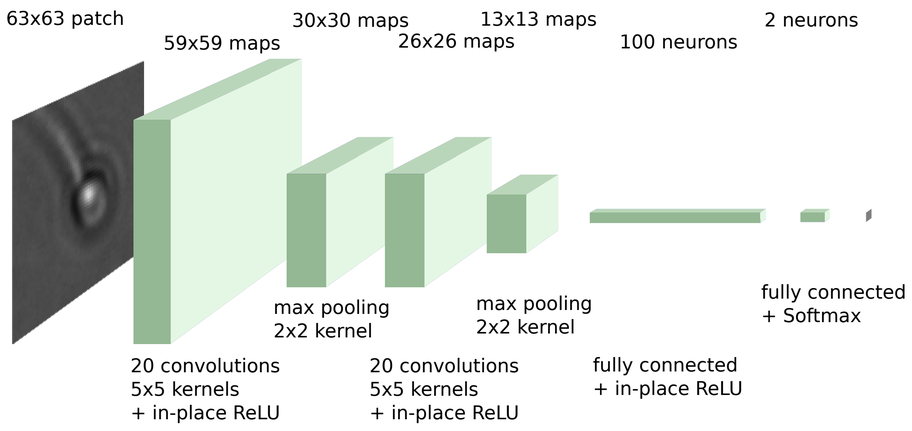


Figure 2: 2-conv

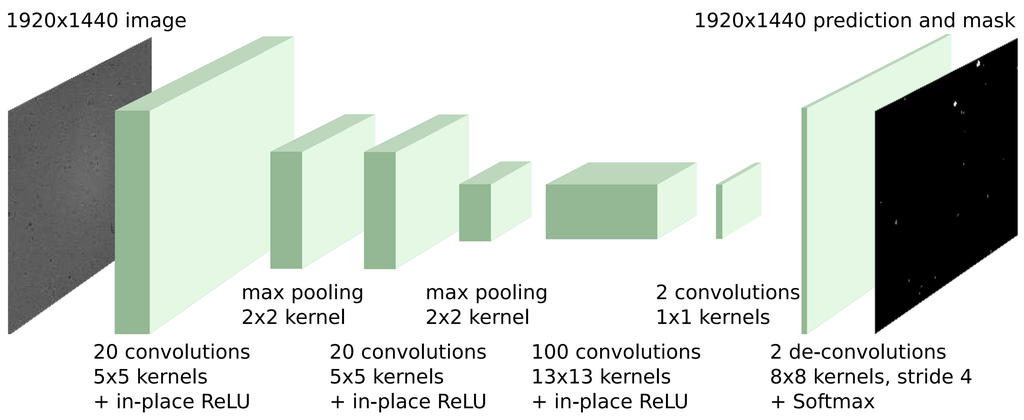


Figure 3: 2-conv-full inspired by the FCN-8s by [2]

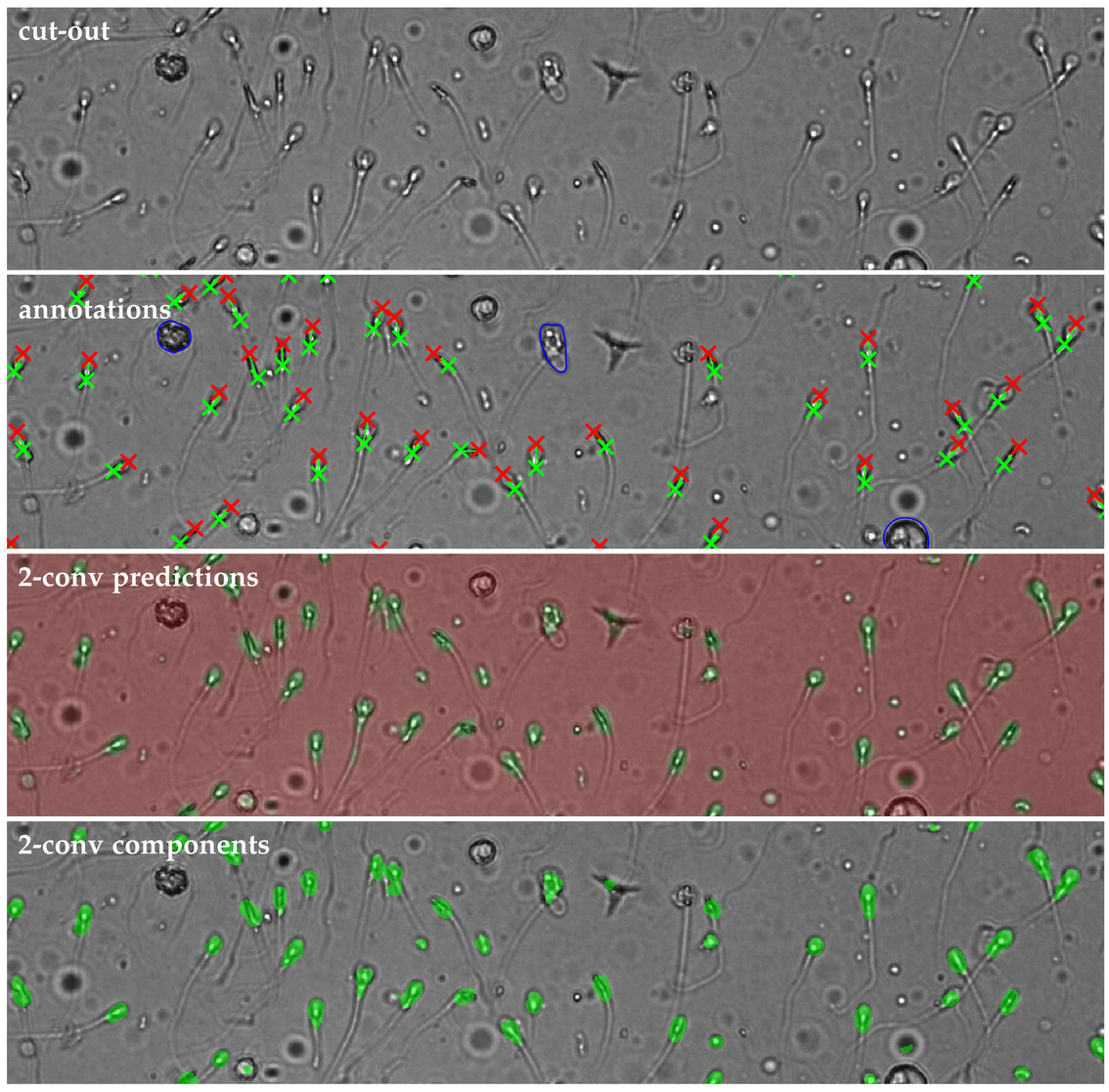
Questions?

Dont hesitate to ask me questions or to let me walk you through my poster.

Not around?

I'm probably looking at one of the other posters. Please find me if you need help or wish to start a discussion.
- Malte S. Nissen

Example



Results

Method	Mean accuracy	Mean IU
2-conv	0.9660	**0.6725**
3-conv	0.5702	0.5086
2-conv-full	**0.9672**	0.5334
3-conv-full	0.9601	0.5210

Table 1: Pixel-based performance measures on the test images.

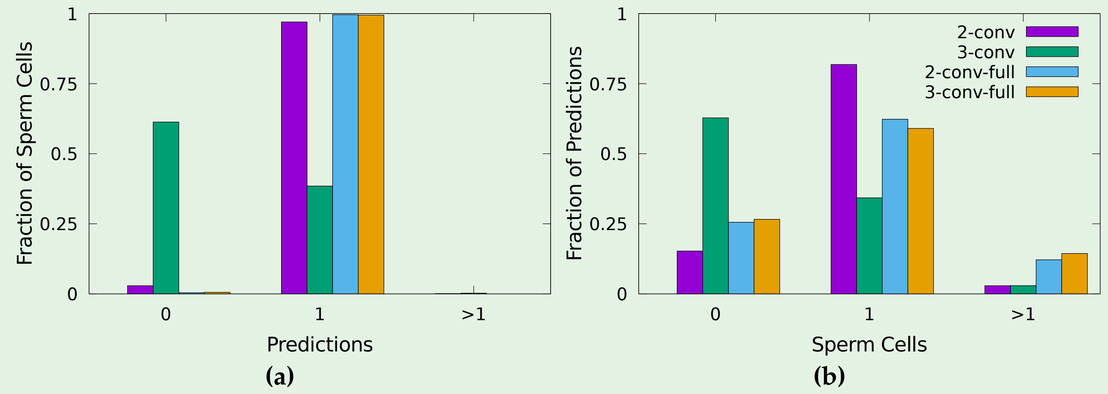


Figure 4: Predictions per sperm cell (4a) and sperm cells per prediction (4b) on the test images.

Acknowledgements

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References

[1] Yangqing Jia, Evan Shelhamer, Jeff Donahue, Sergey Karayev, Jonathan Long, Ross Girshick, Sergio Guadarrama, and Trevor Darrell. Caffe: Convolutional architecture for fast feature embedding. *arXiv preprint arXiv:1408.5093*, 2014.

[2] Jonathan Long, Evan Shelhamer, and Trevor Darrell. Fully convolutional networks for semantic segmentation. *arXiv preprint arXiv:1411.4038*, 2014.