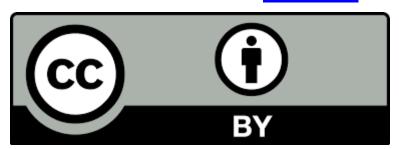
Data science in cell imaging Lecture 5: deep learning in microscopy



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PPTX slides available <u>here</u>



Today and next week

- (Discussing potential course projects)
- Enhancing cell image quality with deep learning
- Generative models for cell structure with deep learning
- Classifying cell state with deep learning

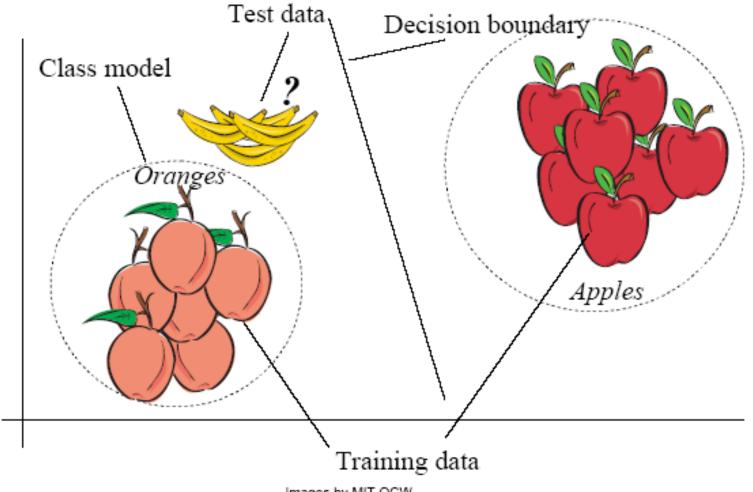
Machine learning 101

Recommended deck for noncomputational students



Supervised machine learning

Data → feature extraction → training → discriminative model



Images by MIT OCW.

Credit: B. Heisele, Y. Ivanov, T. Poggio

Unsupervised machine learning

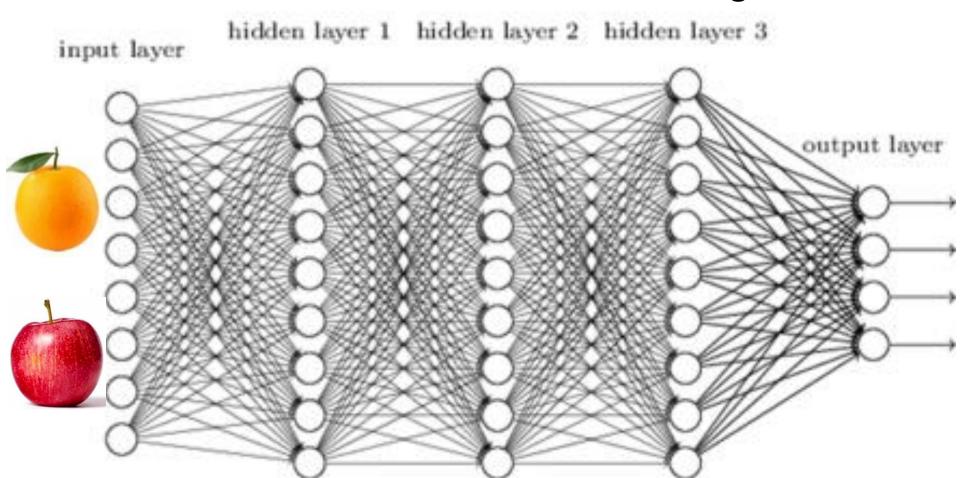
Data → feature extraction → clustering



Source: https://bit.ly/2IJN0NT

Deep learning

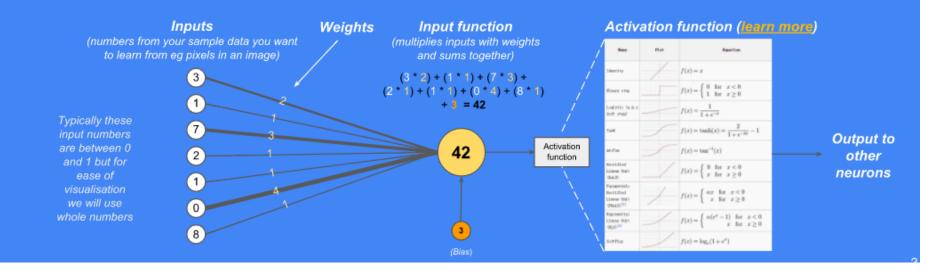
A powerful integration of automated feature extraction and model training



How does it works?

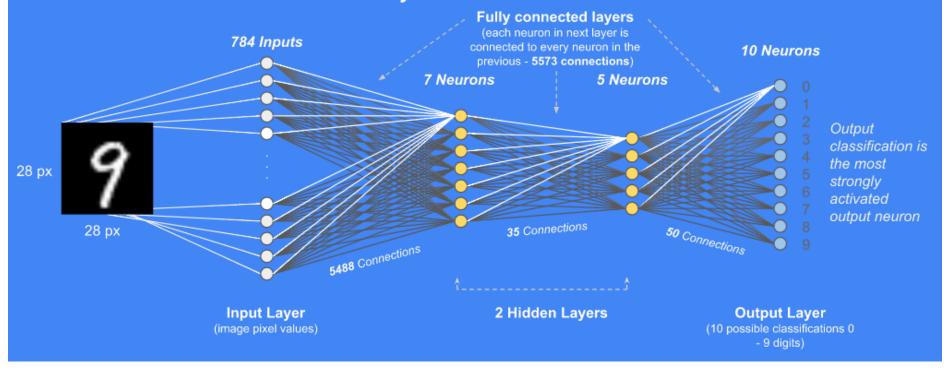
Artificial neuron (perceptron)

A neuron simply has a bunch of weighted inputs (take the input number and multiply by the weight) that are summed together. A bias is then added to this total. The weights and bias are determined when we train the system. If final result is greater than a threshold, it activates, providing an output. Strength of output depends on the activation function chosen. The output is then fed into other neurons and the process repeats.



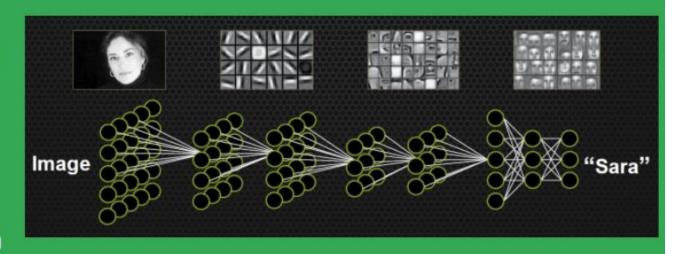
Deep neural network

This is a **multi layered perceptron** (or deep neural network) - one of the oldest forms of "neural nets" - conceptually goes back to the 60s! Each layer is **fully connected** to the next and **data flows forwards only**:



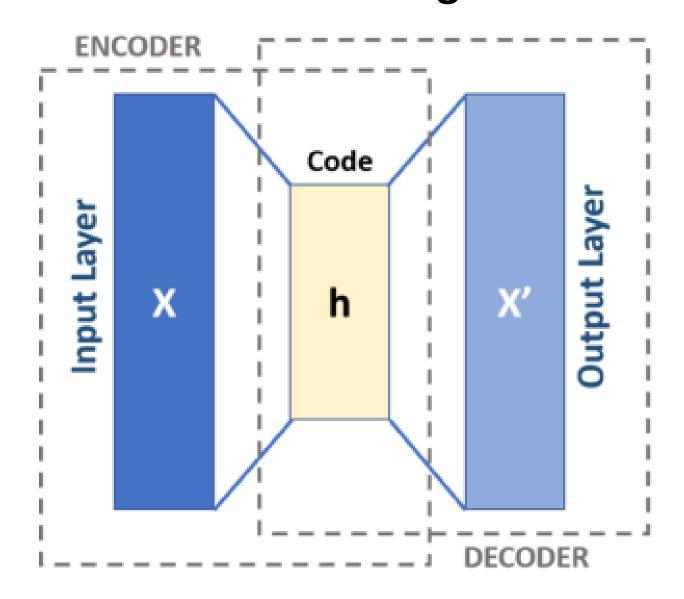
Deep neural network

A Deep Neural Network (DNN) simply consists of many "hidden layers" between the input and the output. Each layer can learn from the one before it from which higher level learning can



take place. These hidden layers typically are of lower dimensionality so they can generalise better and not overfit to the input data. These middle layers in the system can learn features of features. For example bunches of "edges" can lead to "face parts" which lead to "faces" that the system can then recognize.

Autoencoder: unsupervised data encoding

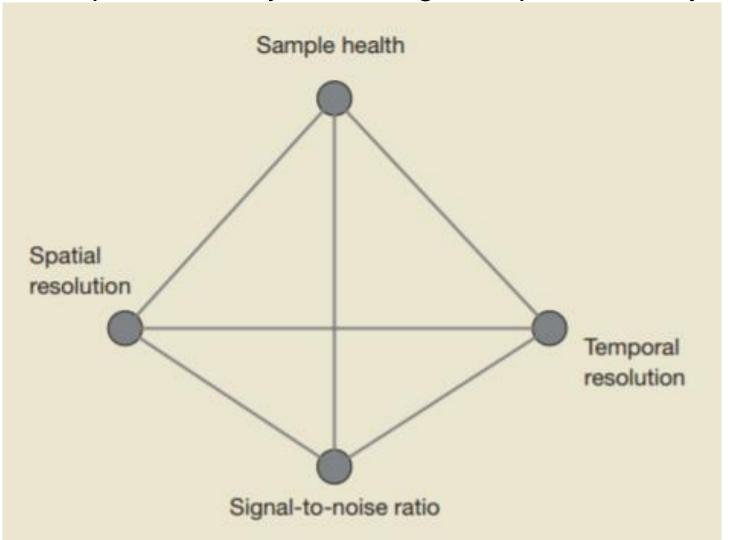


Many applications for ML in cell biology!

Today I'll review a few specific examples on deep learning for (1) image restoration; (2) prediction of (un-labeled) protein localization patterns

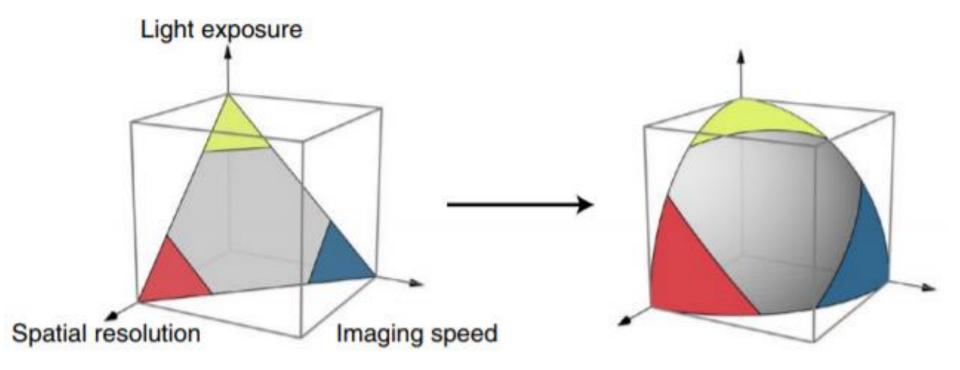
Imaging tradeoffs

Spatial/temporal resolution, experiment time, imaging depth, fluorophore density, bleaching, and photo-toxicity



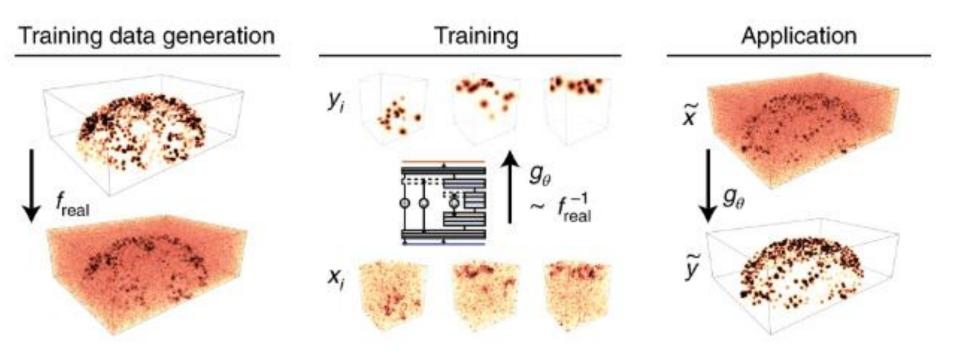
Hadar Aharoni (IDF) from Scherf et al. (2015)

Content aware image restoration (CARE)



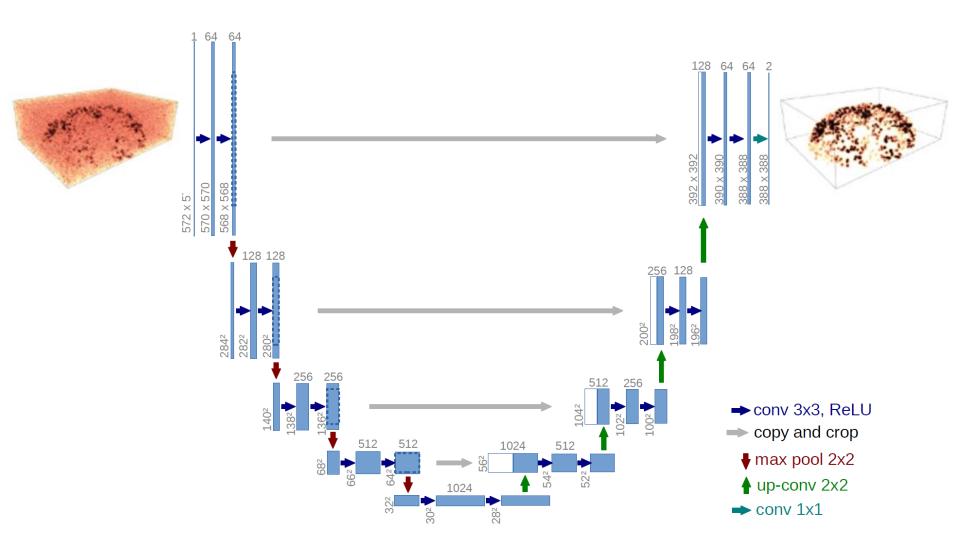
- Traditional methods use general assumptions to perform the restoration
- CARE leverages the available knowledge about the specific experimental task / setup

Content aware image restoration (CARE)



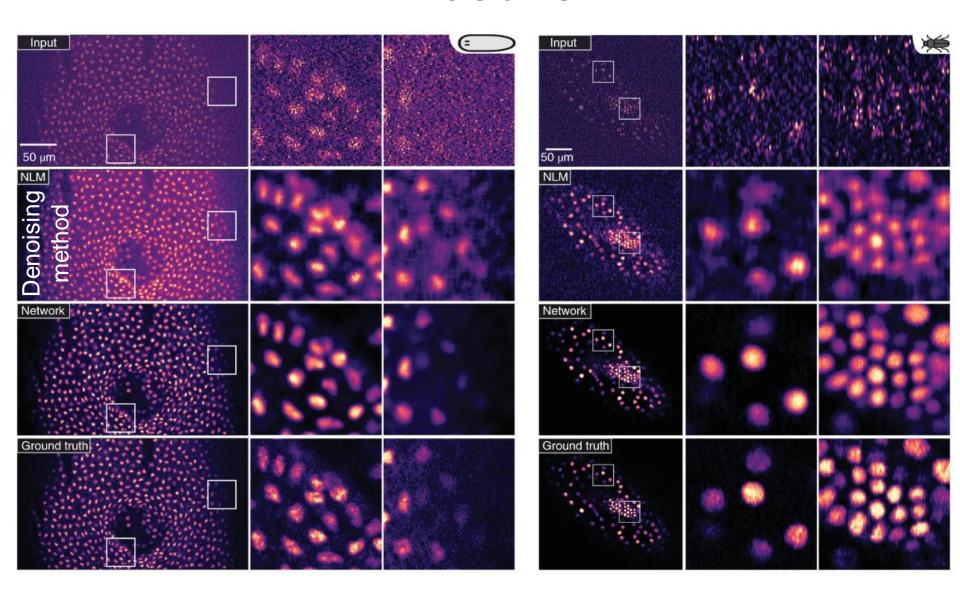
- Traditional methods use general assumptions to perform the restoration
- CARE leverages the available knowledge about the specific experimental task / setup

The machinery: U-Net



Ronneberger et al. (2015)

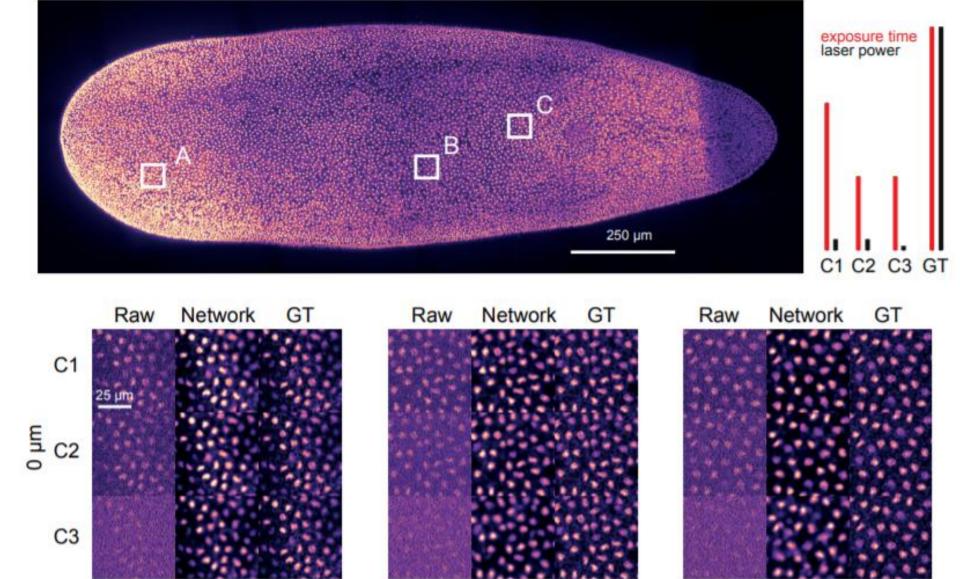
Results



Weigert et al. (2018)

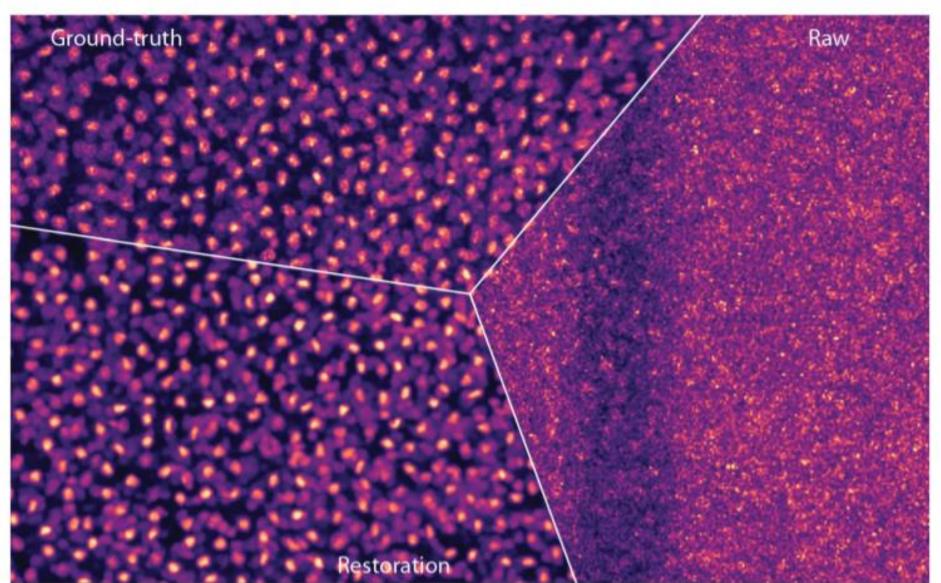


Restoration of low-SNR images

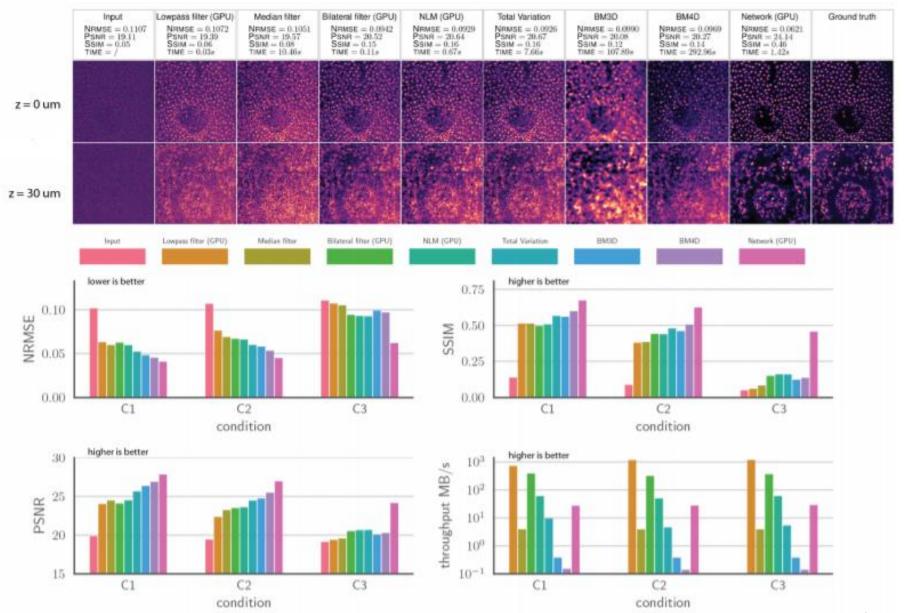


Weigert et al. (2018)

Restoration of low-SNR images



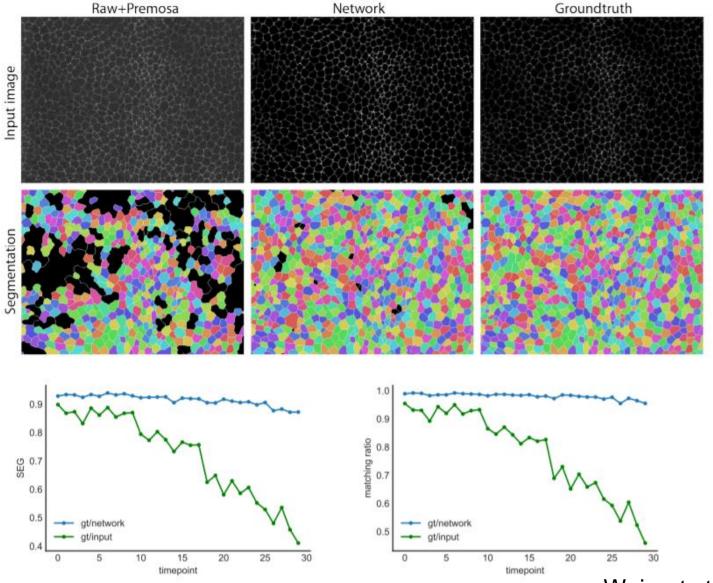
Comparison: different denoising methods



Weigert et al. (2018)

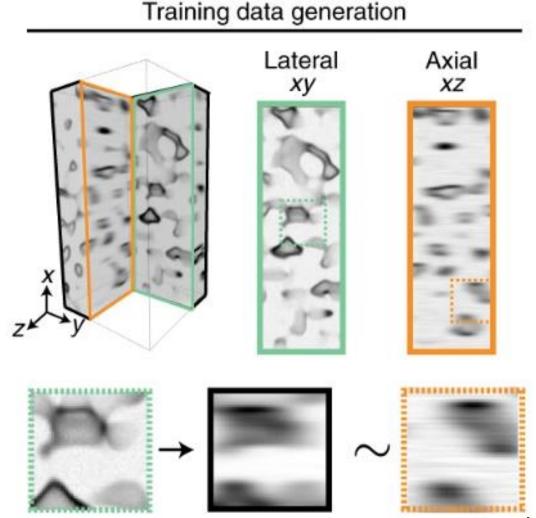
CARE improves downstream analysis

Cell segmentation and tracking of a projected time-lapse

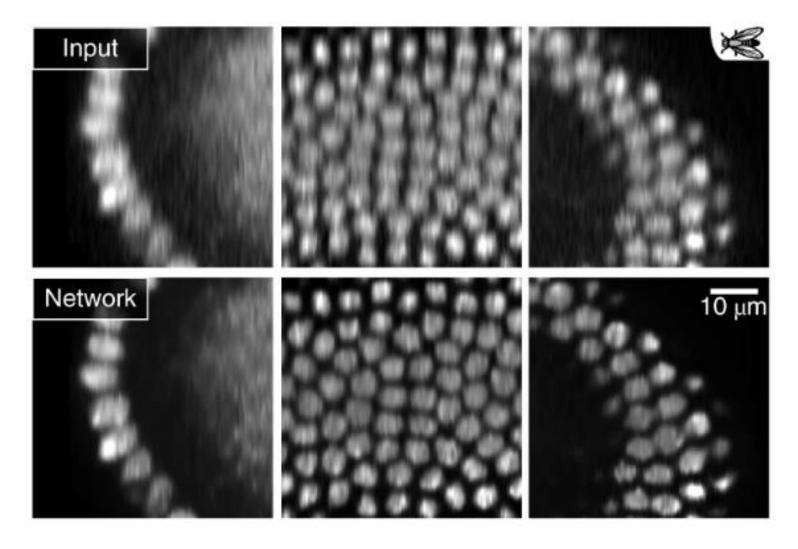


Weigert et al. (2018)

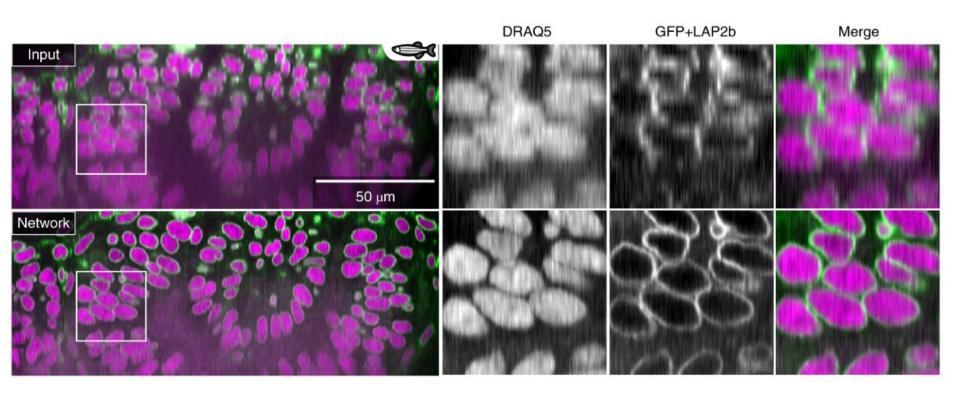
Image restoration of unseen axial slices with <u>semi-synthetic</u> training data



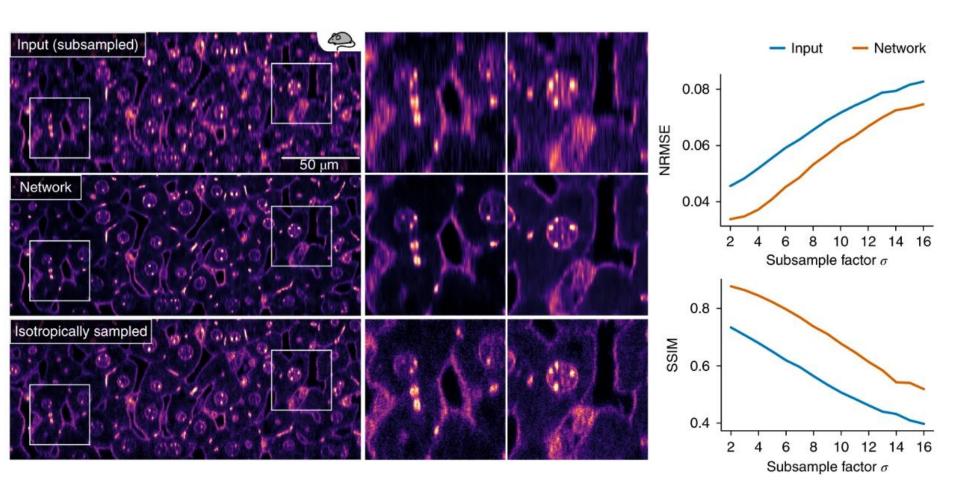
CARE increase axial resolution of acquired volumes



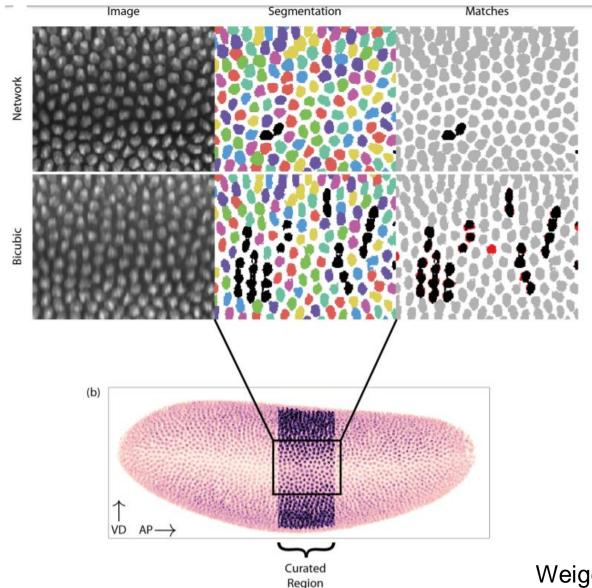
CARE increase axial resolution of acquired volumes



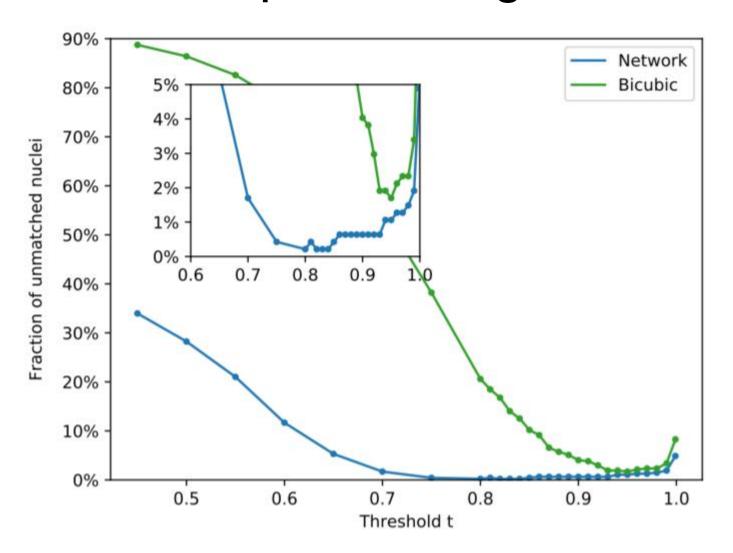
CARE increase axial resolution of acquired volumes



Anisotropic-to-isotropic restoration leads to improved segmentation

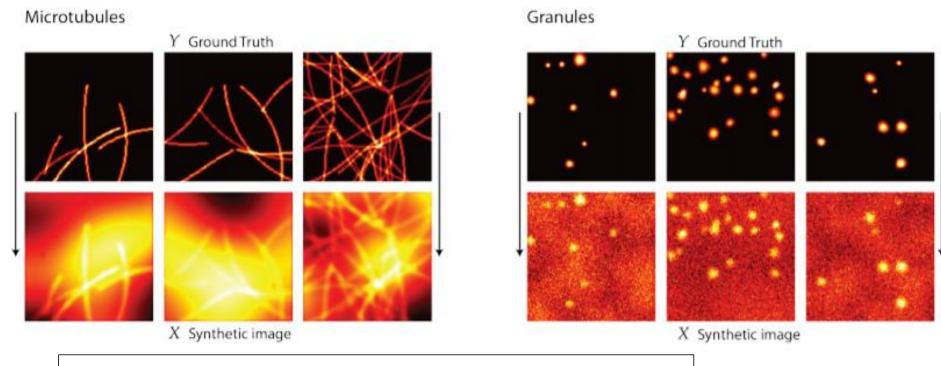


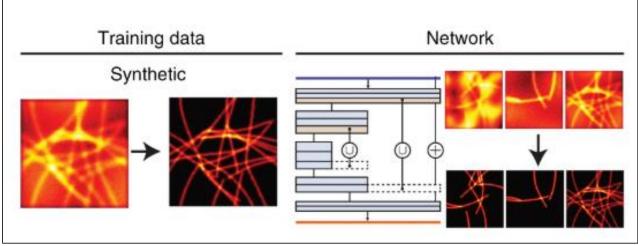
Anisotropic-to-isotropic restoration leads to improved segmentation



Synthetically generated training data

PSF, camera noise, and background auto-fluorescence



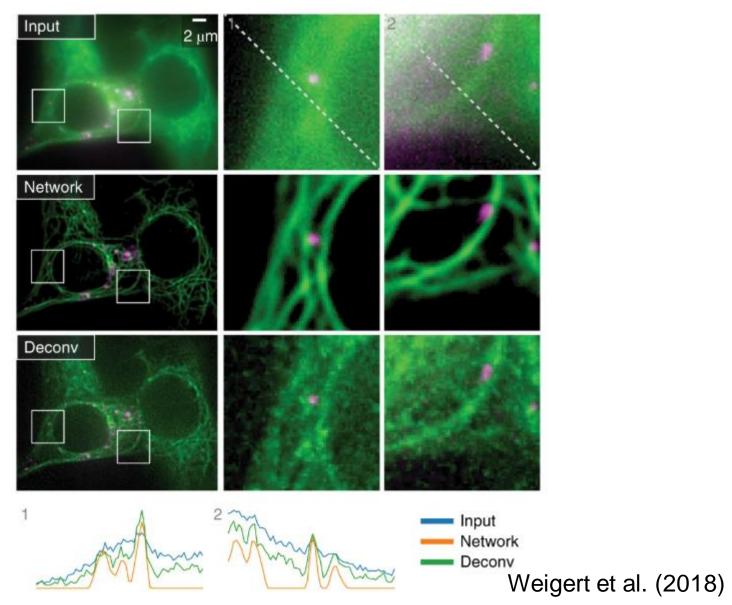


Weigert et al. (2018)

Image restoration with <u>synthetic</u> training data

Restoring sub-diffraction structures using only widefield images

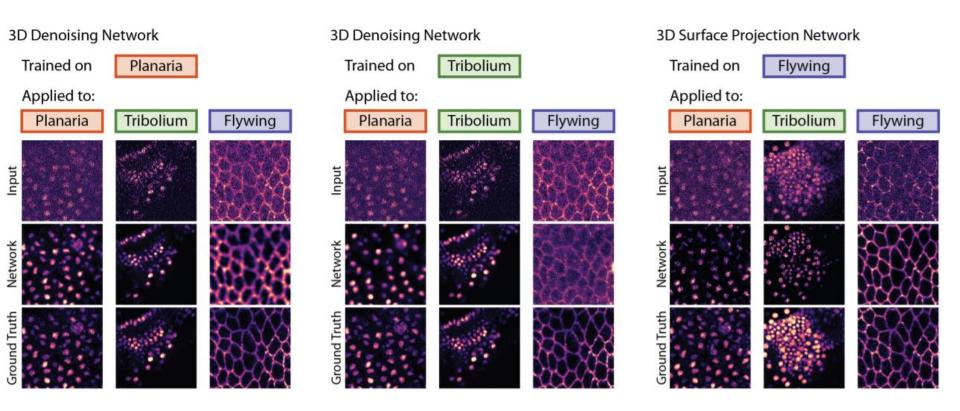
Improved performance of the CARE network over deconvolution



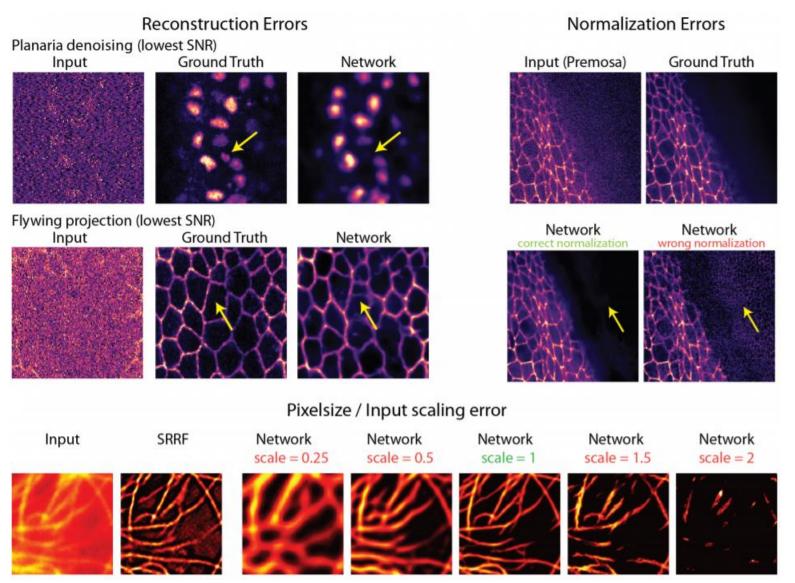
CARE vs. super-resolution radial fluctuations (SRRF)

Enabling 20-fold faster imaging

Cross-application of trained care networks



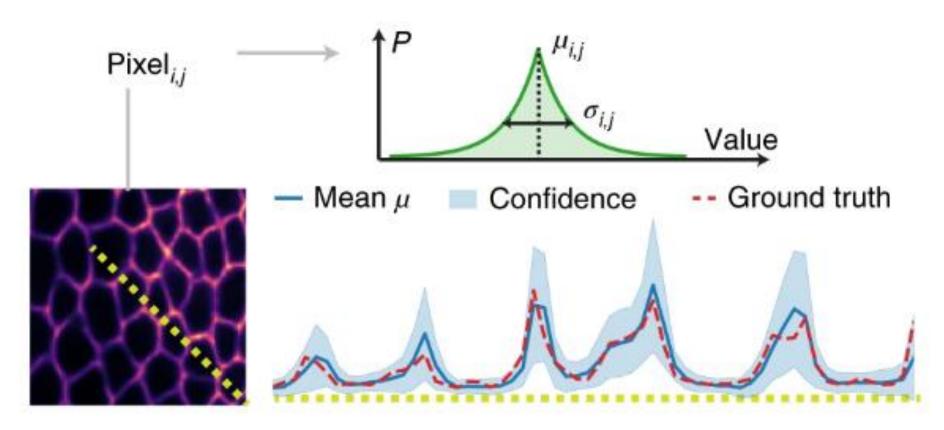
Minimal 'hallucination' effects



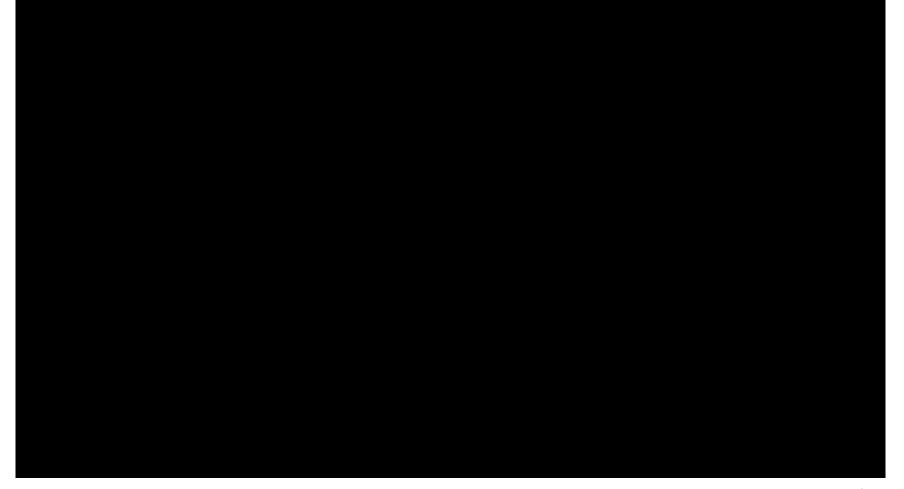
Reliability of image restoration

Calculating pixel-wise confidence intervals

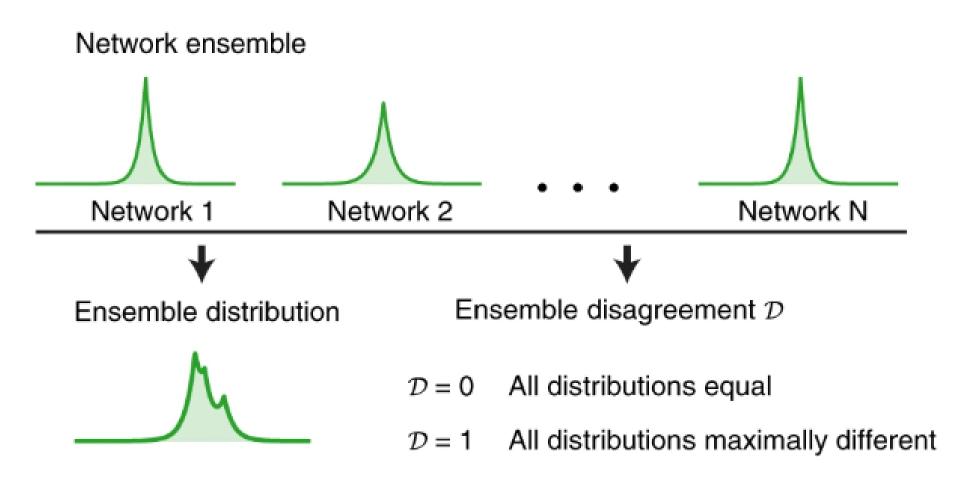
Predicting pixel-wise distributions



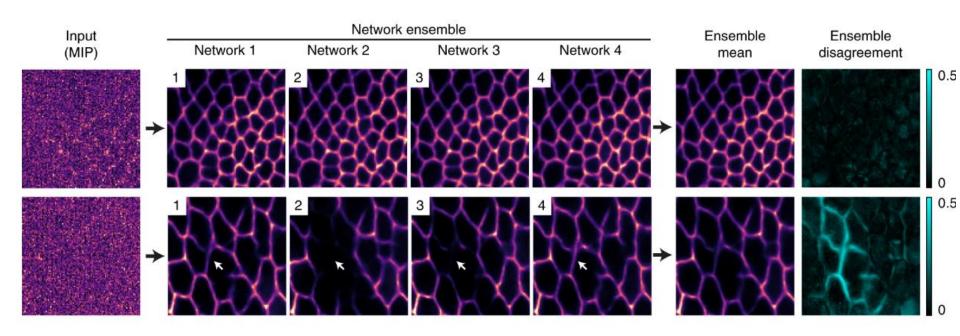
Visualizing the uncertainty by random sampling pixel intensities from their respective distributions

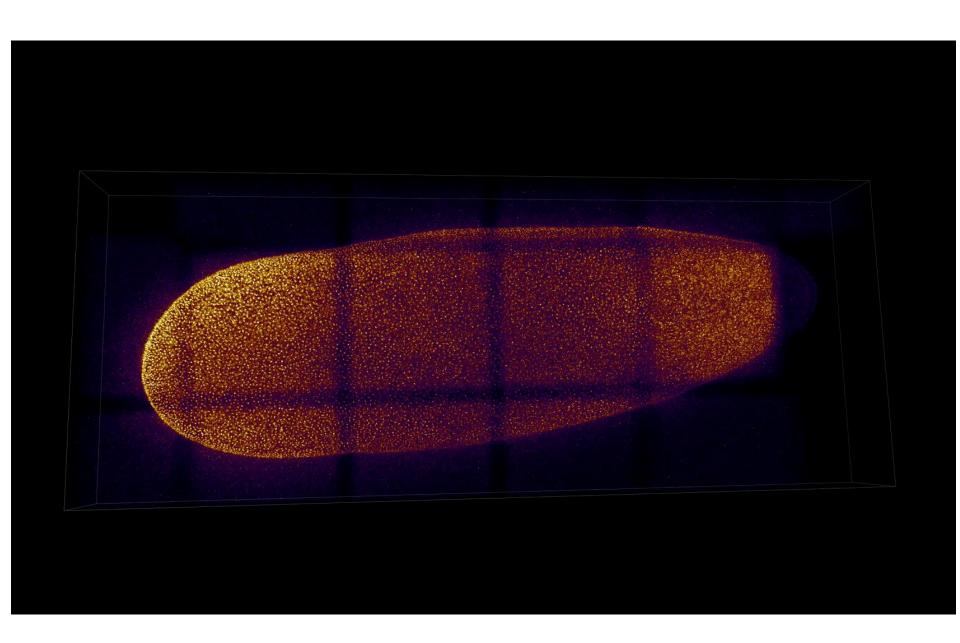


Assessing reliability via consistency of several trained models

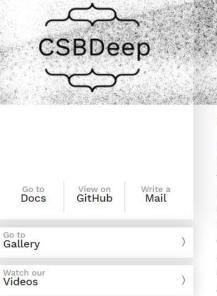


Assessing reliability via consistency of several trained models





Usability is important!



CSBDeep, a toolbox for Content-aware Image Restoration (CARE)

Fluorescence microscopy is a key driver of discoveries in the life-sciences, with observable phenomena being limited by the optics of the microscope, the chemistry of the fluorophores, and the maximum photon exposure tolerated by the sample. These limits necessitate trade-offs between imaging speed, spatial resolution, light exposure, and imaging depth. In this work we show how deep learning enables biological observations beyond the physical limitations of microscopes. On seven concrete examples we illustrate how microscopy images can be restored even if 60-fold fewer photons are used during acquisition, how isotropic resolution can be achieved even with a 10-fold under-sampling along the axial direction, and how diffraction-limited structures can be resolved at 20-times higher frame-rates compared to state-of-the-art methods. All described restoration networks are freely available as open source software in Fiji and KNIME.

How to start

- To use CSBDeep in Python, follow this guide.
- To use CSBDeep in Fiji, follow this guide.
- To use CSBDeep in KNIME, follow this guide.
- (If you have been given access, try CSBDeep on our Paperspace server.)







https://csbdeep.bioimagecomputing.com/ https://github.com/csbdeep/csbdeep

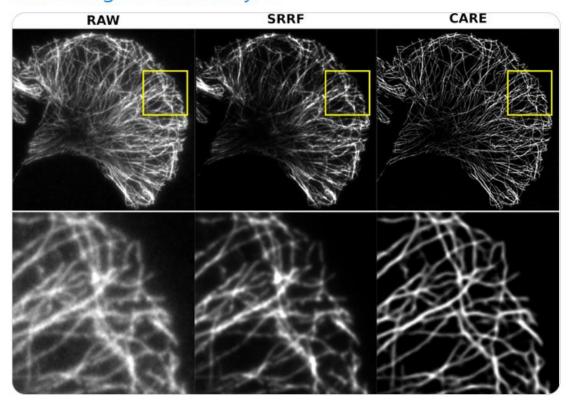
(Sometimes) even works out of the box!



#CARE vs #SRRF on my microtubule images (TIRF 100x).

#CARE work beautifully. I look forward to train it to
work on filopodia! I already have images ready!

biorxiv.org/content/early/...



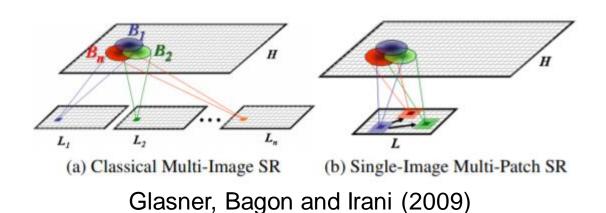
12:09 PM · Jan 4, 2018 · Twitter Web Client

Summary

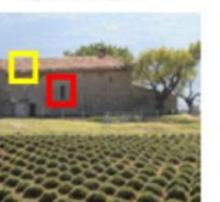
- CARE leverages experiment-specific information to imaging tradeoffs
- Matched images, semi-synthetic and synthetic training data
- High quality denoising models can be trained without the availability of clean ground truth data
- Great for downstream analysis not for intensity-based measurements!
- Could work well "out of the box"
- Usable by others!

"Super resolution" in the context of computer vision

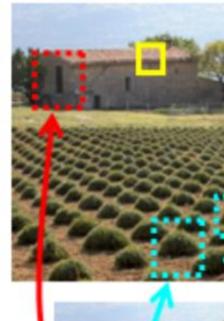
- Recover a high resolution image from one or more low resolution input images
- Classical multi-image super resolution: combining images obtained at subpixel misalignments (Irani & Peleg, 1991)
- Example-Based super-resolution: learning correspondence between matching low and high resolution image patches (Freeman, Pasztor & Carmichael, 2000)



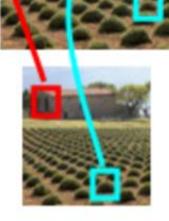
Input image I



Various scales of I

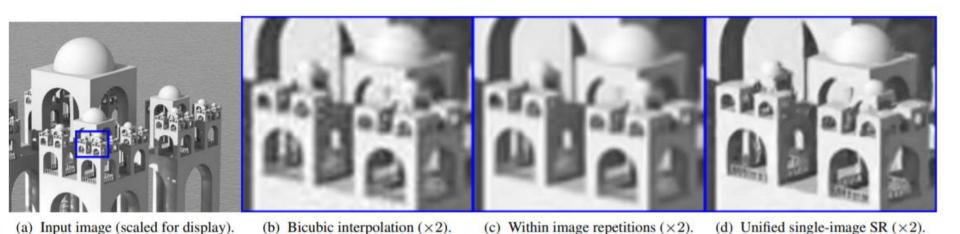


(computer vision) super resolution from a single image



Glasner, Bagon and Irani (2009), see http://www.wisdom.weizmann.ac.il/~vision/SingleImageSR.html

(One) result



Glasner, Bagon and Irani (2009), see http://www.wisdom.weizmann.ac.il/~vision/SingleImageSR.html

2009 vs. 2018

A conceptual lag of (almost) a **decade** between computer vision and microscopy!

There might be other opportunities out there..

Handling noisy images: new extensions from the Jug lab

(could be picked as a student presentation)

- Noise2noise: a mapping between pairs of independently degraded versions of the same training image, requires availability of pairs of noisy images (Lehtinen et. al., 2018)
- Noise2Void: <u>self-supervised</u> training method with "blind-spot" networks – excluding a pixel and learning a mapping from the noisy image to the missing pixel (Krull, Buchholz and Jug, 2019)
- Probabilistic Noise2Void: predict per-pixel intensity distributions (Krull, Vi car and Jug, 2019)

Examples of mapping matched image pairs for image enhancement

- Super resolution: <u>ANNA-PALM</u>, deep STORM, "cross modality" (resolution), PSSR
- 2D → 3D refocusing, Deep-Z

Could be picked as a student presentation

ANNA-PALM: DL accelerates superresolution localization microscopy

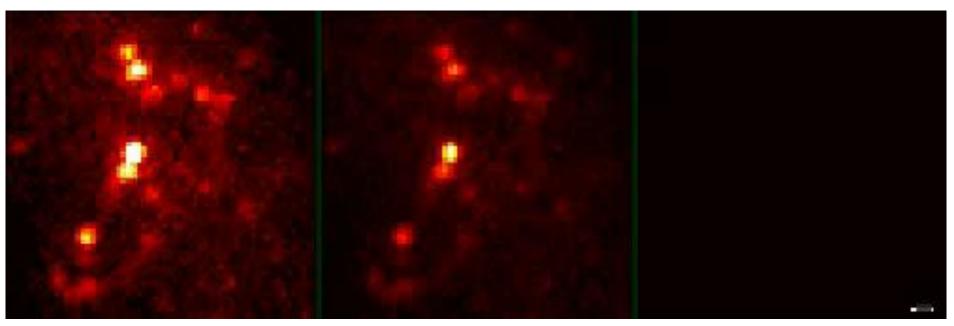
- ANNA-PALM (slightly) preceded CARE
- exploits the structural redundancy of most biological images to reconstruct high-quality images from under-sampled localization microscopy data
- Reducing total number of frames and independent localizations without trading off spatial resolution

Photoactivated localization microscopy (PALM)

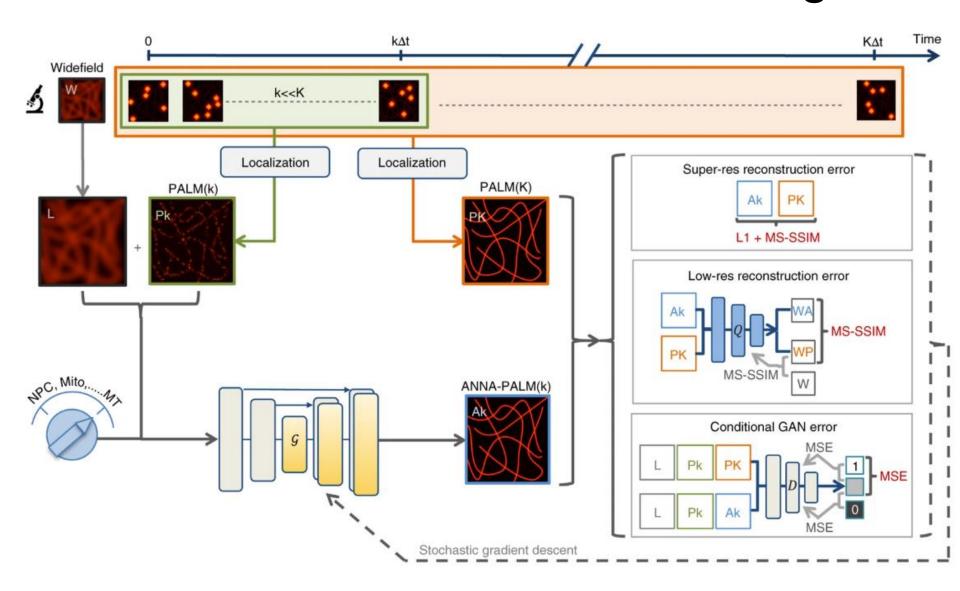
diffraction-limited image sequences

Widefield

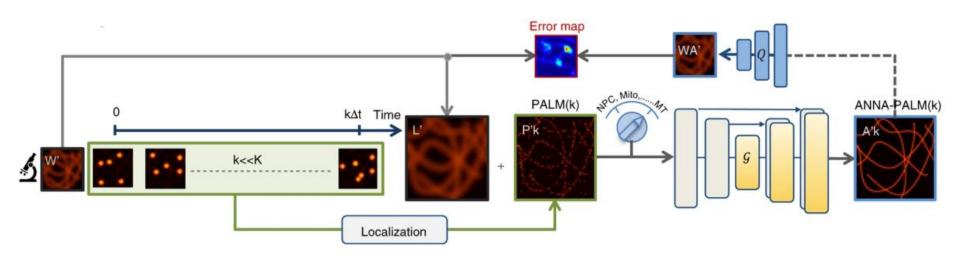
Localization



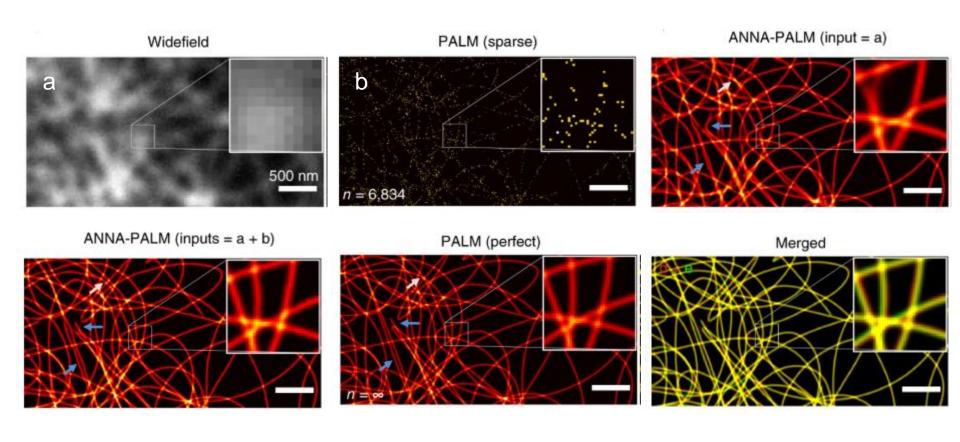
ANNA-PALM network training



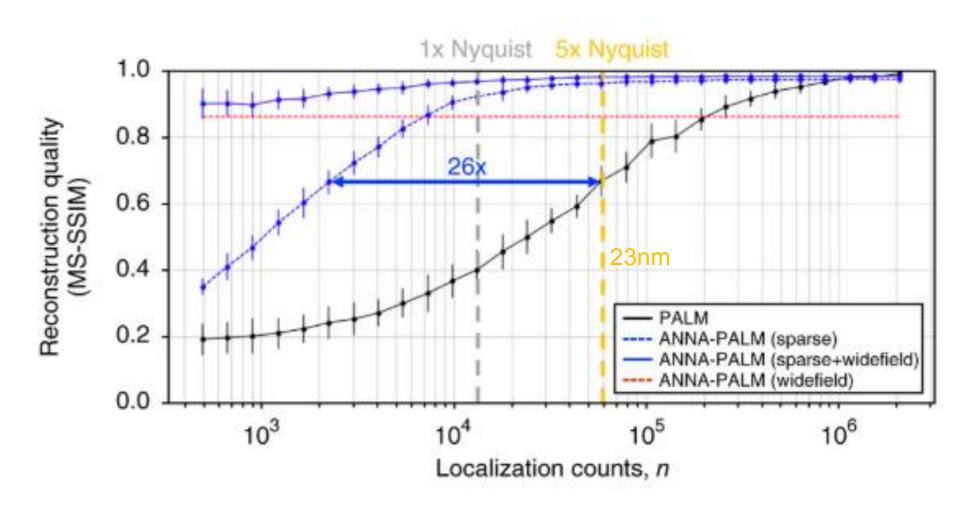
ANNA-PALM inference



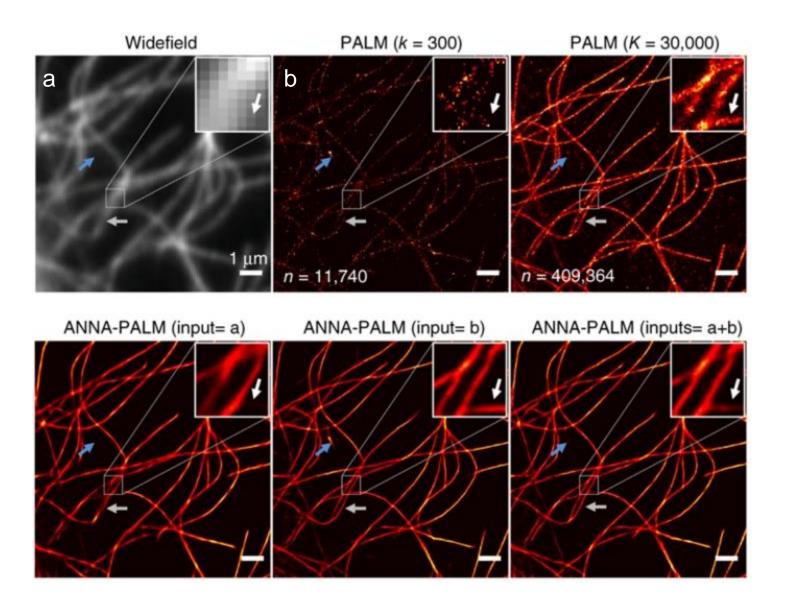
Validation of ANNA-PALM on simulated images



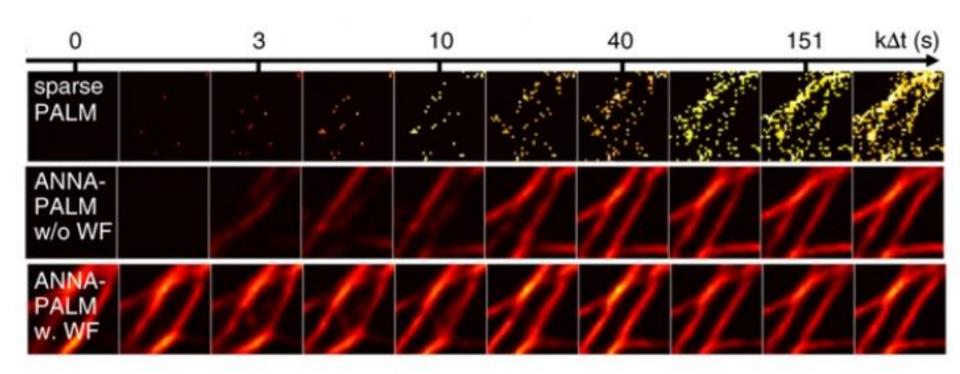
Validation of ANNA-PALM on simulated images



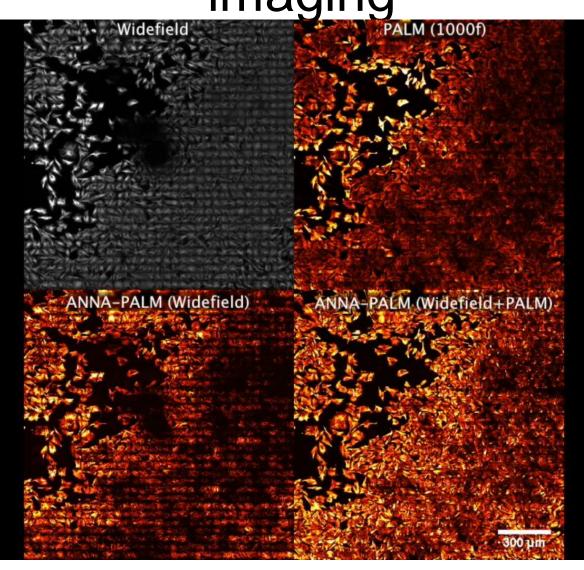
ANNA-PALM imaging of microtubules



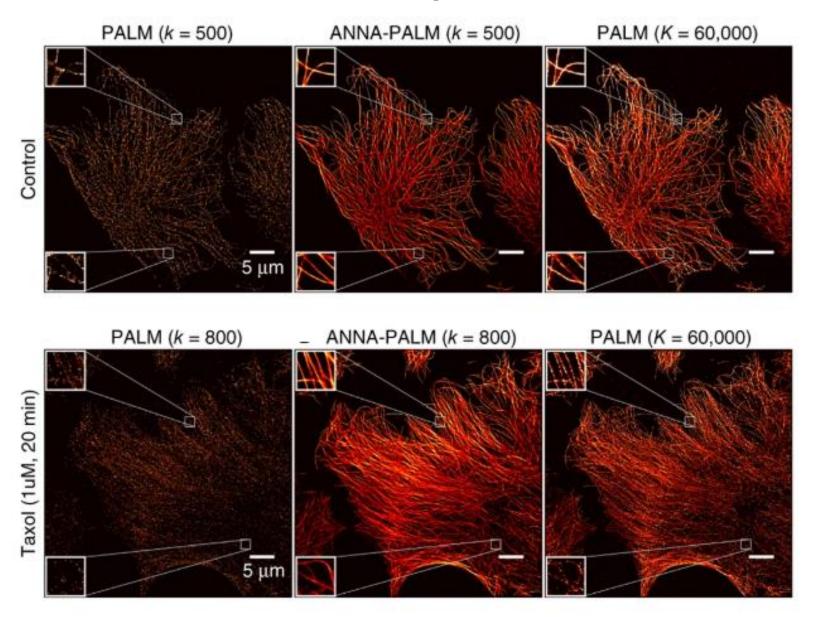
ANNA-PALM imaging of microtubules



High-throughput super-resolution imaging

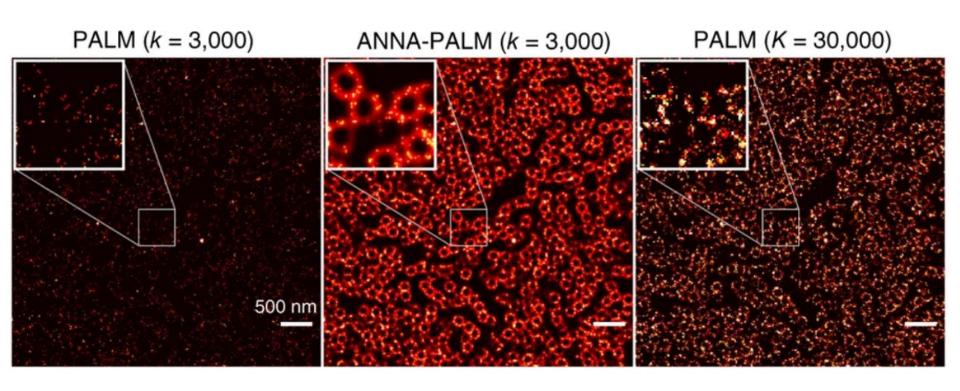


Robustness to perturbations



Ouyang et al. (2018)

Training with microtubules <u>and</u> (one) nuclear pores (imaged here)



Deep STORM

(the Israeli connection!)

Research Article

Vol. 5, No. 4 / April 2018 / Optica 458

Optica

Deep-STORM: super-resolution single-molecule microscopy by deep learning

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Received 13 February 2018; accepted 13 March 2018 (Doc. ID 323156); published 12 April 2018

Pick a paper/s and schedule yourself for class presentation

- Preferably from the list I distributed
- Include key + new (ones that I did not read yet) papers
- One (or more from a common "topic") paper
- Pair > single
- These paper are LONG! (compared to CS papers)
- Focus on the important stuff, in the context of our course: idea & methodology
- Reading tip: you can (mostly) ignore many biological/experimental details.
 - Example: specific molecule names. Very important, but less in the context of our course.

Course projects