



Deep learning and bioimage analysis

Data Driven Life Sciences (DDLS) course

KTH - 2023

Estibaliz Gómez de Mariscal, EMBO Postdoctoral Fellow

Optical Cell Biology Group (Prof. Ricardo Henriques)

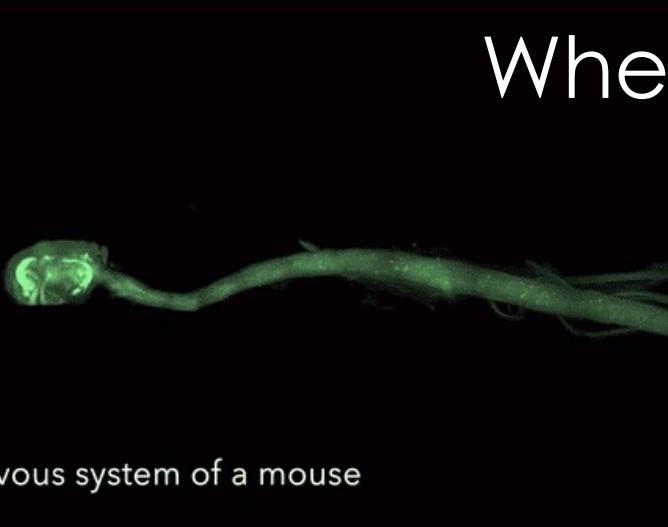
Instituto Gulbenkian de Ciencia

 @gomez_mariscal

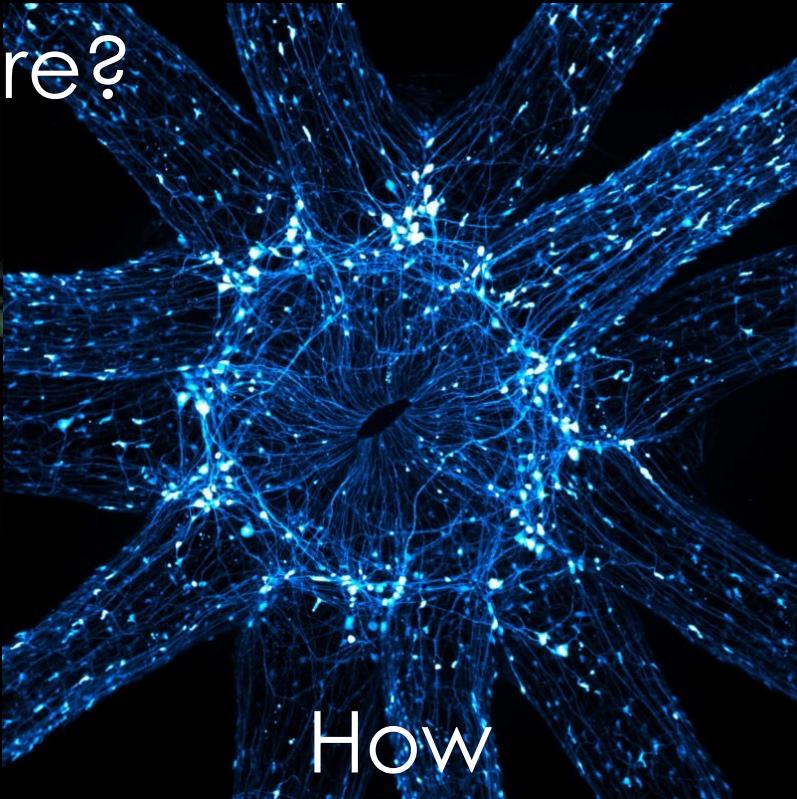
egomez@igc.gulbenkian.pt

Today's lecture

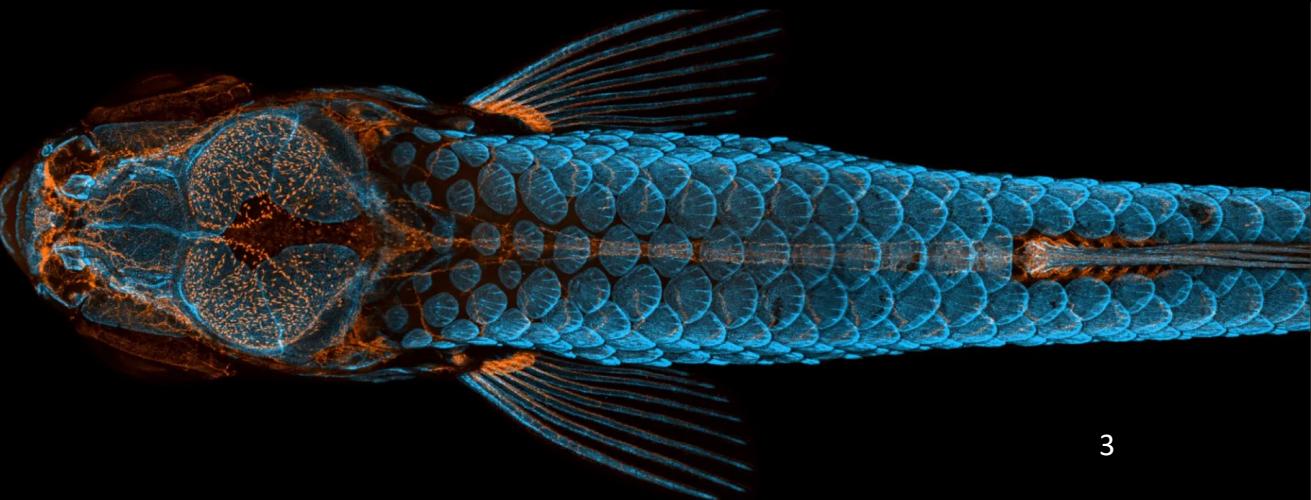
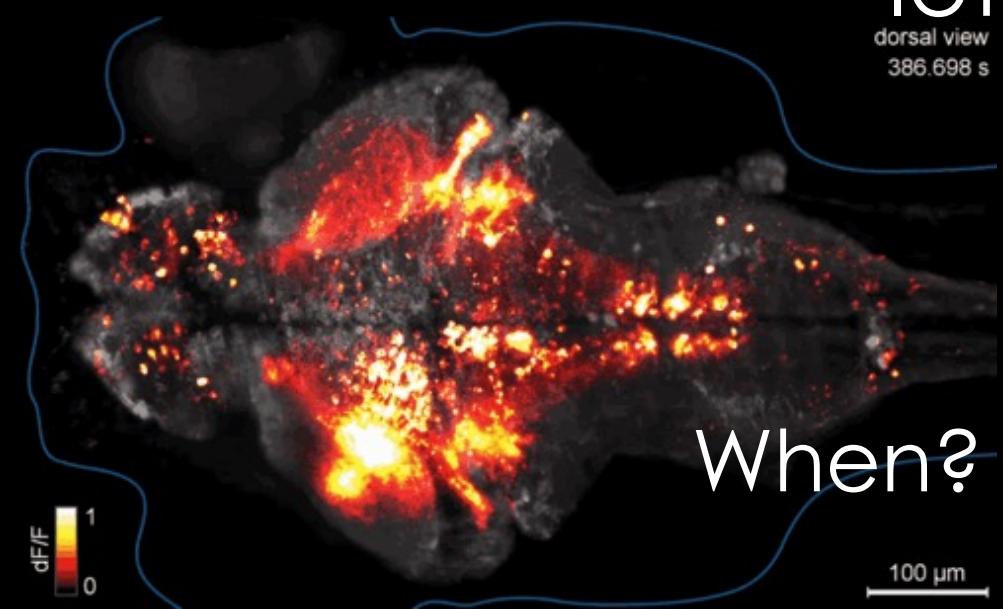
- Biolimage analysis: definition
- Deep learning for image processing
- Segmentation
- Considerations about DL



Where?



Bioimages contain
lot of information



How many cells can we count?

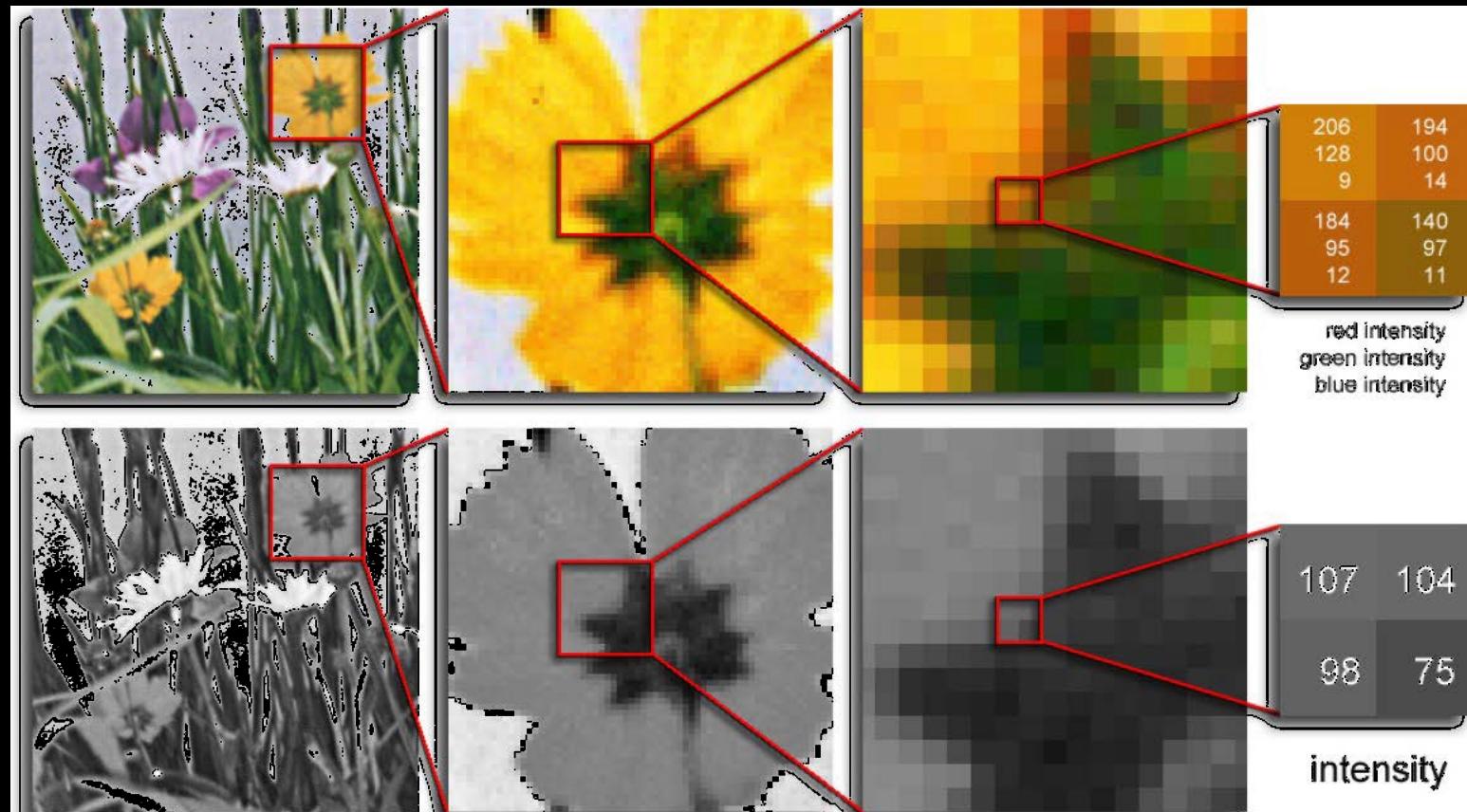


Computational image
processing:

- Precise
- Reproducible
- Transferable
- Automatic → FAST

Digital images

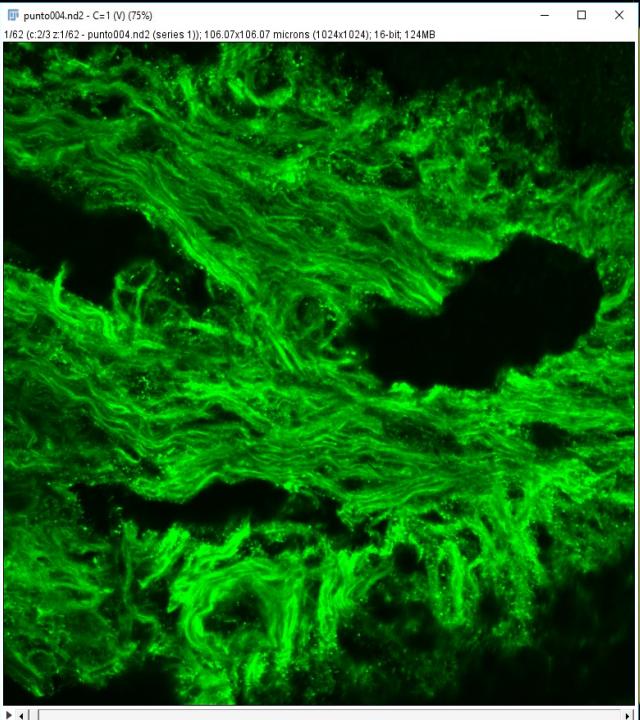
A **digital image** is a mapping of intensities from a 2D grid of (uniformly spaced) discrete points, into a set of numerical values. The grid elements are called **pixels**.



Biolmages: biological information given by numbers

Raw data

Codifies the information contained in the image



| | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|----|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|
| 0 | 0.913862 | 0.984625 | 0.21835 | 0.040914 | 0.745988 | 0.234247 | 0.988077 | 0.319169 |
| 1 | 0.593781 | 0.801641 | 0.283423 | 0.249029 | 0.375144 | 0.134311 | 0.251072 | 0.368147 |
| 2 | 0.536699 | 0.396945 | 0.579795 | 0.990739 | 0.615816 | 0.205092 | 0.0636377 | 0.214259 |
| 3 | 0.666719 | 0.4143736 | 0.495552 | 0.870456 | 0.924456 | 0.816899 | 0.712388 | 0.212872 |
| 4 | 0.282093 | 0.424293 | 0.812224 | 0.736462 | 0.798258 | 0.181772 | 0.1963 | 0.180968 |
| 5 | 0.234833 | 0.595228 | 0.623741 | 0.186595 | 0.297905 | 0.879915 | 0.61341 | 0.0462801 |
| 6 | 0.821762 | 0.491471 | 0.268724 | 0.255439 | 0.127357 | 0.541123 | 0.134237 | 0.762314 |
| 7 | 0.548848 | 0.490773 | 0.985423 | 0.125993 | 0.268893 | 0.8646981 | 0.51265 | 0.719297 |
| 8 | 0.218118 | 0.325782 | 0.459472 | 0.8118880 | 0.288139 | 0.181945 | 0.897689 | 0.719585 |
| 9 | 0.525016 | 0.255971 | 0.157872 | 0.426954 | 0.87146 | 0.324984 | 0.978575 | 0.459743 |
| 10 | 0.231169 | 0.328559 | 0.393136 | 0.87629 | 0.559601 | 0.185497 | 0.341358 | 0.176663 |
| 11 | 0.348081 | 0.410349 | 0.743876 | 0.236652 | 0.524382 | 0.857343 | 0.712128 | 0.445586 |
| 12 | 0.075596 | 0.392205 | 0.00025881 | 0.958719 | 0.544845 | 0.237594 | 0.76893 | 0.167997 |
| 13 | 0.51858 | 0.987361 | 0.955754 | 0.0792741 | 0.117125 | 0.8337119 | 0.192673 | 0.856865 |
| 14 | 0.989562 | 0.532313 | 0.829296 | 0.276368 | 0.498579 | 0.165455 | 0.365422 | 0.037861 |
| 15 | 0.929997 | 0.177880 | 0.594913 | 0.858331 | 0.510879 | 0.029394 | 0.251428 | 0.458976 |
| 16 | 0.572548 | 0.429081 | 0.565412 | 0.352366 | 0.995376 | 0.888374 | 0.248578 | 0.809459 |
| 17 | 0.8328735 | 0.107647 | 0.356802 | 0.996781 | 0.173752 | 0.190765 | 0.9989551 | 0.436135 |
| 18 | 0.793344 | 0.419179 | 0.0466559 | 0.6449771 | 0.8594911 | 0.213729 | 0.3862644 | 0.212385 |
| 19 | 0.180833 | 0.8998789 | 0.281579 | 0.168074 | 0.769454 | 0.19305 | 0.831869 | 0.876054 |
| 20 | 0.2435 | 0.310843 | 0.520687 | 0.830611 | 0.592553 | 0.980714 | 0.643541 | 0.534982 |
| 21 | 0.631555 | 0.197771 | 0.0288182 | 0.279186 | 0.419381 | 0.8029542 | 0.561324 | 0.369116 |
| 22 | 0.429872 | 0.261335 | 0.661441 | 0.644851 | 0.899366 | 0.838013 | 0.459745 | 0.0756821 |
| 23 | 0.488912 | 0.182647 | 0.143884 | 0.358812 | 0.392998 | 0.721193 | 0.895807 | 0.145355 |
| 24 | 0.283615 | 0.34975 | 0.550145 | 0.544887 | 0.498918 | 0.342482 | 0.379545 | 0.265943 |
| 25 | 0.0023189 | 0.18338 | 0.248245 | 0.980539 | 0.370947 | 0.800439 | 0.217019 | 0.753996 |
| 26 | 0.573237 | 0.902549 | 0.329727 | 0.576902 | 0.30266 | 0.759982 | 0.170411 | 0.141302 |
| 27 | 0.156159 | 0.367303 | 0.539944 | 0.861447 | 0.213495 | 0.116079 | 0.453791 | 0.248593 |
| 28 | 0.591882 | 0.585813 | 0.170423 | 0.299442 | 0.783162 | 0.847421 | 0.867145 | 0.938113 |
| 29 | 0.237085 | 0.114423 | 0.533174 | 0.655568 | 0.463769 | 0.463523 | 0.262685 | 0.954846 |

Metadata

Set of text data providing additional information about the image.

| Key | Value |
|-----------------------------|----------------------------|
| BitDepth | 12 |
| DimensionOrder | X,Y,C,Z |
| Interleaved | false |
| isRGB | false |
| LittleEndian | true |
| PixelFormat | uint16 |
| Series 0 Name | punto004.nd2 (series 1) |
| SizeC | 3 |
| SizeT | 1 |
| SizeX | 1024 |
| SizeY | 1024 |
| SizeZ | 62 |
| - Device | Ti.ZDrive |
| - Step | 0.1 nm |
| Average | 1 |
| AverageToQuality | 0 |
| CH1 (Laser Wavelength) #1 | 408.0 (Laser Power): 100.0 |
| CH1 (Laser Wavelength) #2 | 408.0 (Laser Power): 100.0 |
| CH1 (Laser Wavelength) #3 | 408.0 (Laser Power): 100.0 |
| CH1 (Laser Wavelength) #4 | 408.0 (Laser Power): 100.0 |
| CH2LEMBrightness | 4 |
| CH2LEMEnoughSignalThreshold | 800 |
| CH2LEMInputSignalThreshold | 200 |
| CH2ChannelIndex | 16711680 |
| CH2ChannelName | DAPI |
| CH2ChannelLaserIndex | 0 |
| CH2LaserPower | 100 |
| CH2LaserStimulationPower1 | 0 |
| CH2LaserStimulationPower2 | 0 |
| CH2LaserStimulationPower3 | 0 |
| CH1PMTHighVoltage | 121 |
| CH1PMTOffset | 9 |
| CH2 (Laser Wavelength) #1 | 486.0 (Laser Power): 85.6 |
| CH2 (Laser Wavelength) #2 | 486.0 (Laser Power): 85.6 |
| CH2 (Laser Wavelength) #3 | 486.0 (Laser Power): 85.6 |
| CH2 (Laser Wavelength) #4 | 486.0 (Laser Power): 85.6 |
| CH2CLEMBrightness | 4 |
| CH2LEMEnoughSignalThreshold | 800 |
| CH2LEMInputSignalThreshold | 200 |
| CH2ChannelColor | 65280 |
| CH2ChannelName | FITC |
| CH2ChannelLaserIndex | 3 |
| CH2LaserPower | 85.6625 |
| CH2LaserStimulationPower1 | 0 |
| CH2LaserStimulationPower2 | 0 |
| CH2LaserStimulationPower3 | 0 |
| CH2PMTHighVoltage | 78 |

BIO-FORMATS

The solution for reading proprietary microscopy image data and metadata

Digital (bio)-image analysis



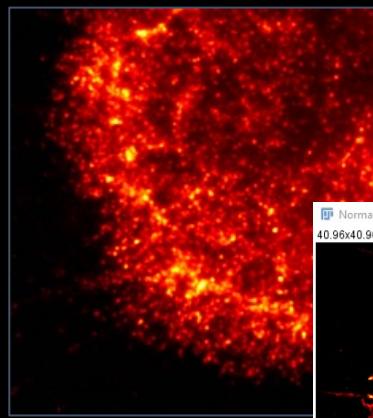
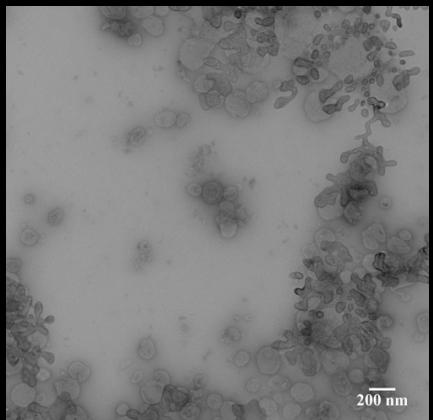
Image processing

Image Processing is any form of data processing for which the input is an image – the output is not necessarily an image.

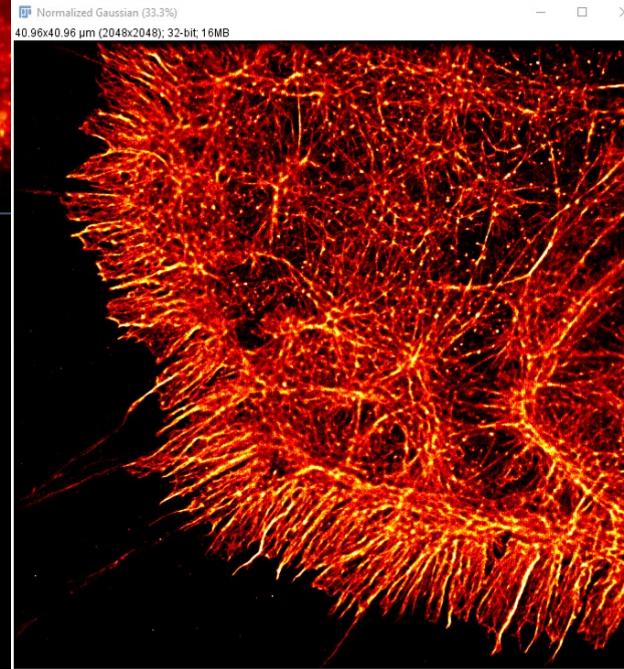
Input: Image - Output: Coordinates (bounding boxes)



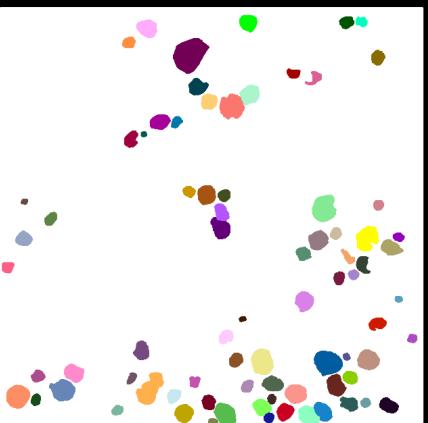
Input: Image
Output: Coordinates (bounding boxes)



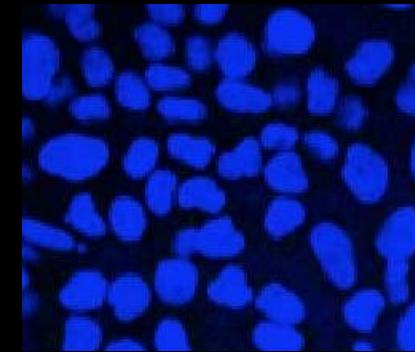
Input: Image
Output: Coordinates (bounding boxes)



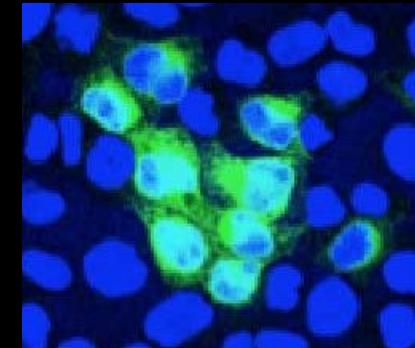
Input: Image
Output: Coordinates (bounding boxes)



Input: Image
Output: Label



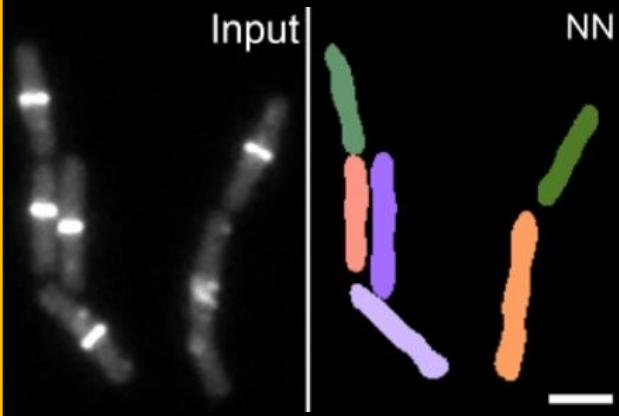
Non infected



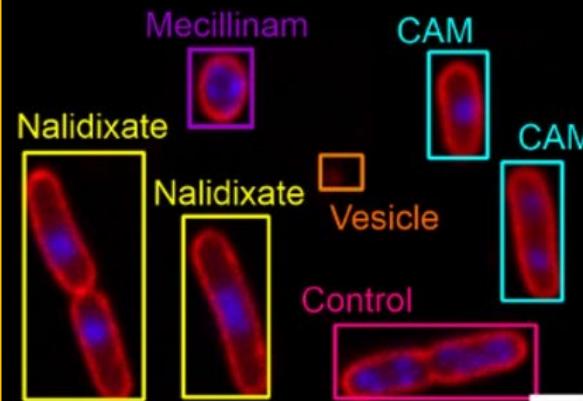
Infected

(Classical) image processing tasks

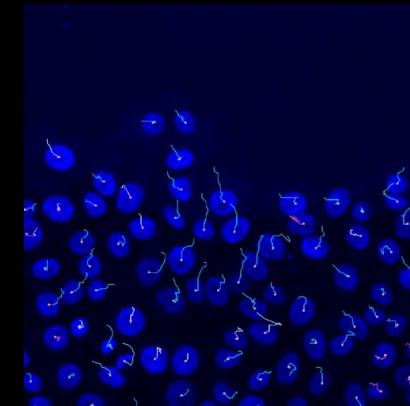
(1) Segmentation



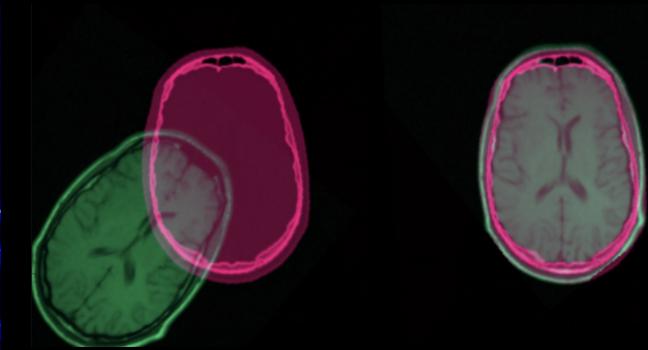
(2) Object detection



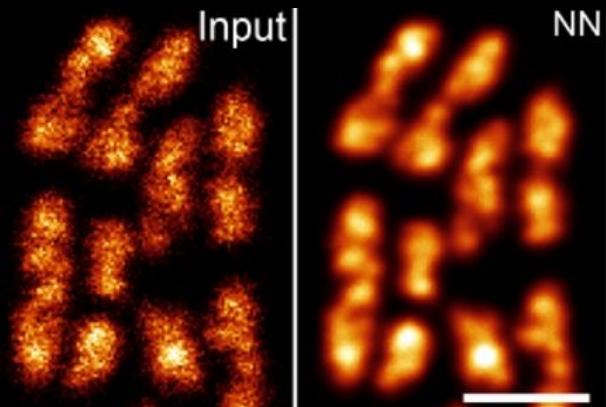
(3) Object tracking



(4) Image registration



(5) Denoising



(6) Super-resolution

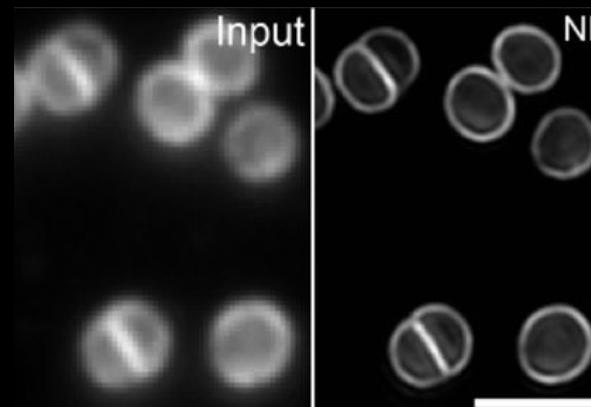
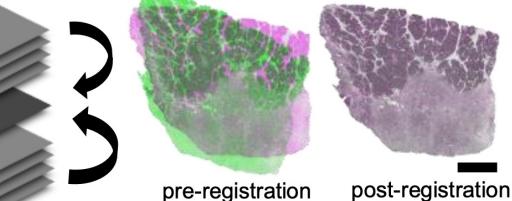


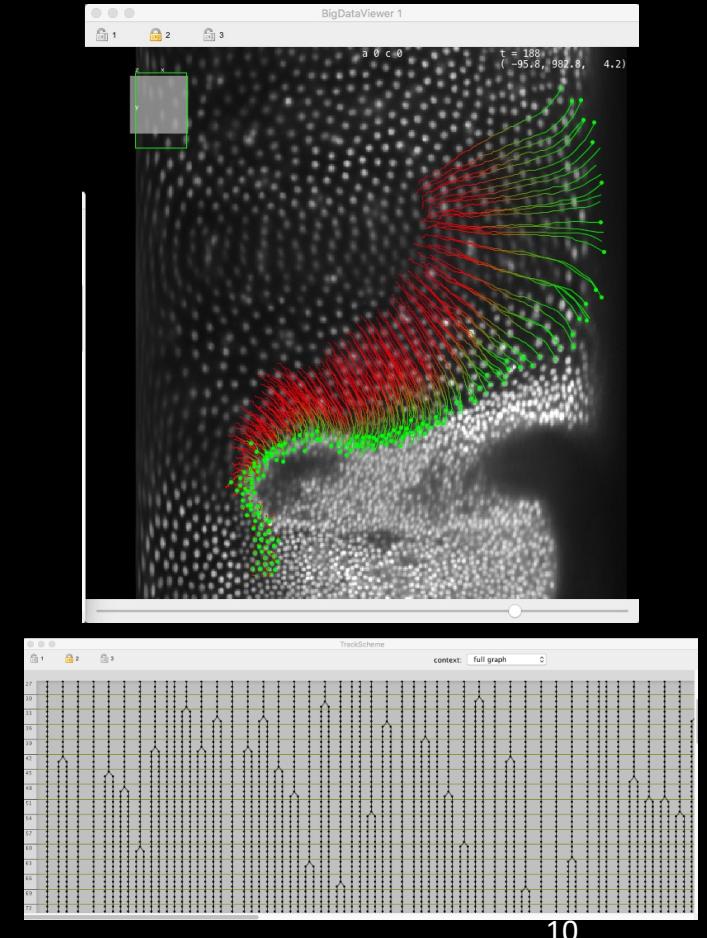
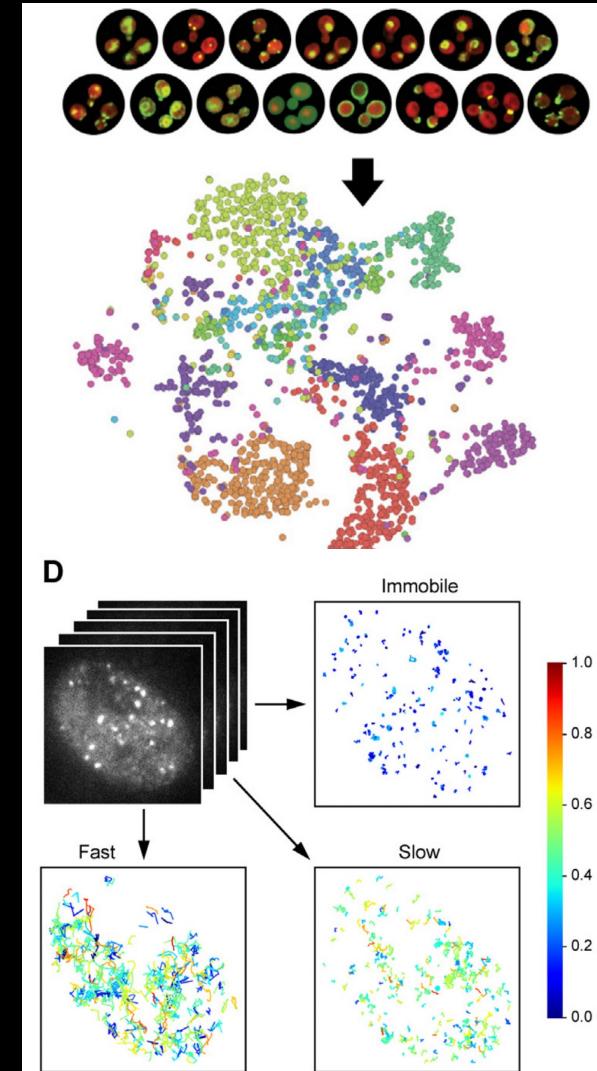
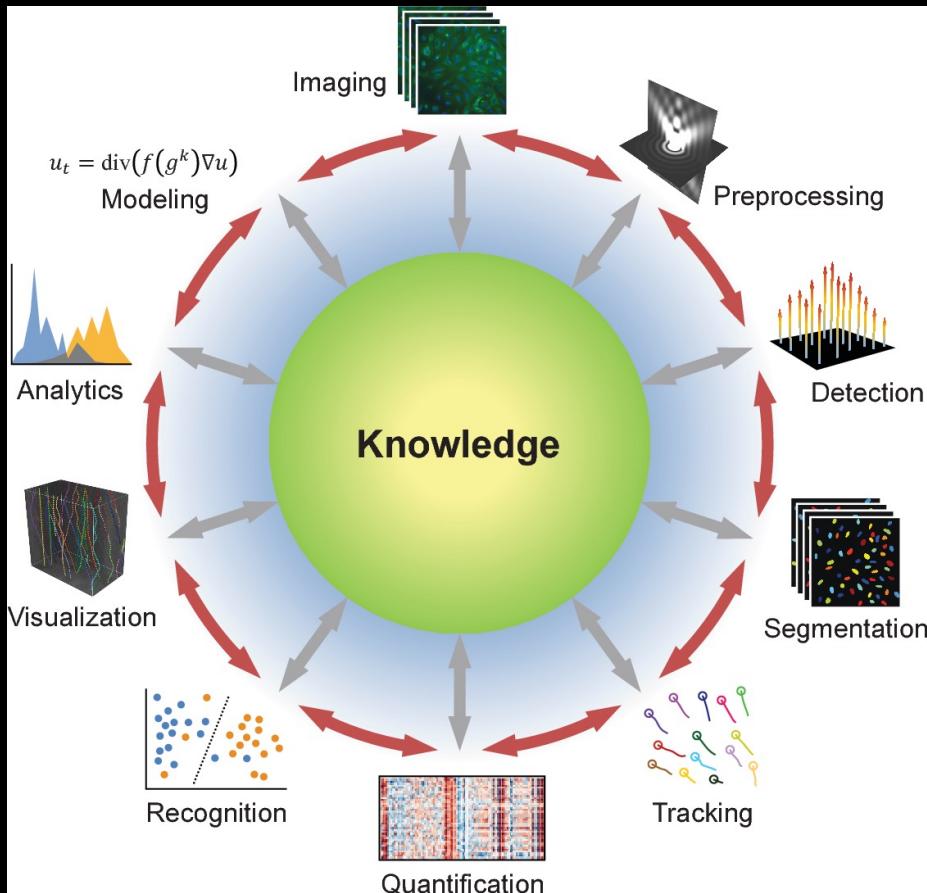
image 1
...
center
...
image n



Christoph Spahn, et al., bioRxiv, 2021
Eliaz Fazeli, et al., F1000Research 2020
Ashley Kiemen, et al., bioRxiv 2020

Biolimage analysis

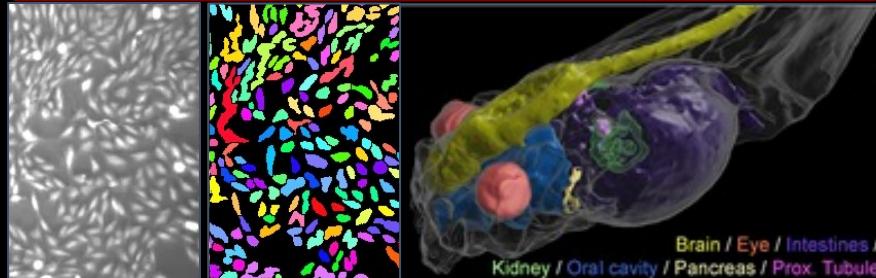
Collection of image processing techniques to extract numerical information from scientific images



Deep learning:
an extremely hot topic in the field 🔥

The deep learning landscape for microscopy imaging

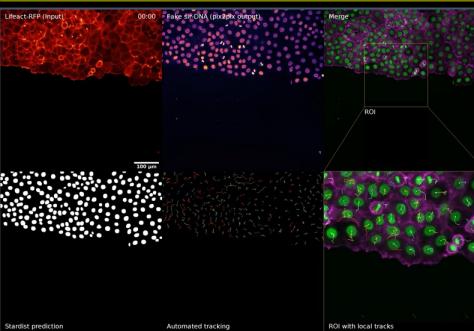
Segmentation



F. Lux & P. Matula, arXiv, 2020

Naert et al., Development 2021

Artificial labelling



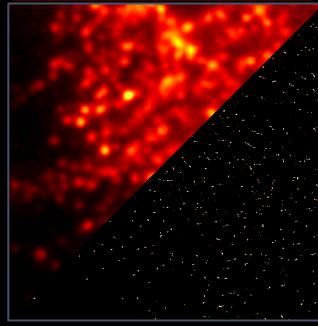
L. Von Chamier, ..., R. Henriques, Nat
Comms 2021

Resolution enhancement & restoration



Imaging modality: LLSM
Specimen: HeLa cell
Labelled structure: Mito, ER, and chromosomes

SMLM



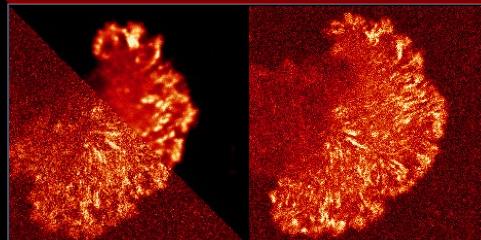
E. Nehme et al.,
Optica, 2018

Detection

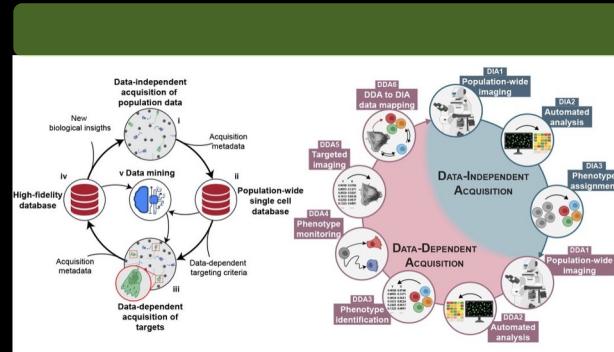


C. Spahn et al., Comm
Biology 2022

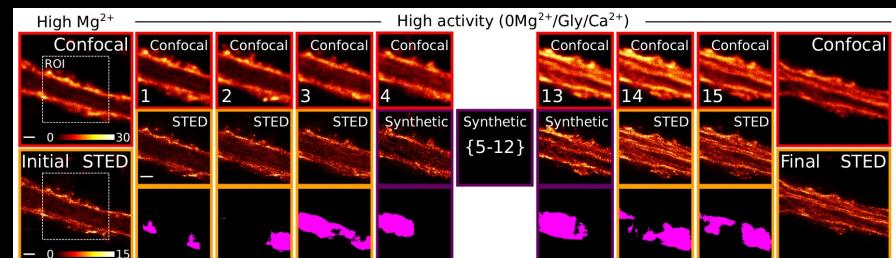
Denoising



L. Von Chamier, ..., R. Henriques, Nature Communications 2021

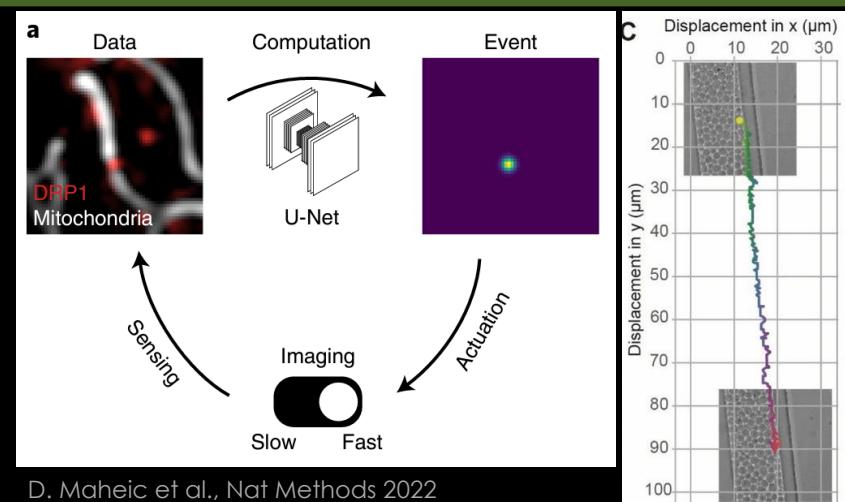


O. André et al., Cell
reports 2023



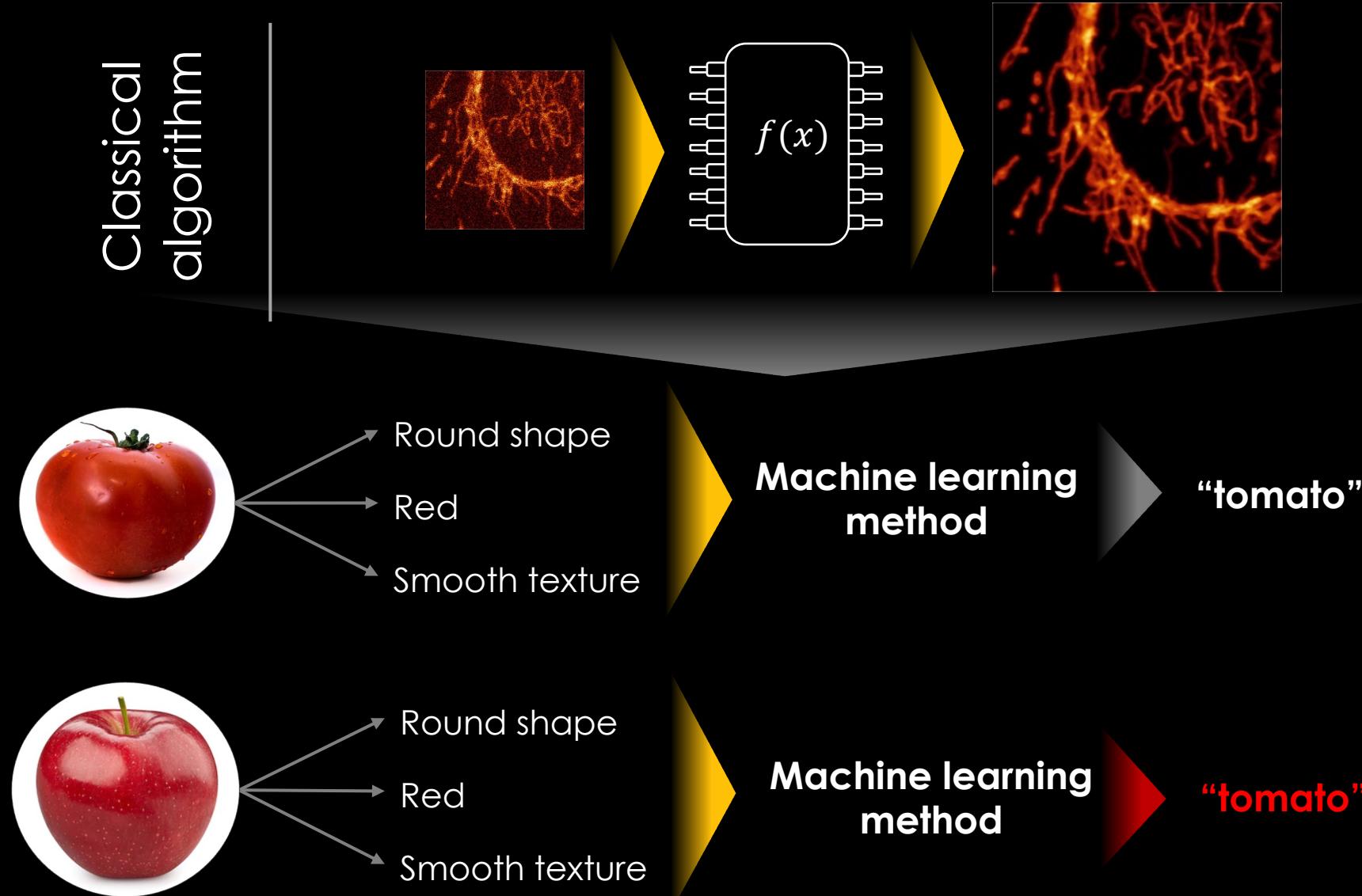
D. Maheic et al., Nat Methods 2022

C.Bouchard et al., bioRxiv 2023

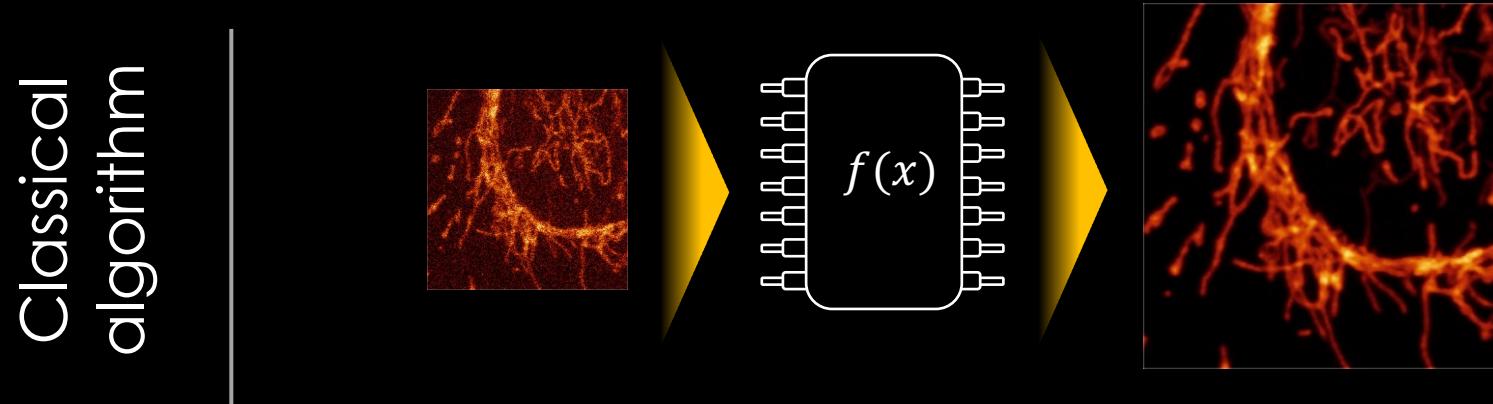


L. Chiron et al., Sci
Reports 2022

Why does deep learning pose a new paradigm?

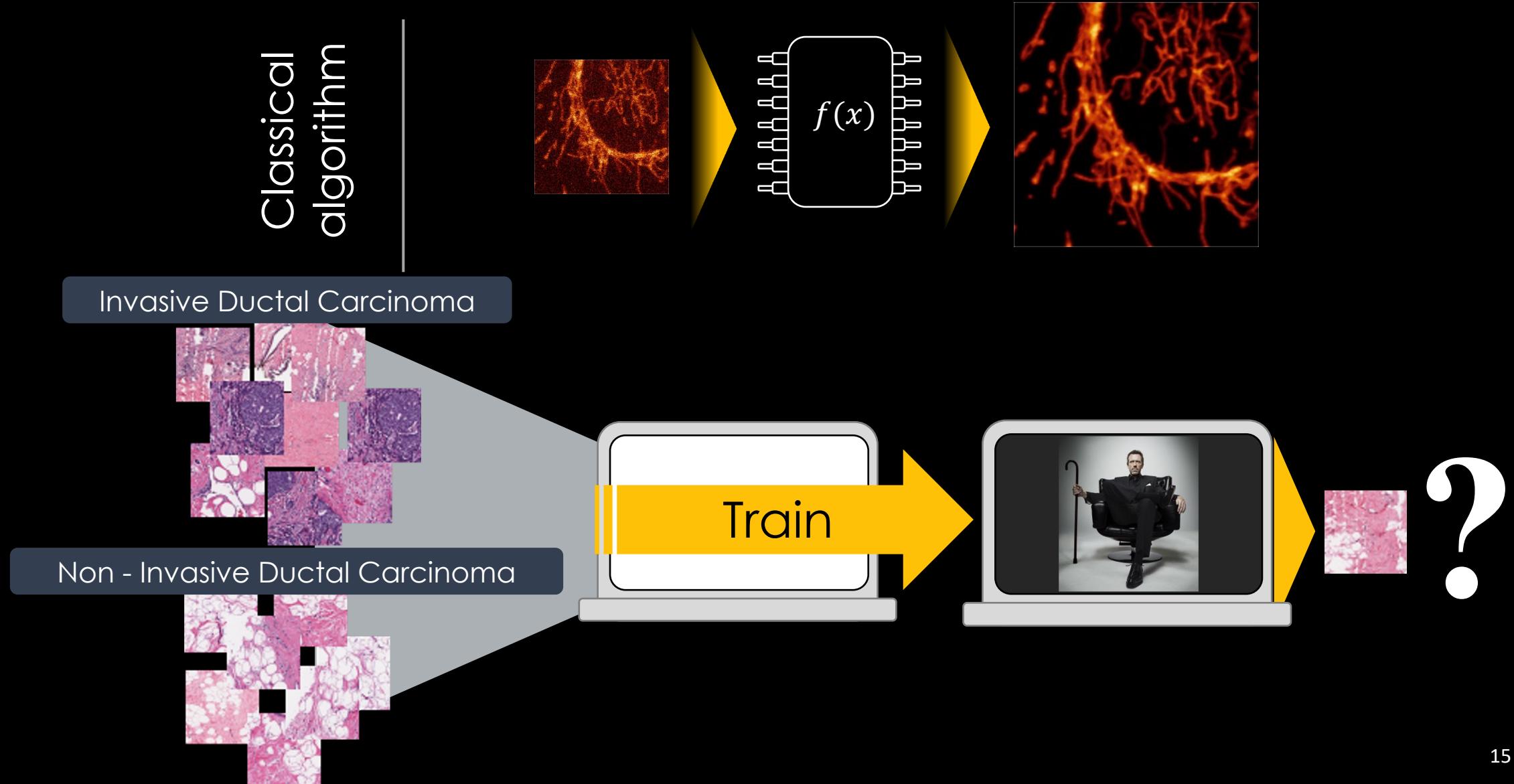


Why does deep learning pose a new paradigm?

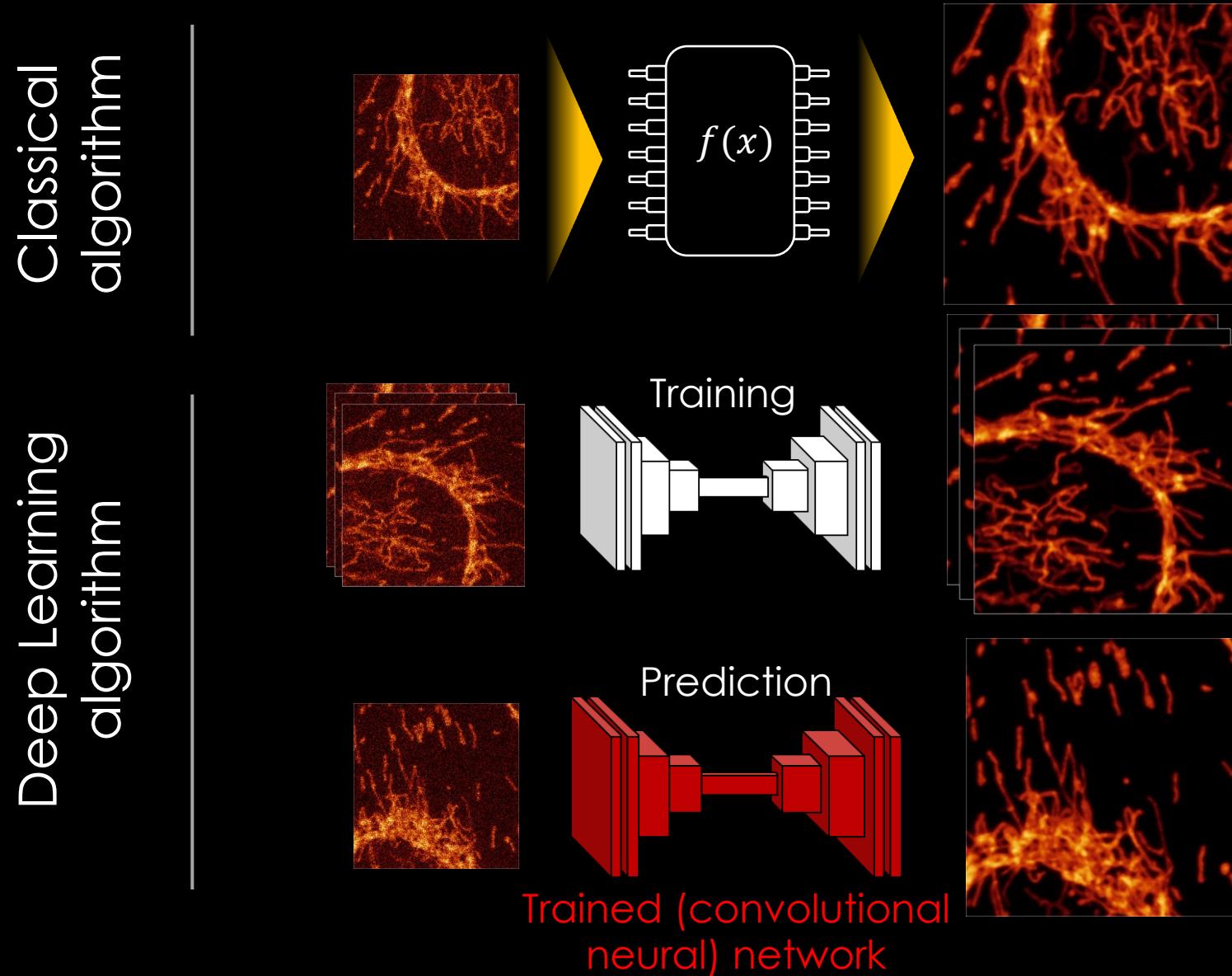


What if the system could learn
automatically from the **data**?

Why does deep learning pose a new paradigm?



Why does deep learning pose a new paradigm?



What are (convolutional) neural networks?

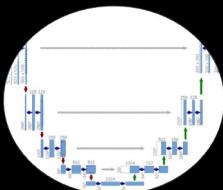
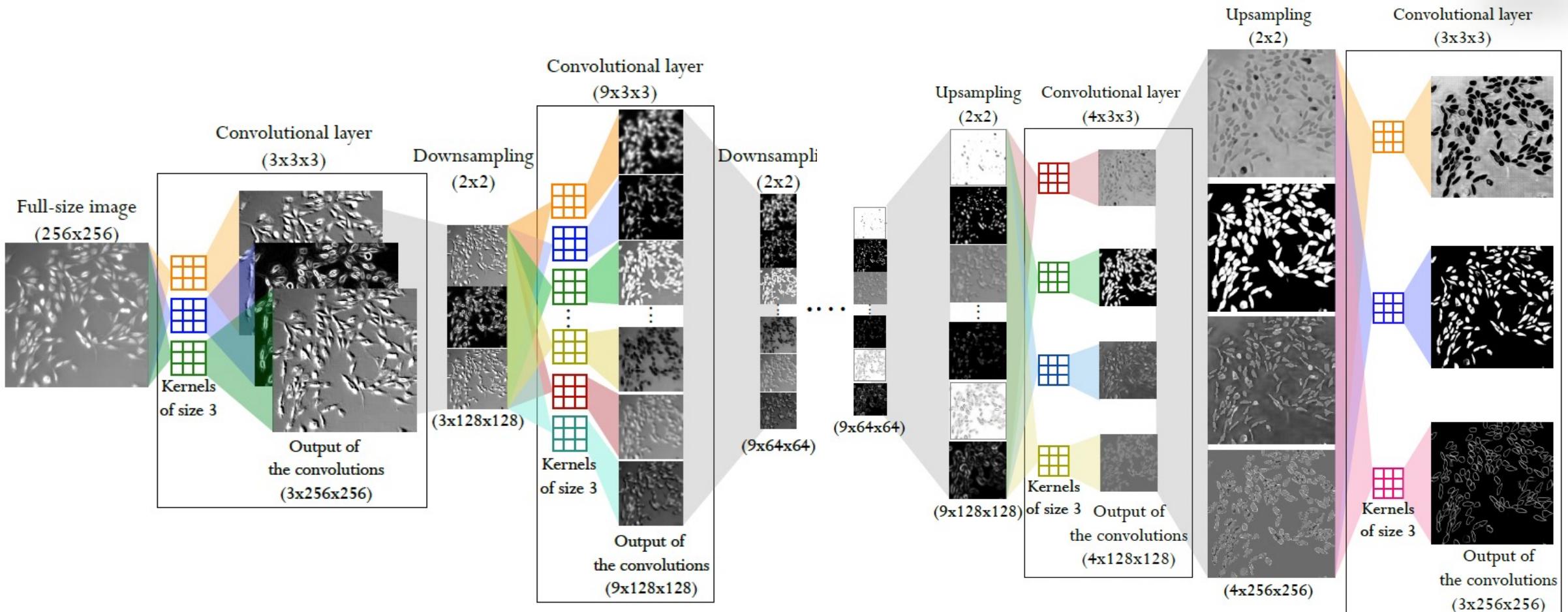
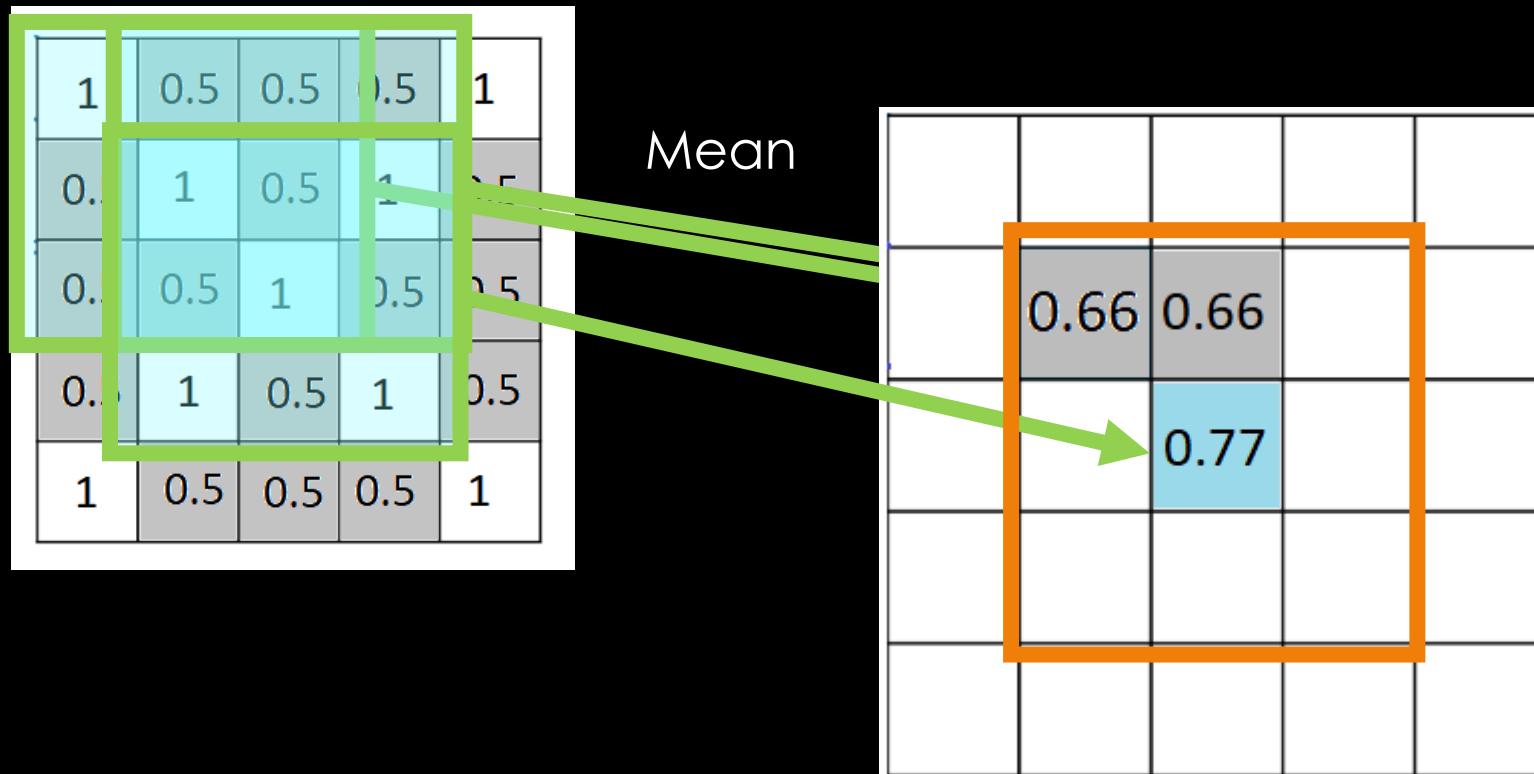


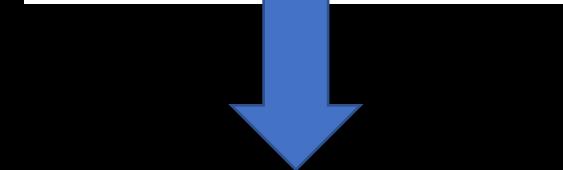
Image segmentation convolutional neural network arquitecture (2D U-Net)



Convolutions

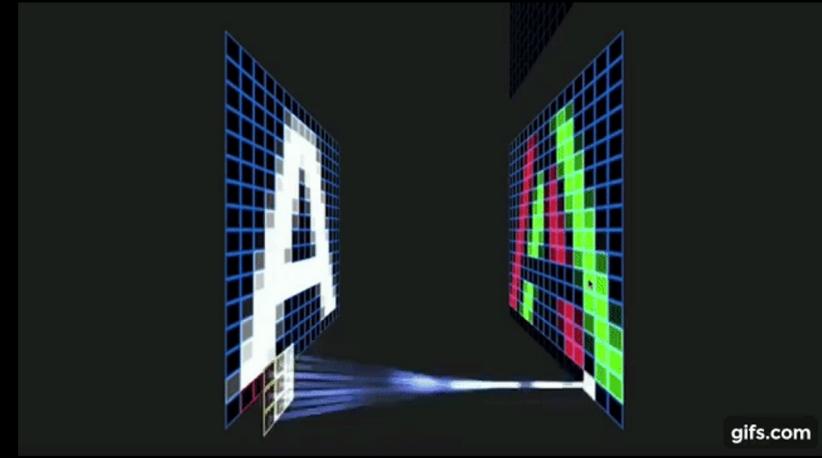
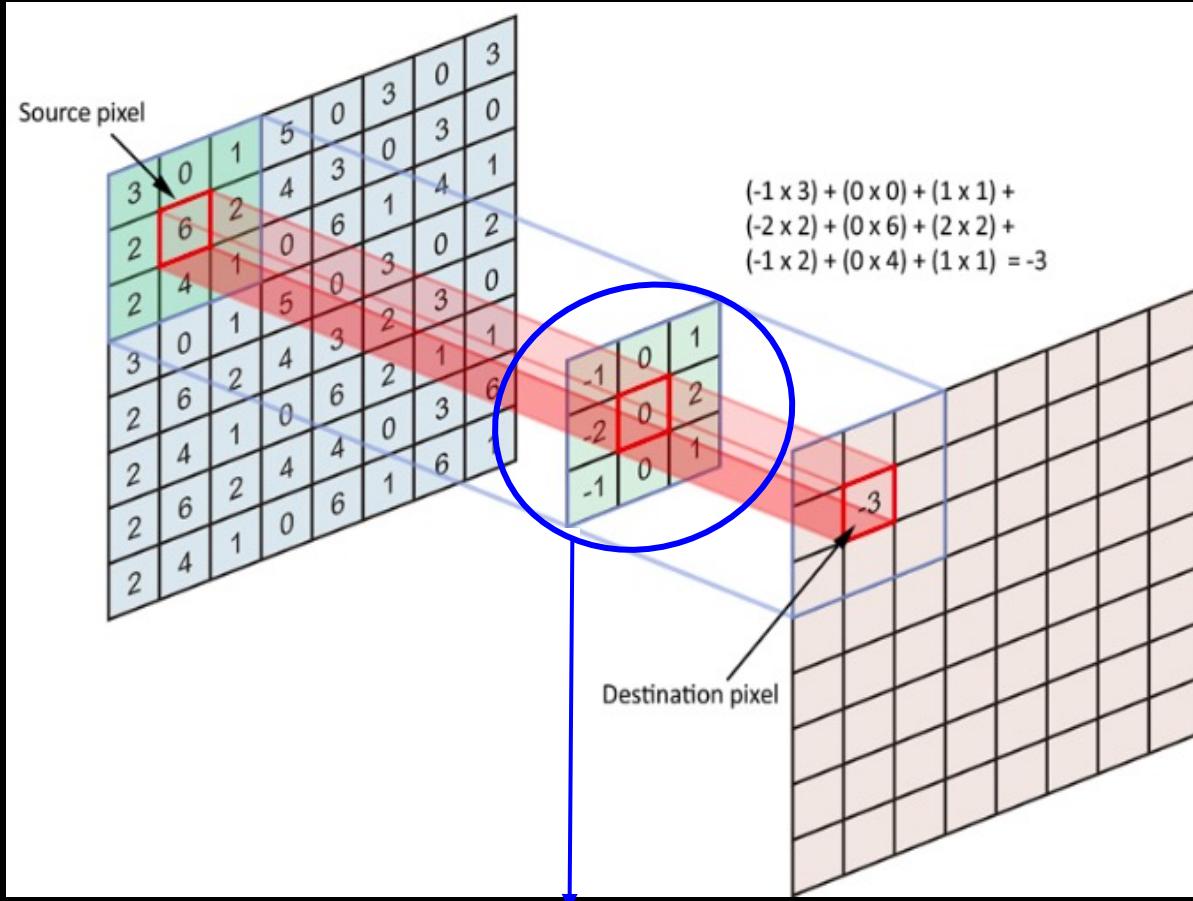


| | | | | |
|-----|-----|-----|-----|-----|
| 1 | 0.5 | 0.5 | 0.5 | 1 |
| 0.5 | 1 | 0.5 | 1 | 0.5 |
| 0.5 | 0.5 | 1 | 0.5 | 0.5 |
| 0.5 | 1 | 0.5 | 1 | 0.5 |
| 1 | 0.5 | 0.5 | 0.5 | 1 |



| | | |
|------|------|------|
| 0.66 | 0.66 | 0.66 |
| 0.66 | 0.77 | 0.66 |
| 0.66 | 0.66 | 0.66 |

Convolutions

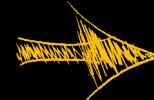


Contextual information around the pixel

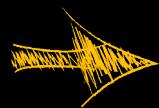
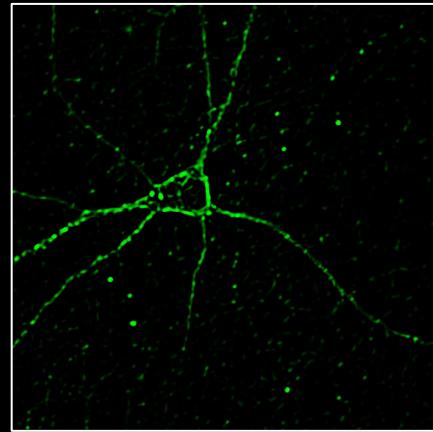
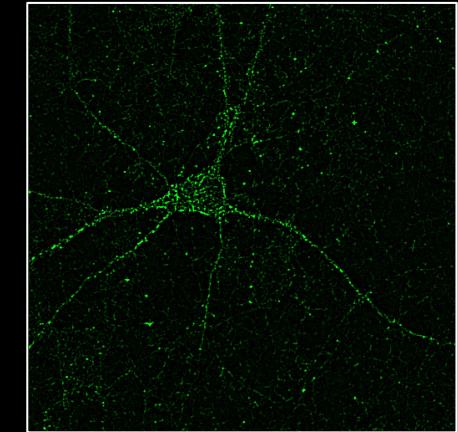
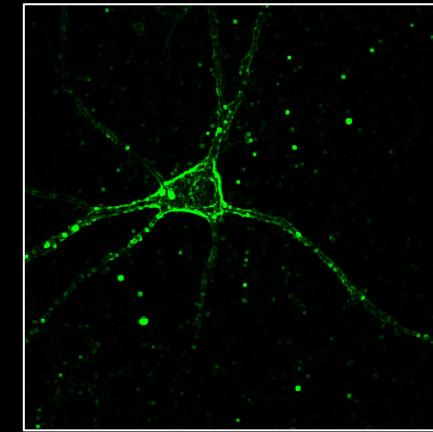
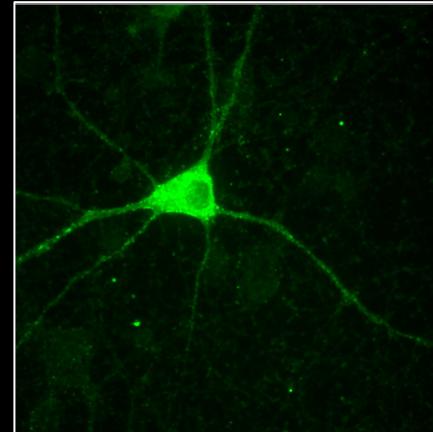
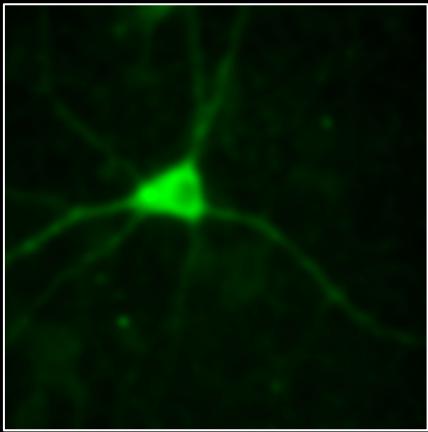
Convolutional kernel: determines de feature to enhance

↓
Spatial filtering

Convolutions



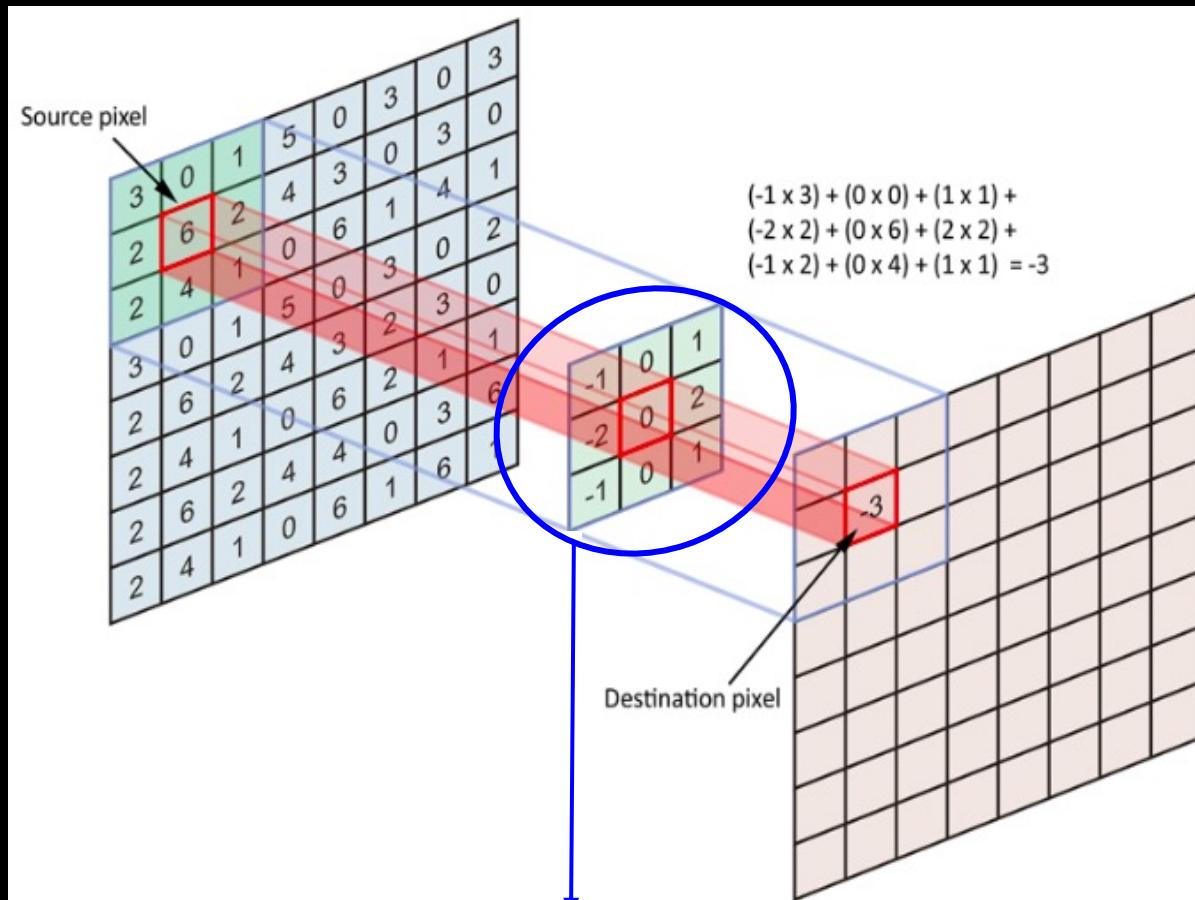
Capacity to quantify and enhance features of interest in the image



Filtered images and image filters can be combined in multiple ways

What if the system could learn the optimal combinations **automatically** from the **data**?

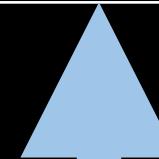
What are (convolutional) neural networks?



Convolutional kernel: determines de feature to enhance

Trainable filter (convolutional layer)

| | | |
|----------|-----------|----------|
| w_{00} | $w_{01}b$ | w_{02} |
| w_{10} | w_{11} | w_{12} |
| w_{20} | w_{21} | w_{22} |

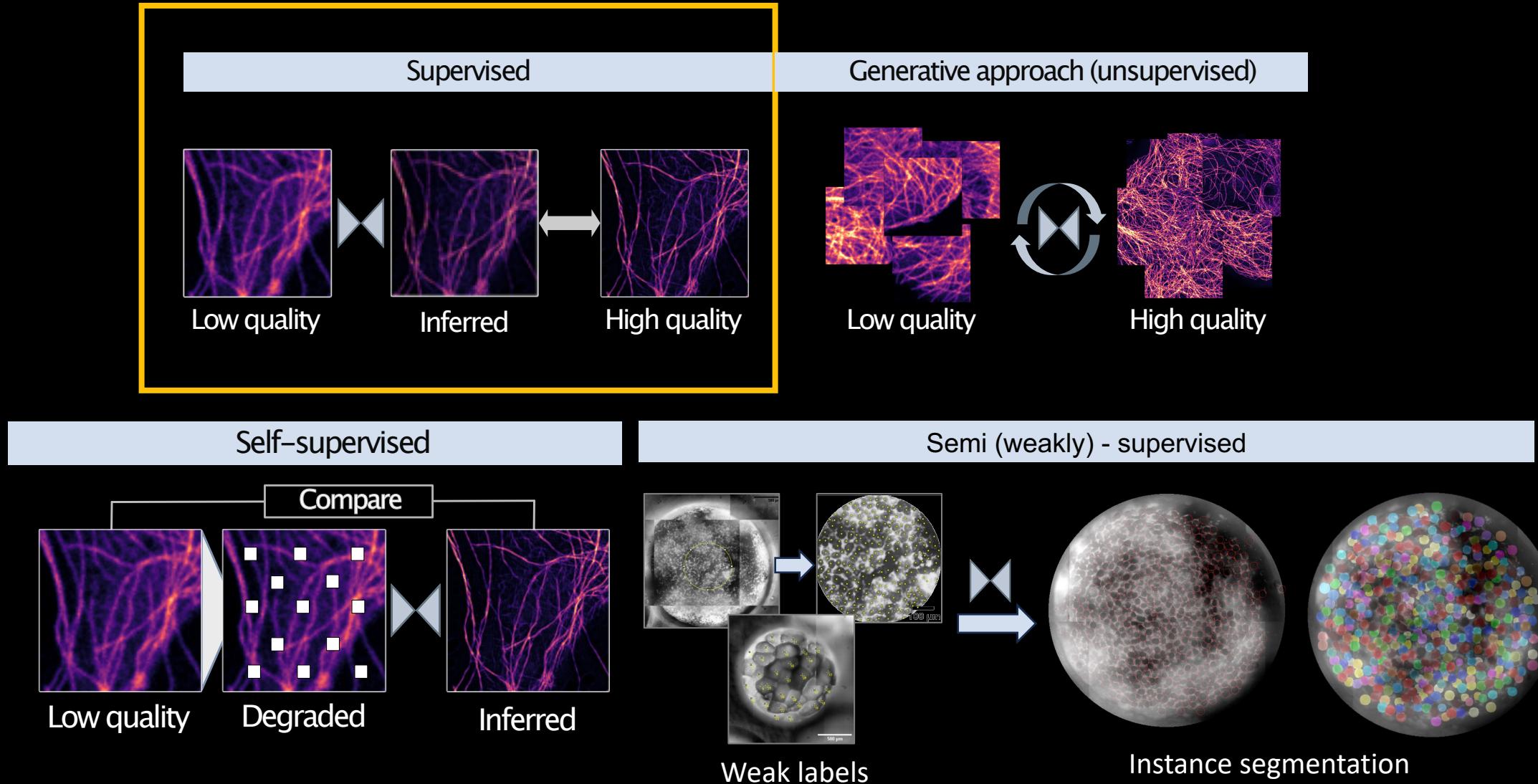


Note: Each unit in the kernel will have its weight, but each convolutional filter will also have a bias:

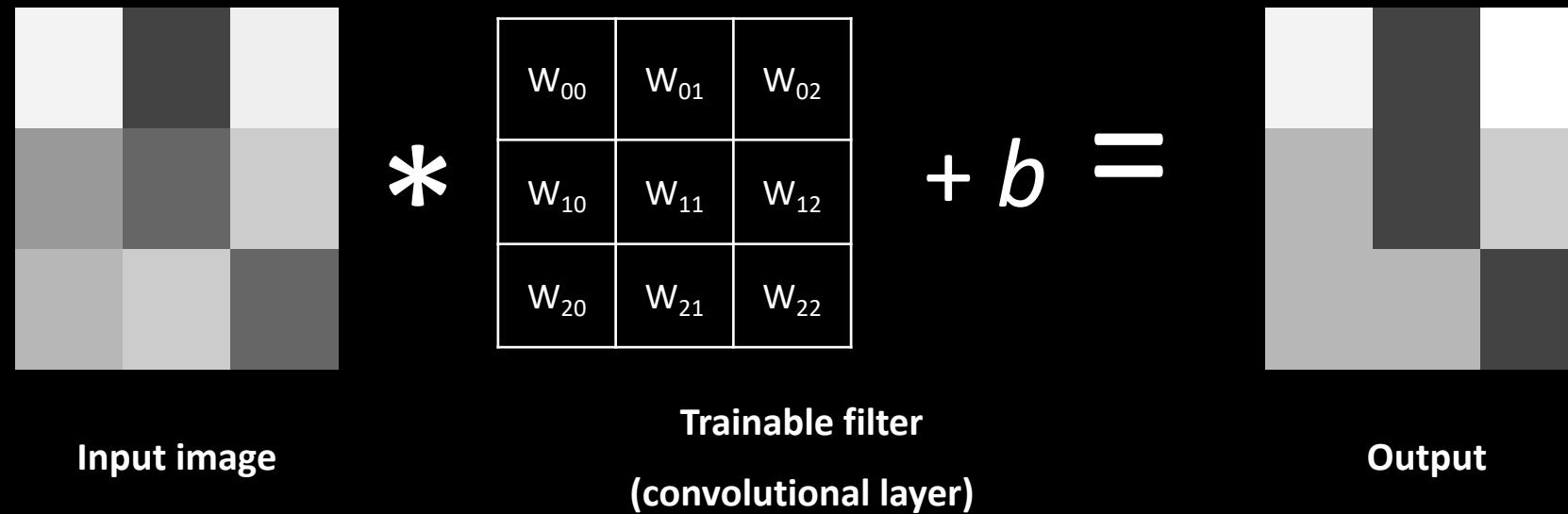
$$C(x) = W \otimes x + b,$$

where x is an input image

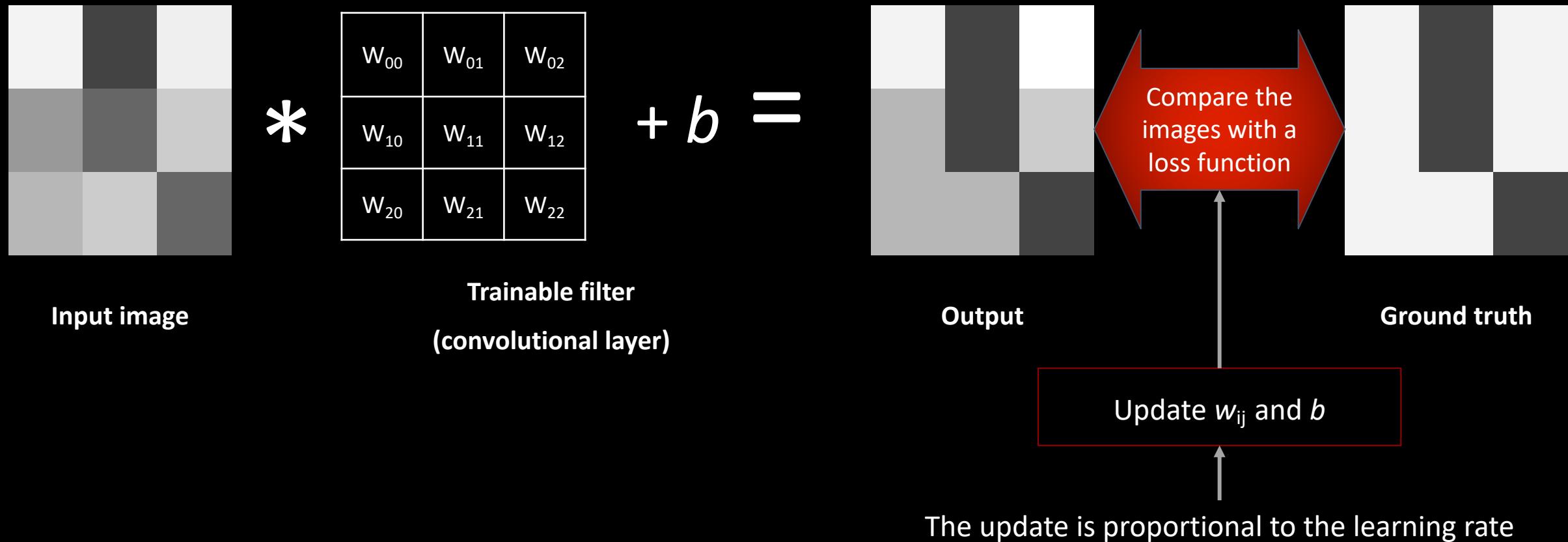
The learning process



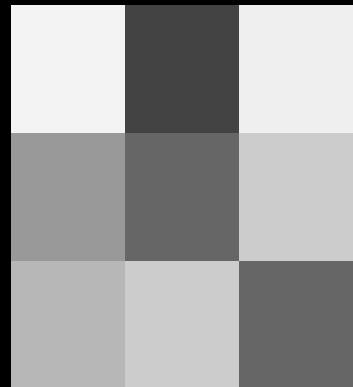
Supervised CNNs training



Supervised CNNs training



Supervised CNNs training

 $*$

| | | |
|----------|----------|----------|
| W_{00} | W_{01} | W_{02} |
| W_{10} | W_{11} | W_{12} |
| W_{20} | W_{21} | W_{22} |

 $+ b =$ 

Input image

Trainable filter
(convolutional layer)

Output

Ground truth

Supervised CNNs training: backpropagation

- Optimization → Gradient descent

- Gradients computation → Backpropagation (use the chain rule for derivatives):

After each forward pass through the network, a backward pass is performed to adjust the model's parameters (weights and biases) according to the error made by the output of the network.

Loss function: quantitative measure of the error

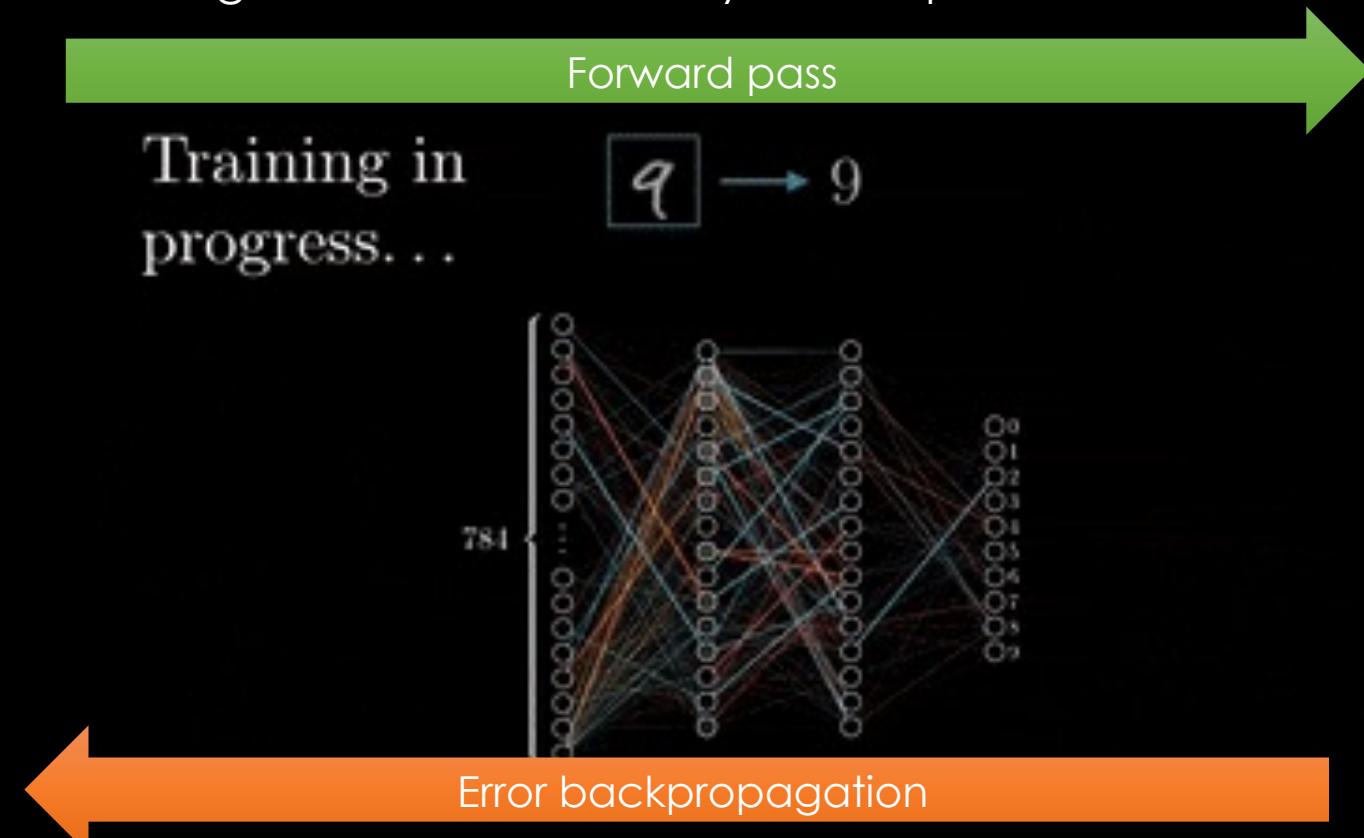
Learning rate: proportion used to update the parameters on each pass

Most used loss functions:

- Mean Squared Error (MSE or L1)
- Mean Absolute Error (MAE or L2)
- Binary Cross Entropy (Categorical cross entropy)

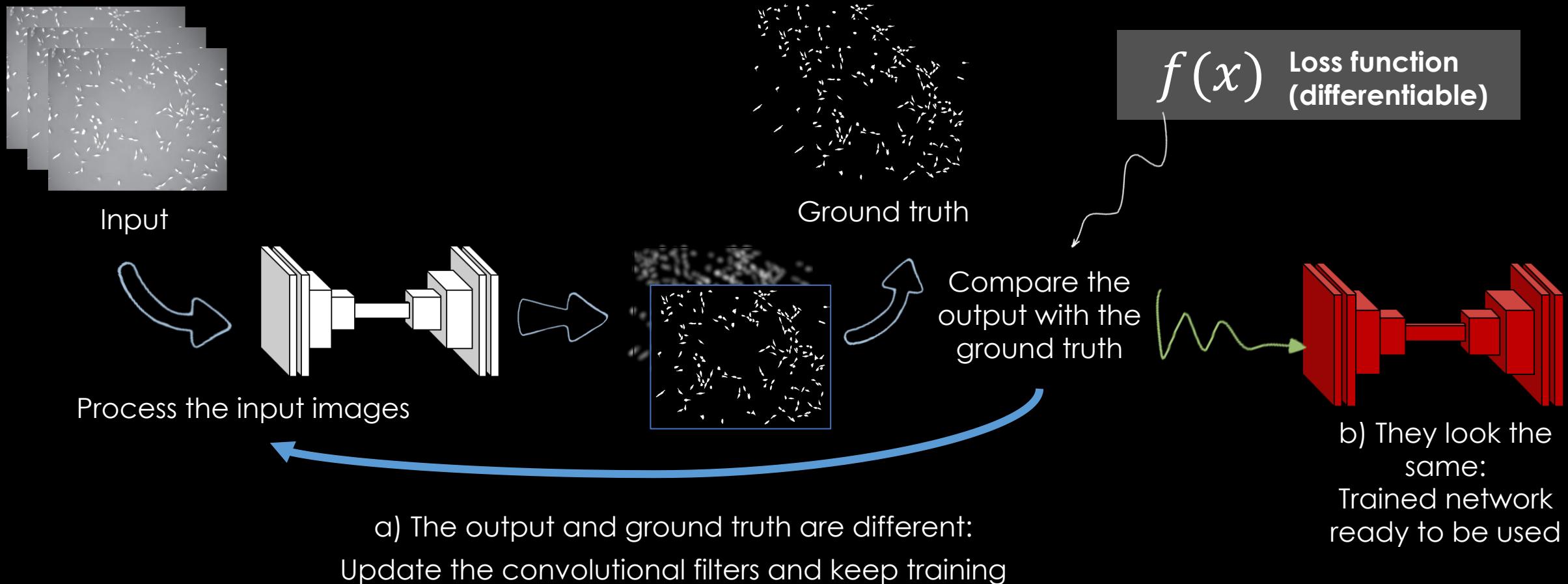
Introduced in 1960s

Popularized by Rumelhart, Hinton and Williams in "Learning representations by back-propagating errors", 1989

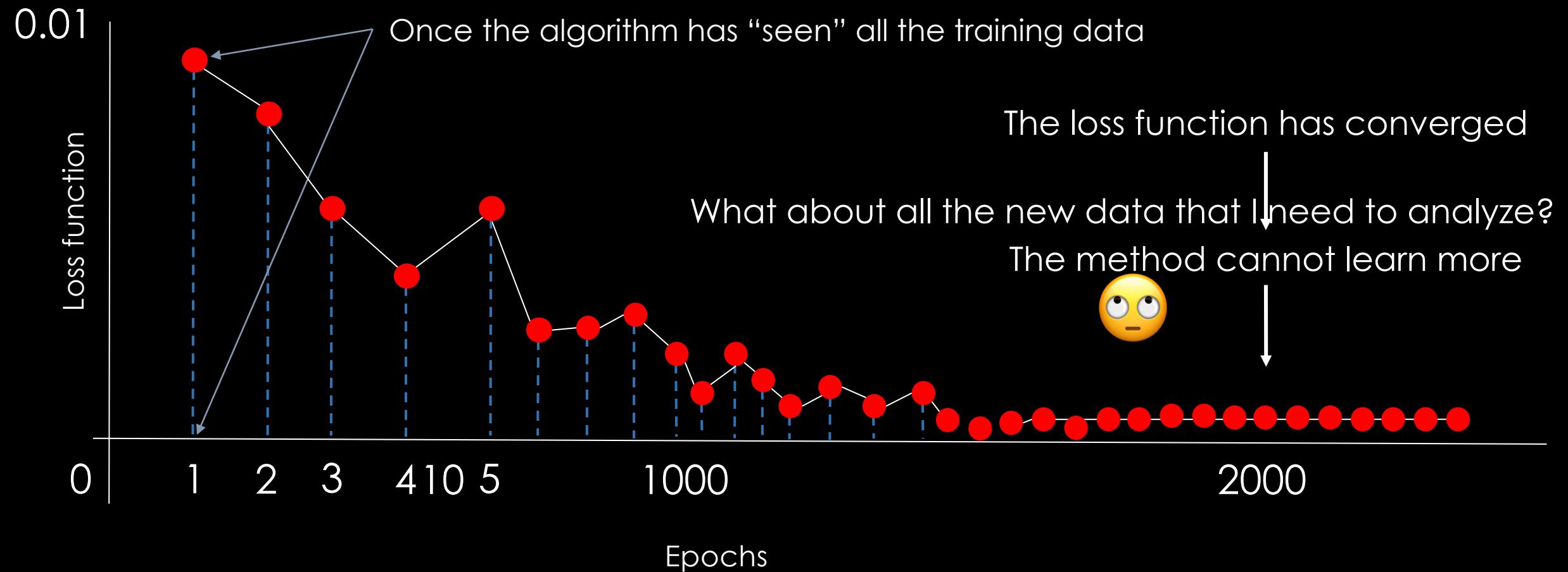


Supervised CNNs training

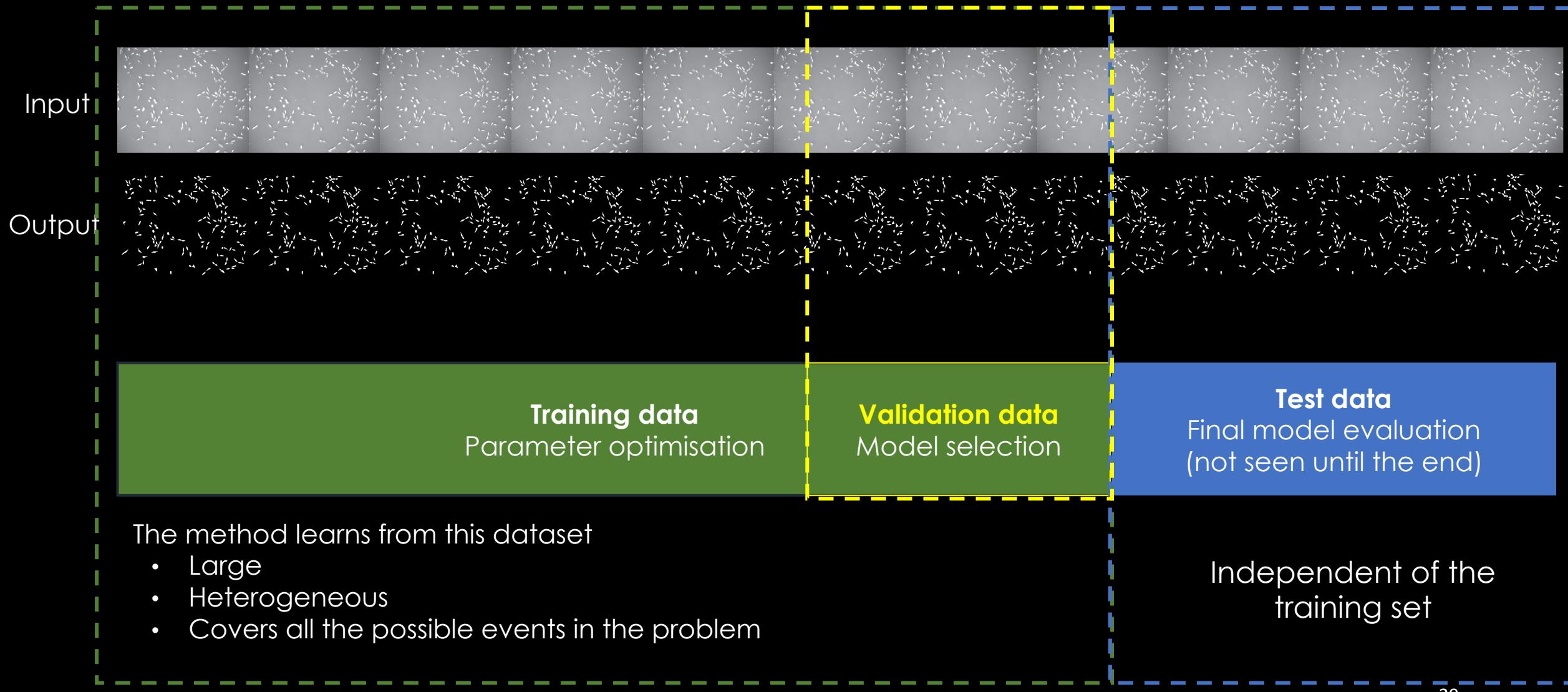
Pairs of inputs and desired outputs (i.e., ground truth)



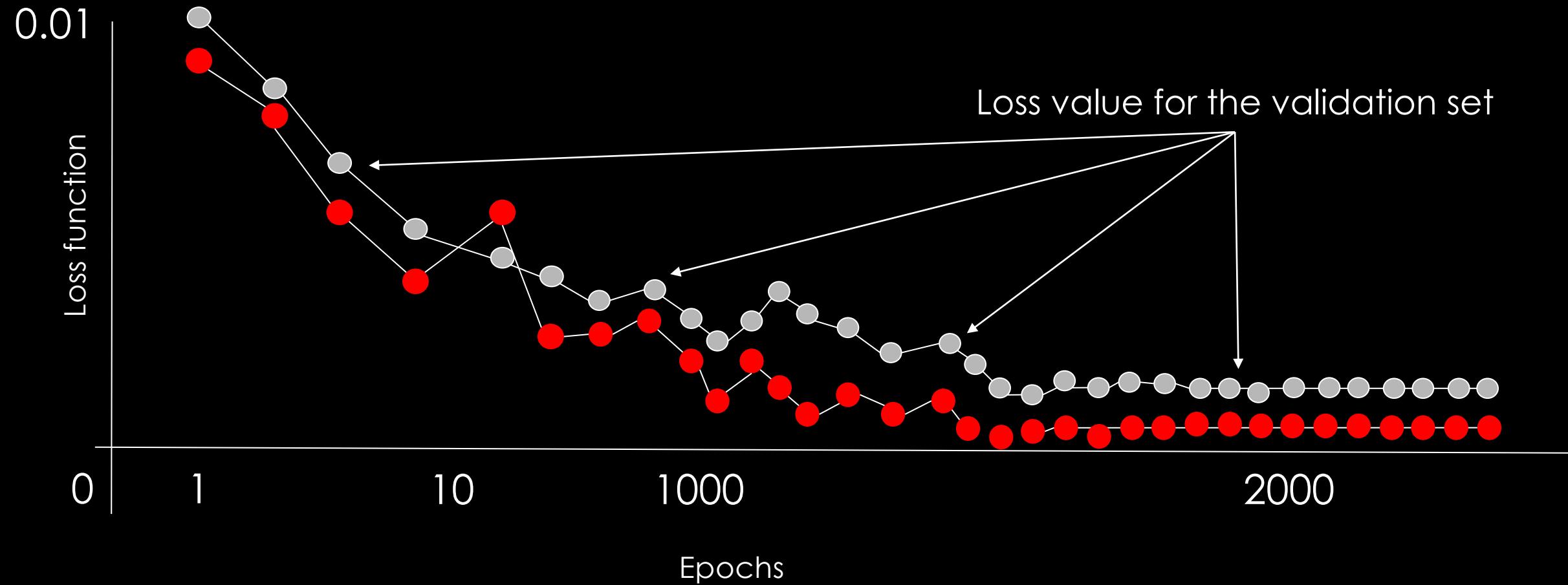
Training a neural network



Training a neural network: data

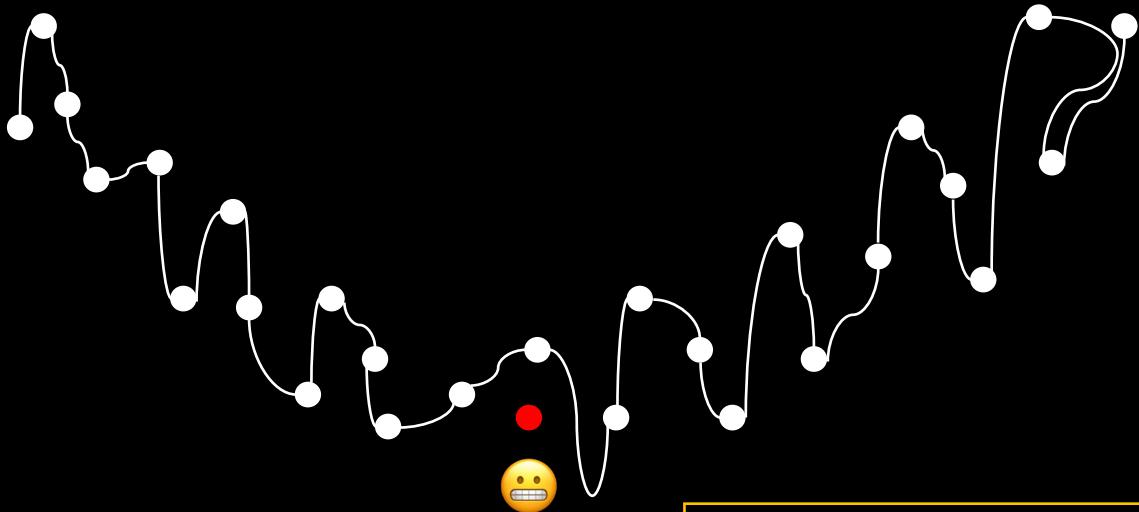


Training a neural network: data

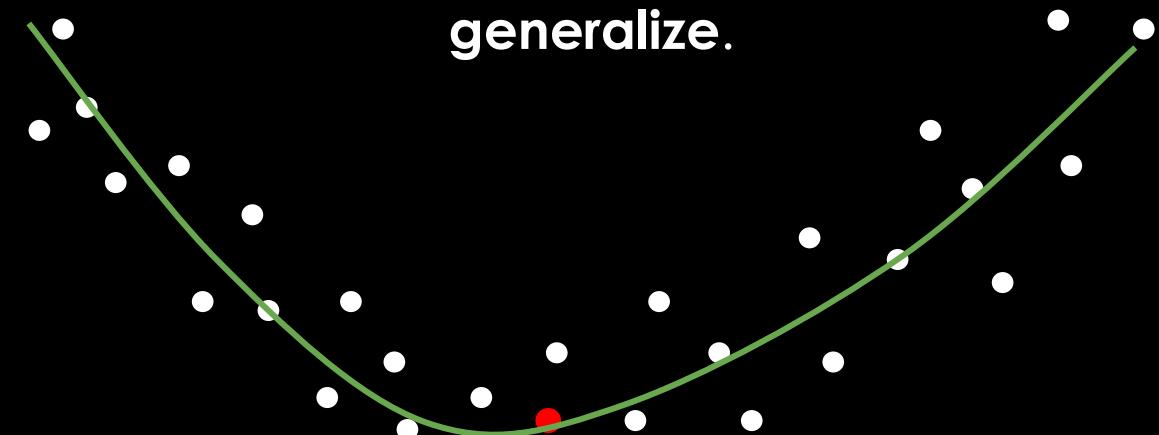


Training a neural network: data

If the method fails in the validation data, then it is called **overfitting**.



If the test processing is as good as in the training data, then we say that it can **generalize**.



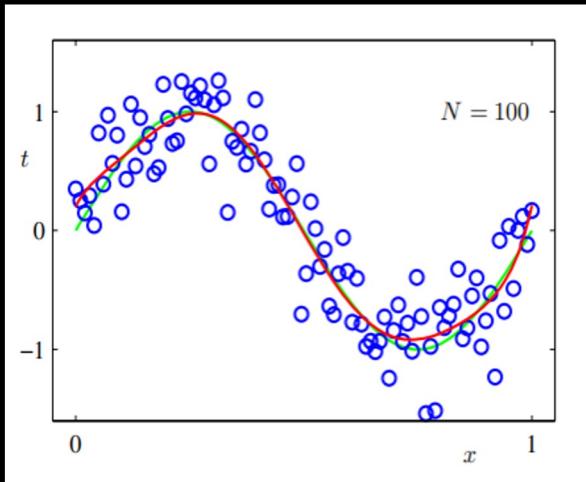
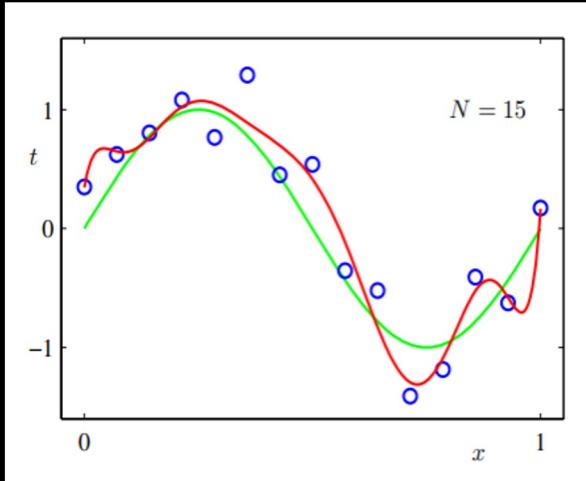
You: how do I prevent overfitting?

Esti & Wei: more data 😊

You: 🤯 😷

Training a neural network: data

The bigger the data the better
→ Cover a real scenario



Data augmentation

All of them are cats, indeed, the same cat

No doubt, it is a fox or an airplane

image classification

It is always the number 6

Most common strategies to augment data in image classification

Crop

Symmetry

Rotation

Scale

Original

Noise

Hue

Obstruction

Blur

Training a neural network: data augmentation in microscopy

- I. The ground truth also needs to be augmented with the same transformations.
- II. Image transformations need to preserve the meaning and biophysical properties of the data.

Geometrical transformations

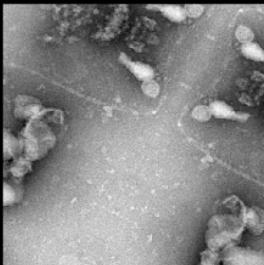
Linear transformations (preserve shape)

- Rotation
- Translation

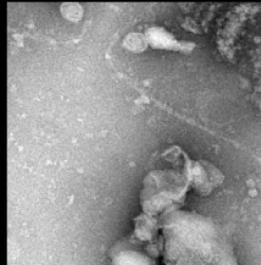
Linear transformations



Original patch



Rotation + Shift



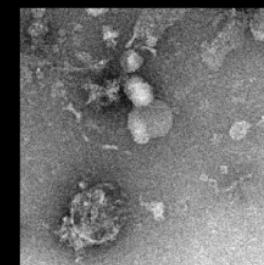
Rotation



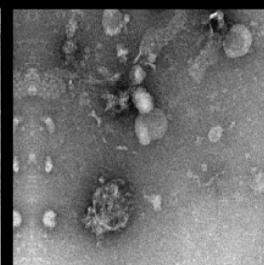
Non-linear (elastic) transformations
(shape changes)

- Zooming
- Shearing

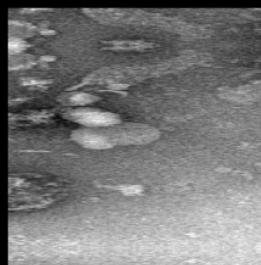
Non-linear transformations



Original patch



Zoom



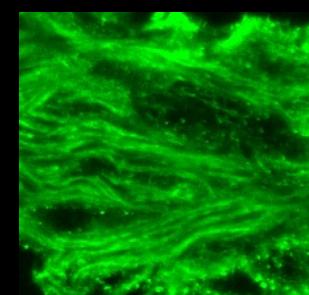
Shearing



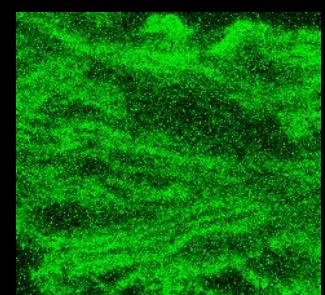
Signal artifacts:

- Noise
- Contrast
- Blurring

Adding noise



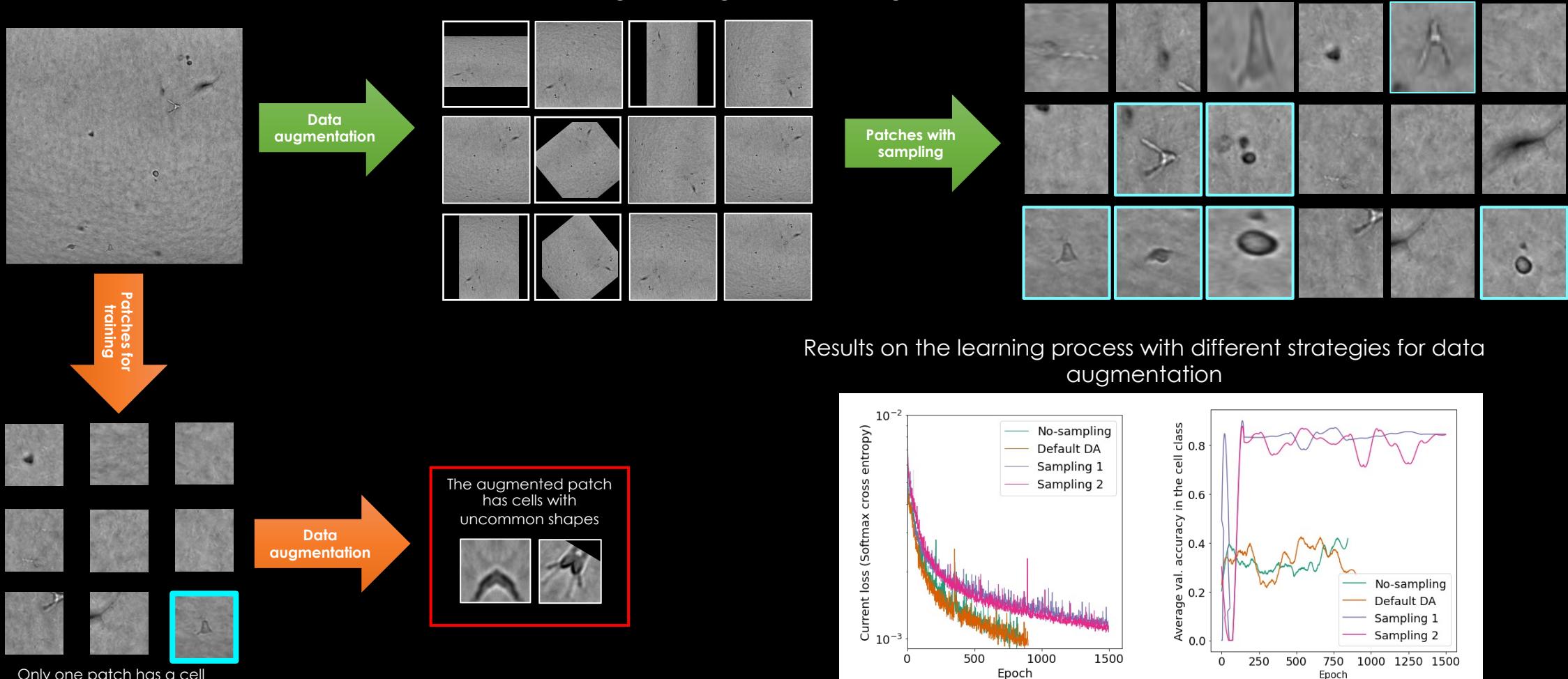
Original image



Noisy

Segmentation with CNNs: patches and data augmentation

Make sure that artifacts are not introduced when augmenting the patching



Training a neural network: data

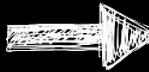
Data collection (&curation) is expensive.



Small datasets for bioimage analysis

Fine tuning

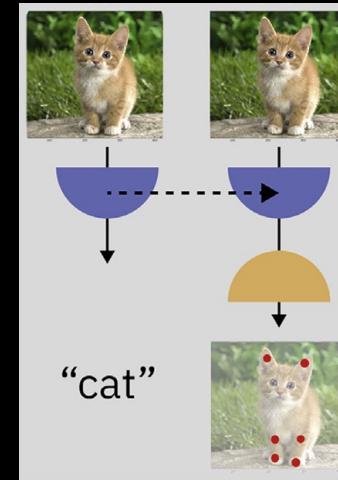
Pretrained model
for boundary
segmentation



Same task, similar
features, different
data distribution



Transfer learning



Classification



Segmentation

Classification



Pose estimation

Deep learning systems

Model architecture

- U-Net
- ResNet
- MobileNetV2
- (cycle)GANS
- DenseNets

Loss function

- Mean Squared Error
- Mean Absolute Error
- (binary)cross-entropy
- Focal loss
- Dice loss

Optimisation

- Stochastic gradient descent
- ADAM

Data (curation)

- Labelled masks
- Keypoints&landmarks
- Paired images (high&low SNR)
- Bounding boxes
- Tracks

Influence the final performance and behaviour of your system

Deep learning systems

Model architecture

Loss function

Optimisation

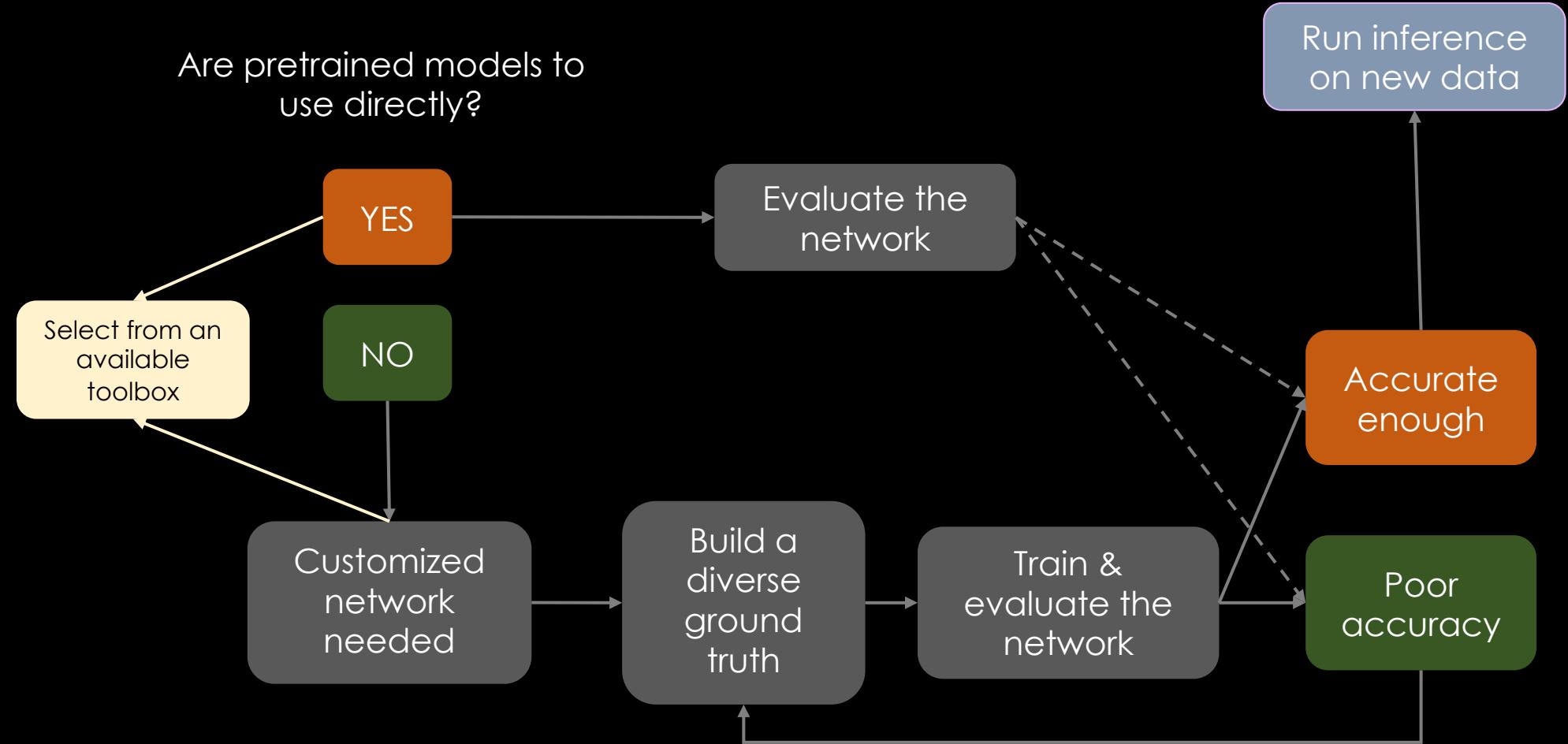
Data

- Each configuration affects the inference speed, training data requirements, memory demands.
- Task specific:
 - 2D, 3D, time lapse, multichannel.
 - Image-to-image vs.image-to-vector processing.
 - Criterion needed to learn: regression vs classification.

Deep learning systems

Identify the sample type(s) and features you need to analyse

Questions to consider:
What features give me the info I need?
Live or fixed?
Highly accurate?
Multichannel?

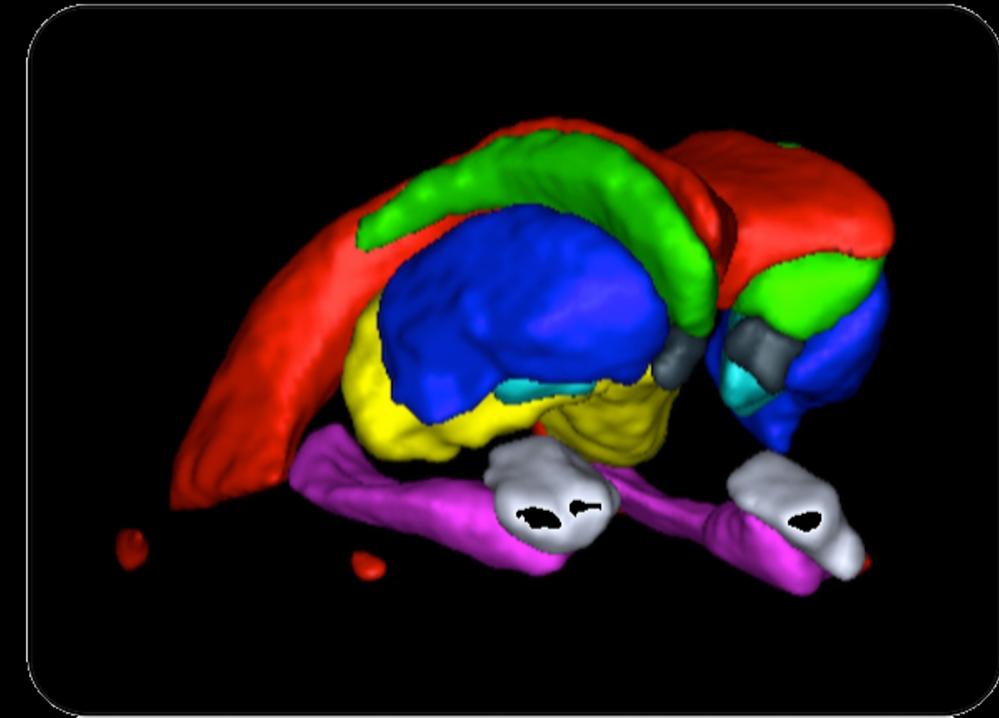
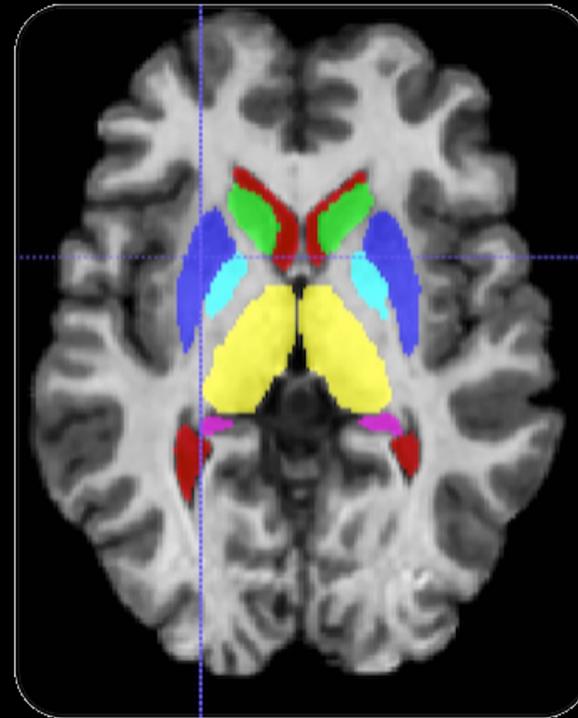


Segmentation

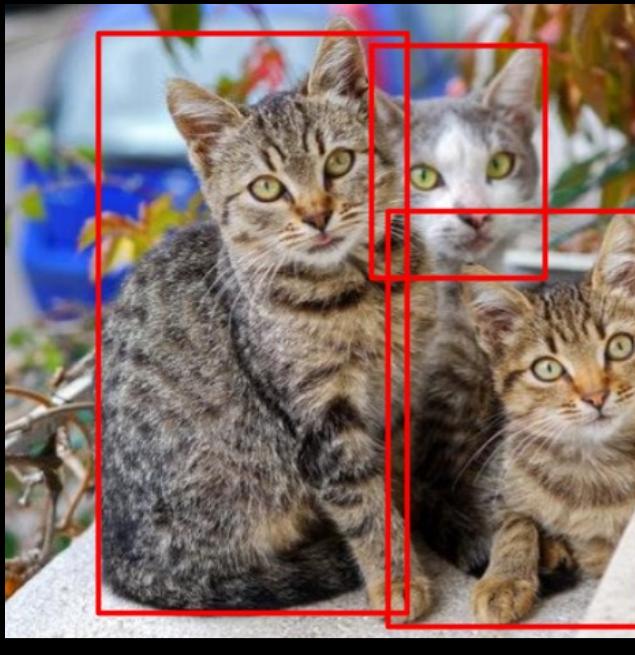
Segmentation

Formal definition: partitioning of the image domain Ω into several (usually disjoint) regions Ω_i

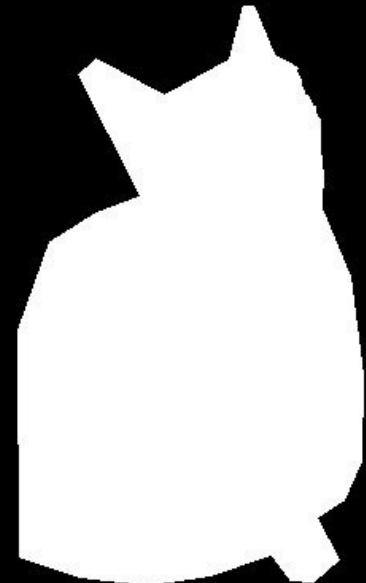
$$\Omega = \bigcup_i \Omega_i, \quad \Omega_i \cap \Omega_j = \emptyset, \forall i \neq j$$



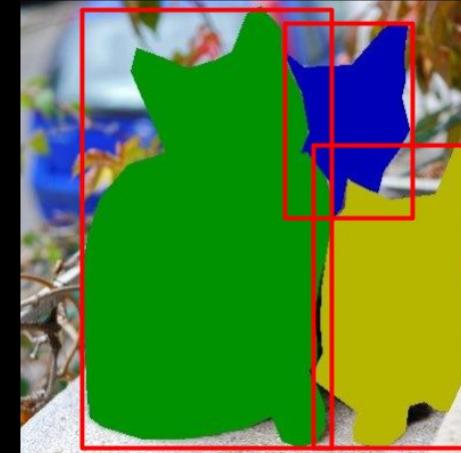
Segmentation



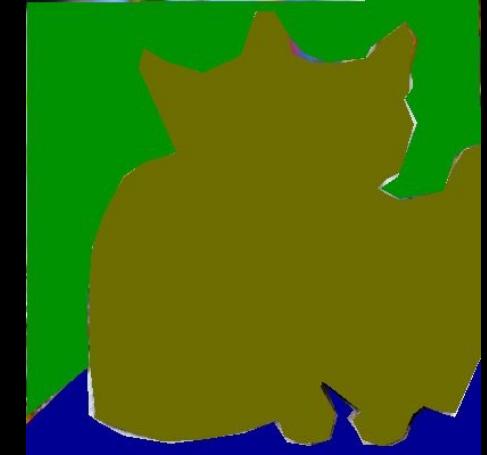
Detection



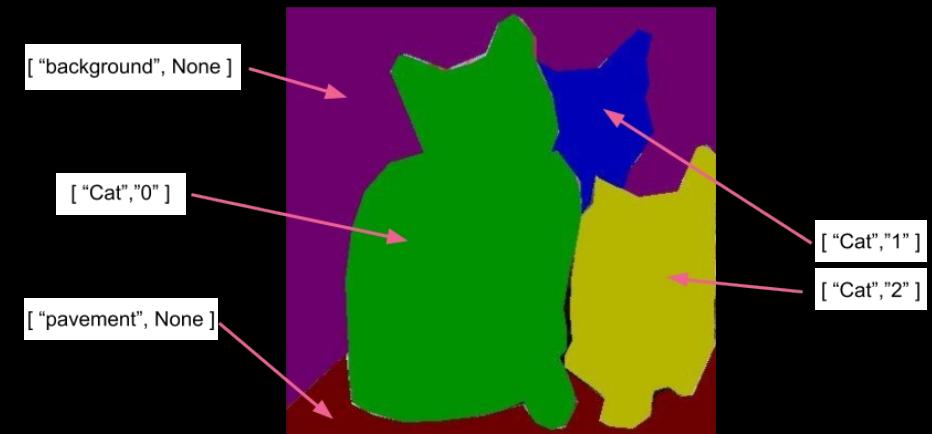
Binary segmentation



Instance segmentation
(Detection + segmentation)



Semantic segmentation

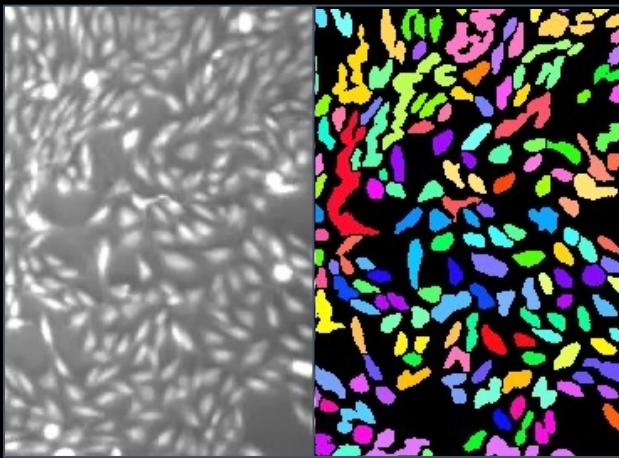


Panoptic segmentation
(Instance + Semantic segmentation)

Segmentation

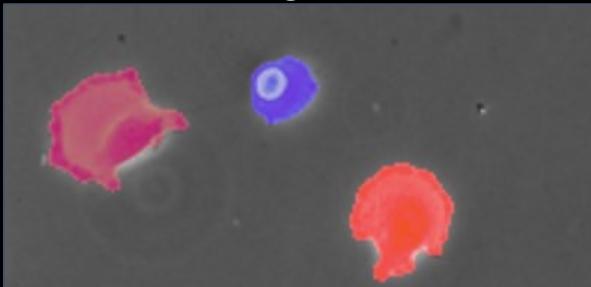
The information is partitioned in different segments to simplify its representation into something that is easier to analyze

Cell counting



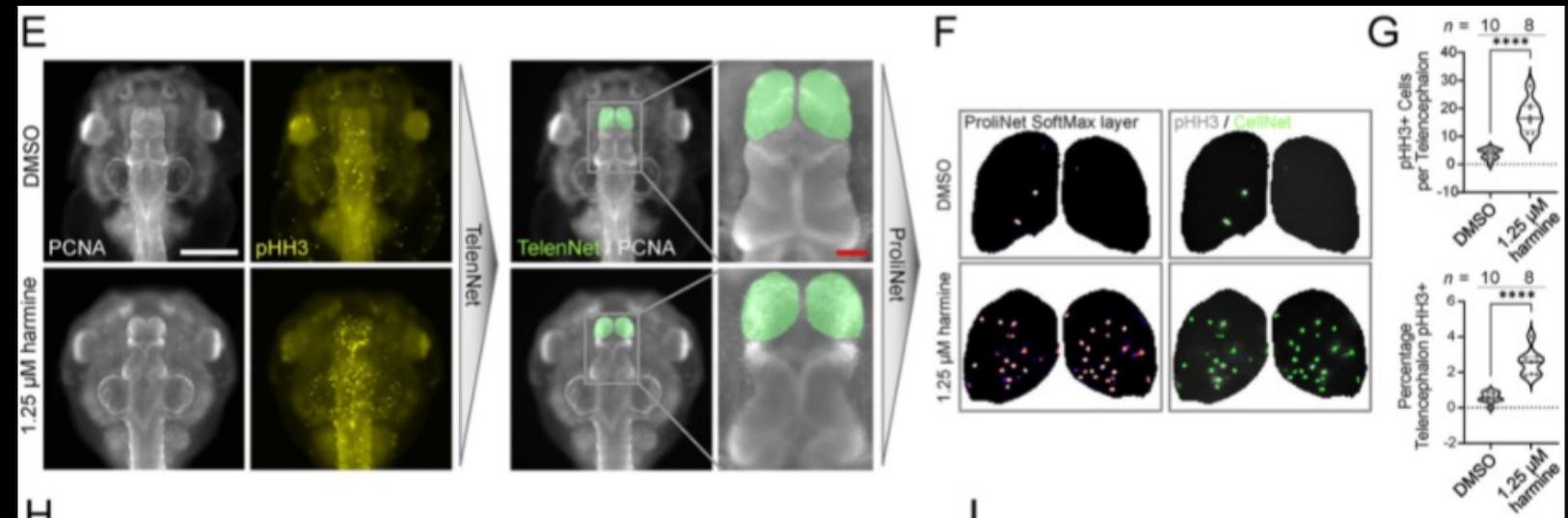
F. Lux & P. Matula, arXiv, 2020

Morphology assessment

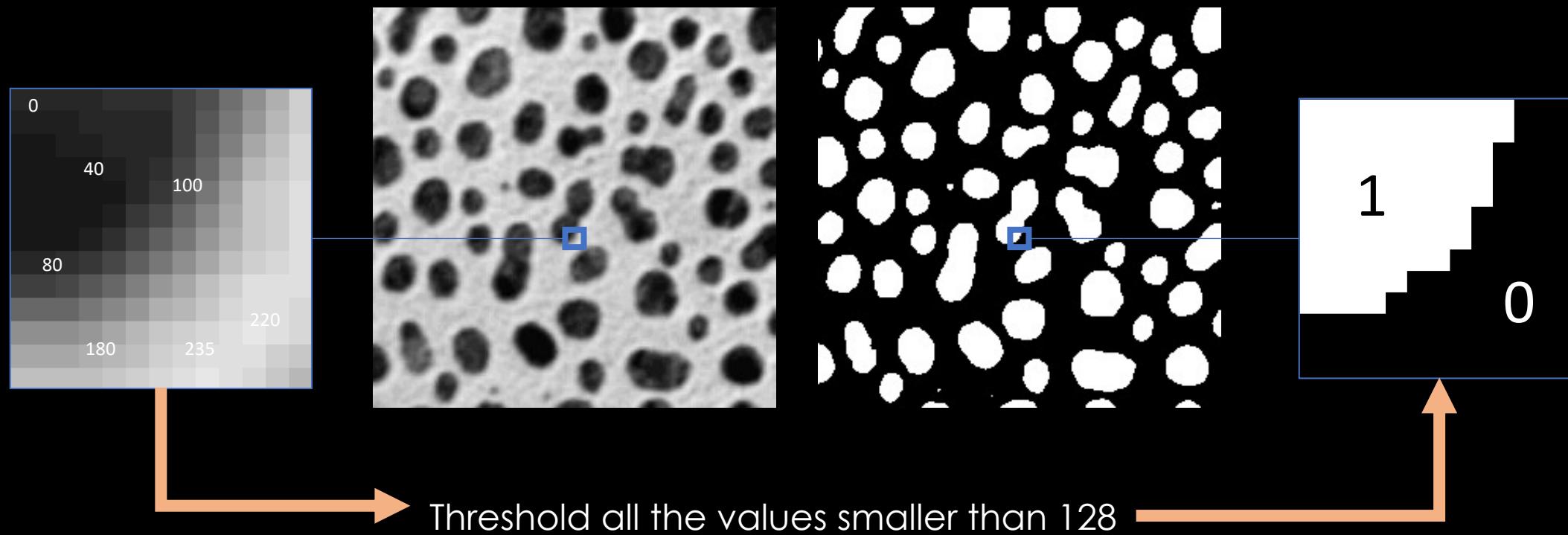


Data: Cell Tracking Challenge (Ulman, V., et al., Nat Methods 2017), Training: João Luis Soares Lopes (EPFL)

Determine anatomical regions (telencephalons) to measure cell activity (proliferating pHH3+ cells)



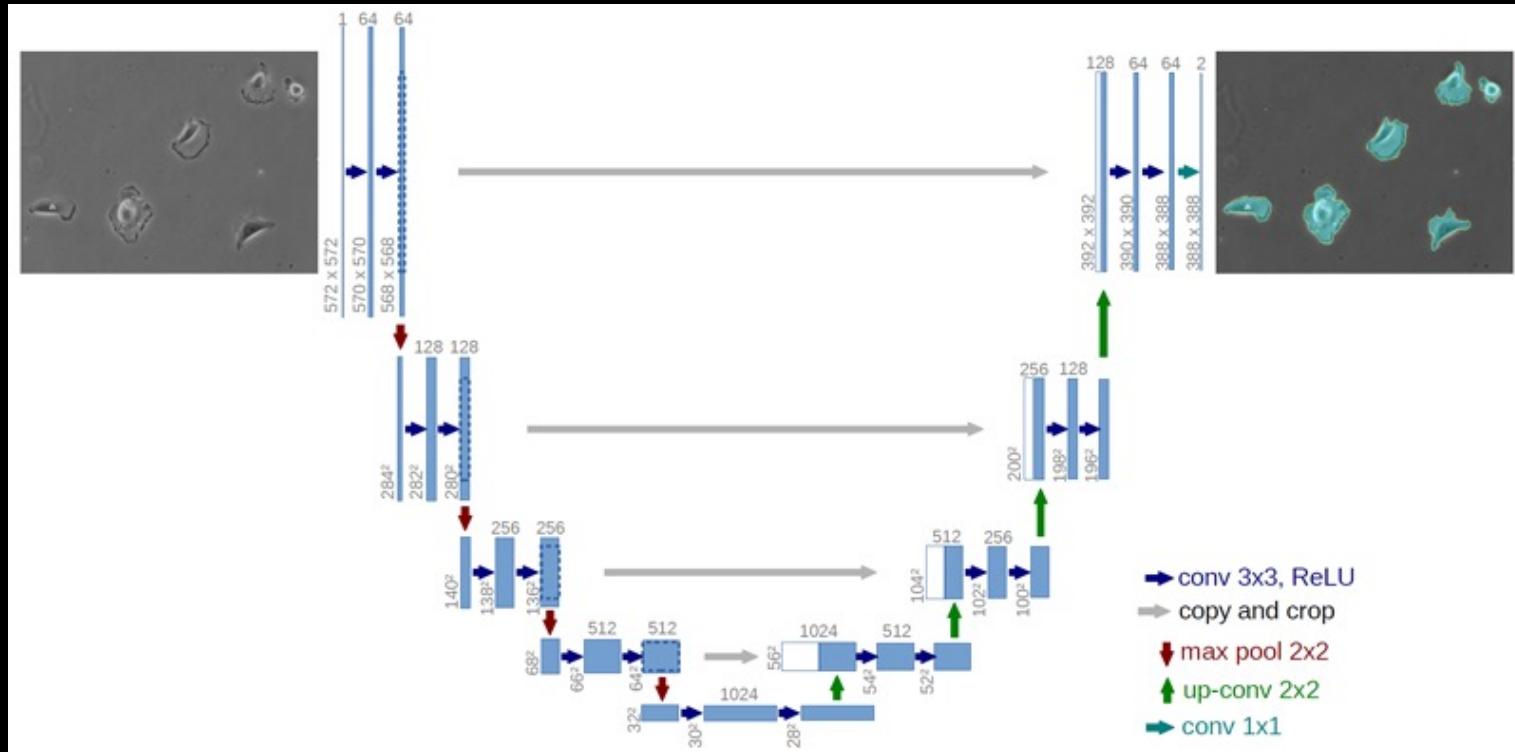
Segmentation: Thresholding is the most basic form of obtaining binary images



Segmentation with CNNs: U-Net encoder-decoder for binary segmentations

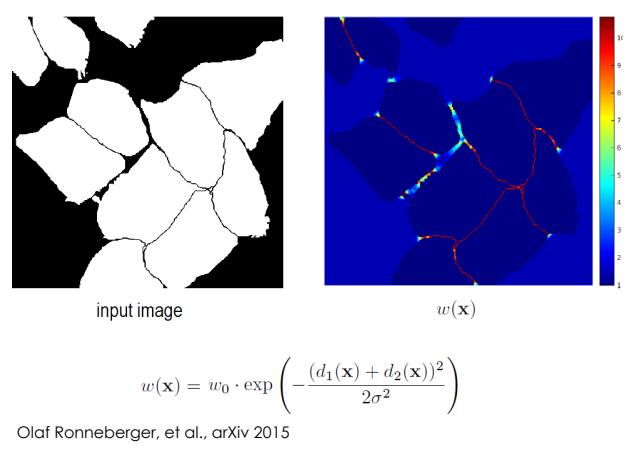
Skip connections:

Take the output of each level in the encoder path and copy it with the input of the decoder path. It helps preserving high resolution details during decoder process.

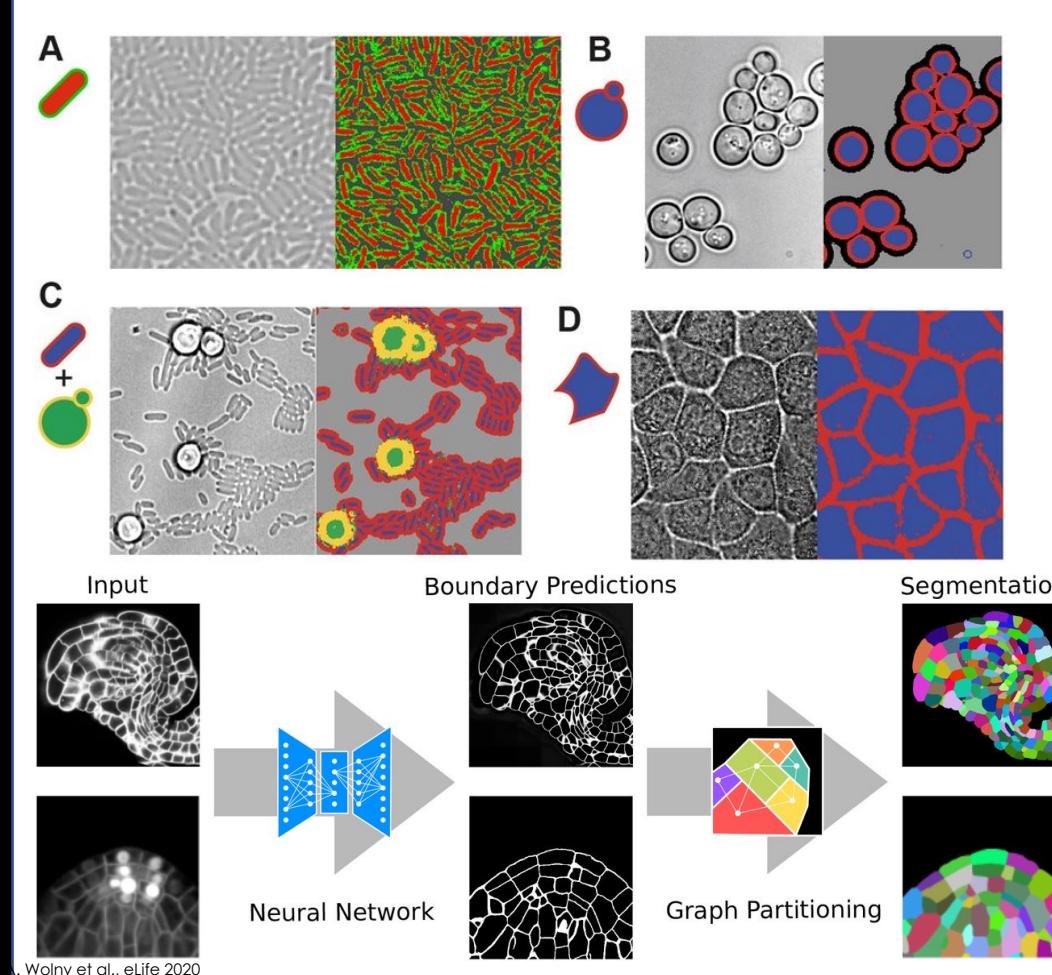


Segmentation: alternative strategies

Weighted loss functions



Use different labels



Limitations of binary image segmentation

- Will not work with dense, packed or clustered objects.
→ Additional labels to split independent objects
- Overlapping objects cannot be represented in one single mask
- ROIs need to be predefined and do not scale well to cellular shapes

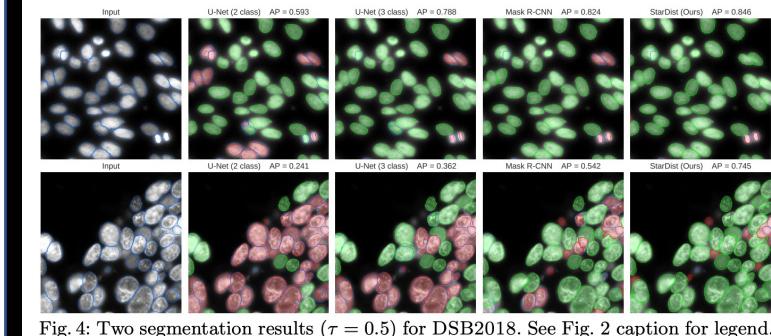
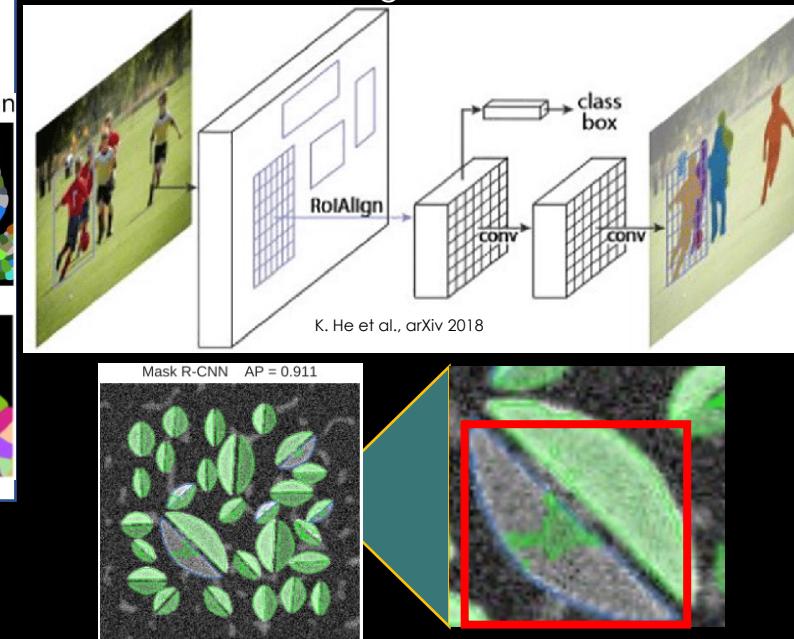


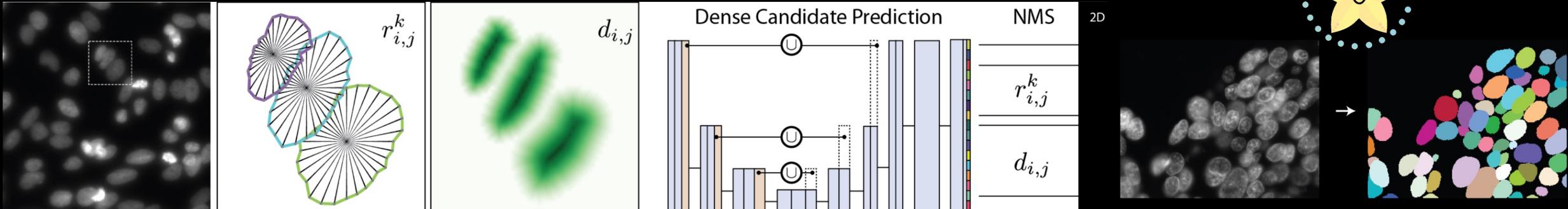
Fig. 4: Two segmentation results ($\tau = 0.5$) for DSB2018. See Fig. 2 caption for legend.
https://github.com/maweinert/neubias_academy_starDist
Schmidt, Weigert et al 2018

Instance segmentation with ROI classification and segmentation



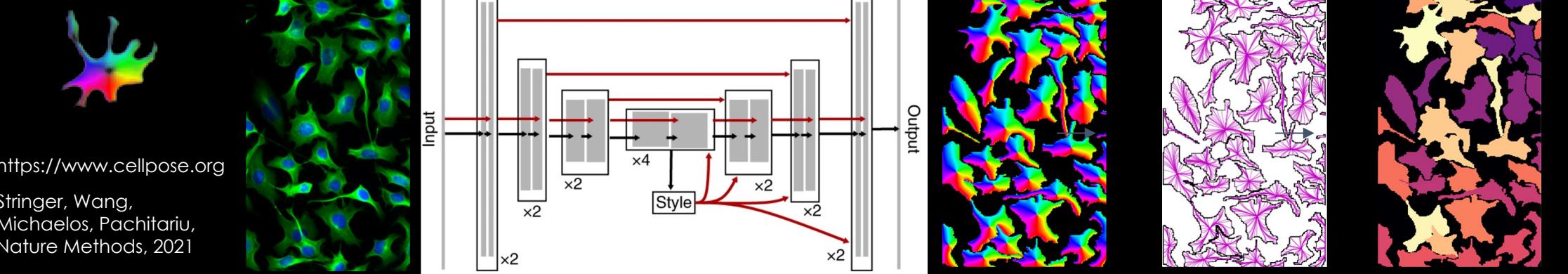
Segmentation: learn deterministic features rather than discrete labels

StarDist



https://github.com/mawiegert/neubias_academy_stardist
Schmidt, Weigert et al 2018

Cellpose



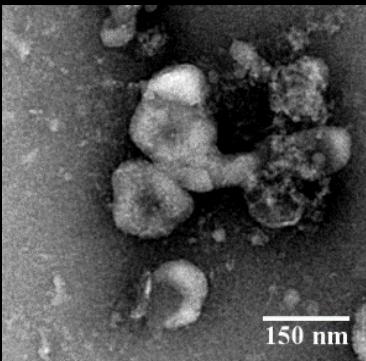
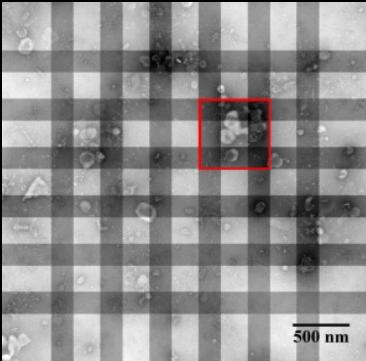
<https://www.cellpose.org>

Stringer, Wang,
Michaelos, Pachitariu,
Nature Methods, 2021

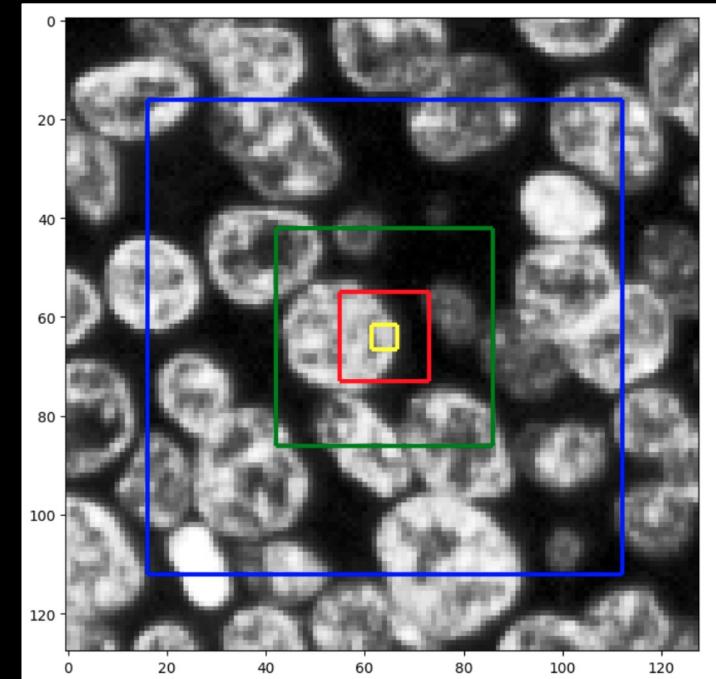
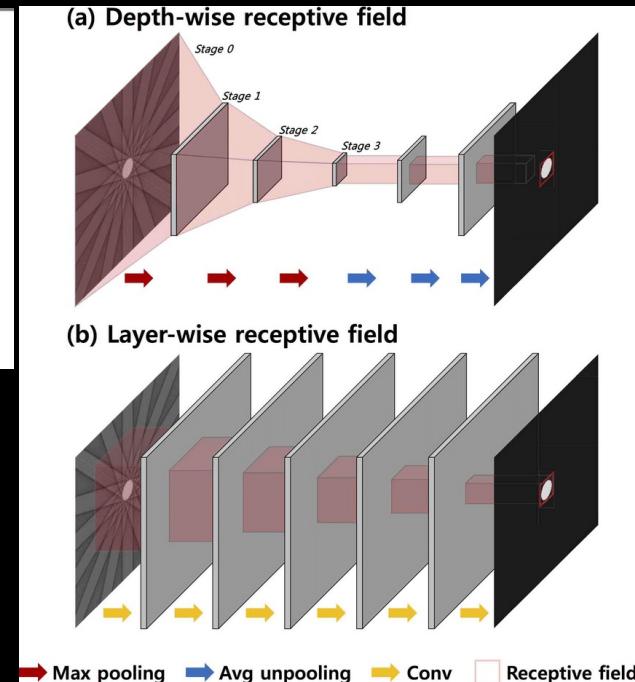
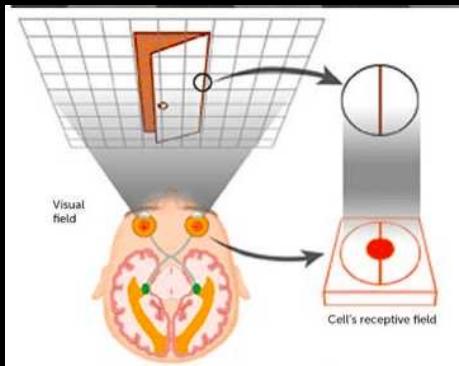
Segmentation with CNNs: image preparation and features

Biomedical images can get really large (up to TB for electron microscopy) → GPU memory a major limitation

Divide images into patches → increase the training data variability



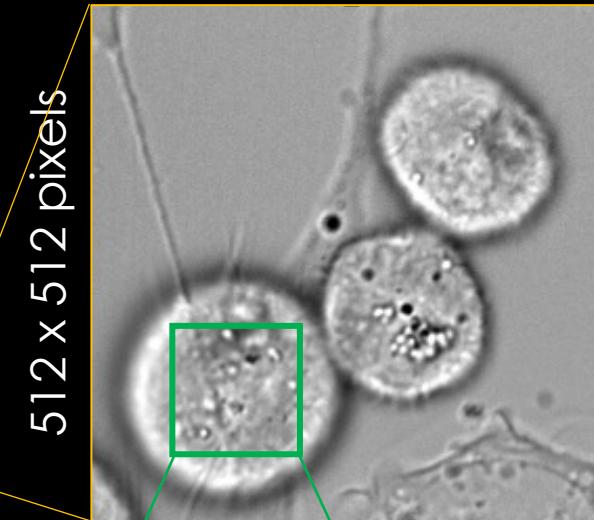
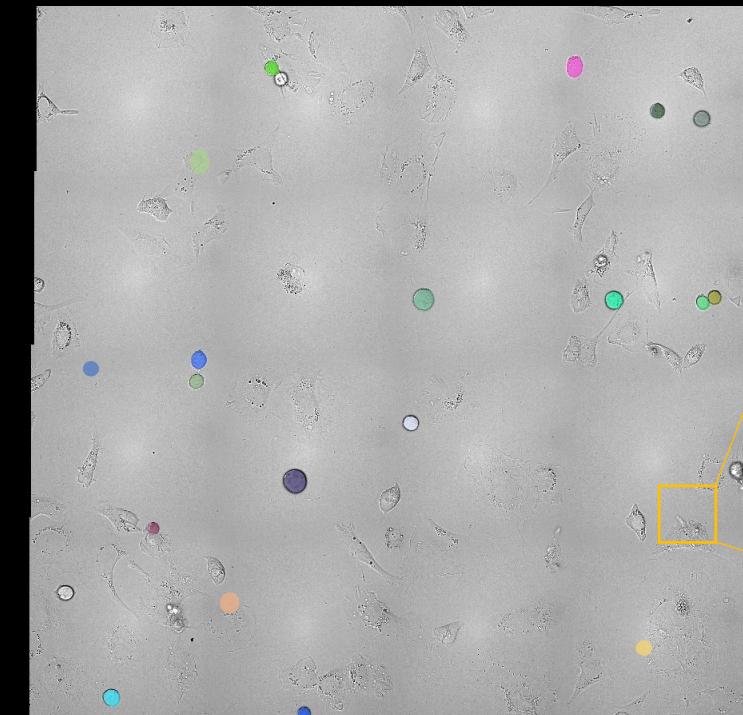
How big? → Receptive field of the network → it needs to have enough information to learn and discriminate



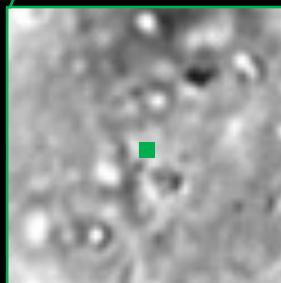
TissueNet,
Greenwald, Miller et al 2021

Segmentation with CNNs: image preparation and features

Image processing task: segment cells in mitosis

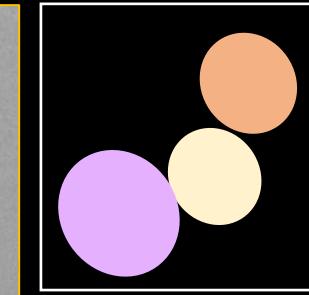


Receptive field of StarDist: "What the network sees to determine the value of one pixel"

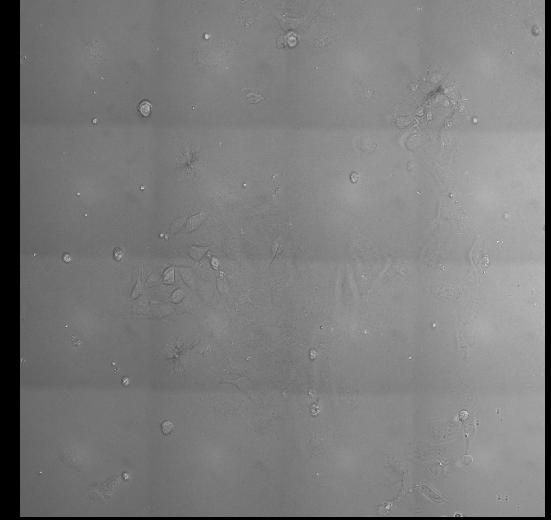


Original videos: 4x4 field of views (x63)

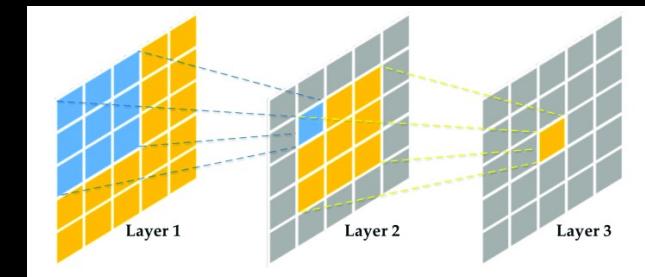
Pixel size = 0.108 µm/pixel



Training patch size
for StarDist



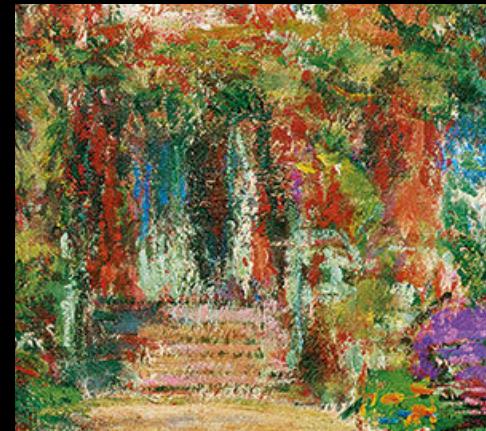
Result: empty
masks



Schmidt, Weigert et al 2018

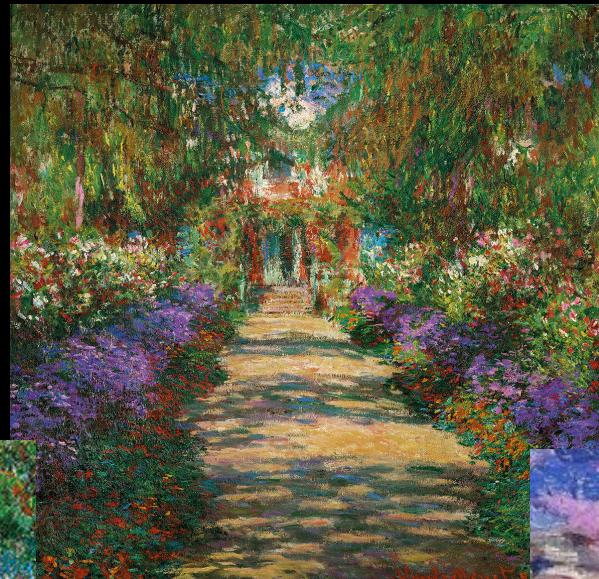
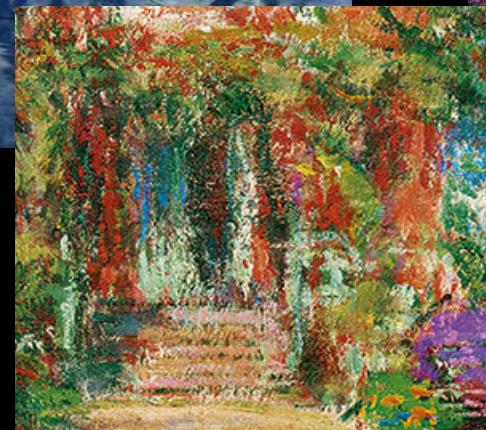
Segmentation with CNNs: image preparation and features

A way to understand could be... asking what is the perfect distance to decipher the scenes of Claude Monet's art
→ enough as to get the context with still meaningful details



Segmentation with CNNs: image preparation and features

A way to understand could be... asking what is the perfect distance to decipher the scenes of Claude Monet's art
→ enough as to get the context with still meaningful details



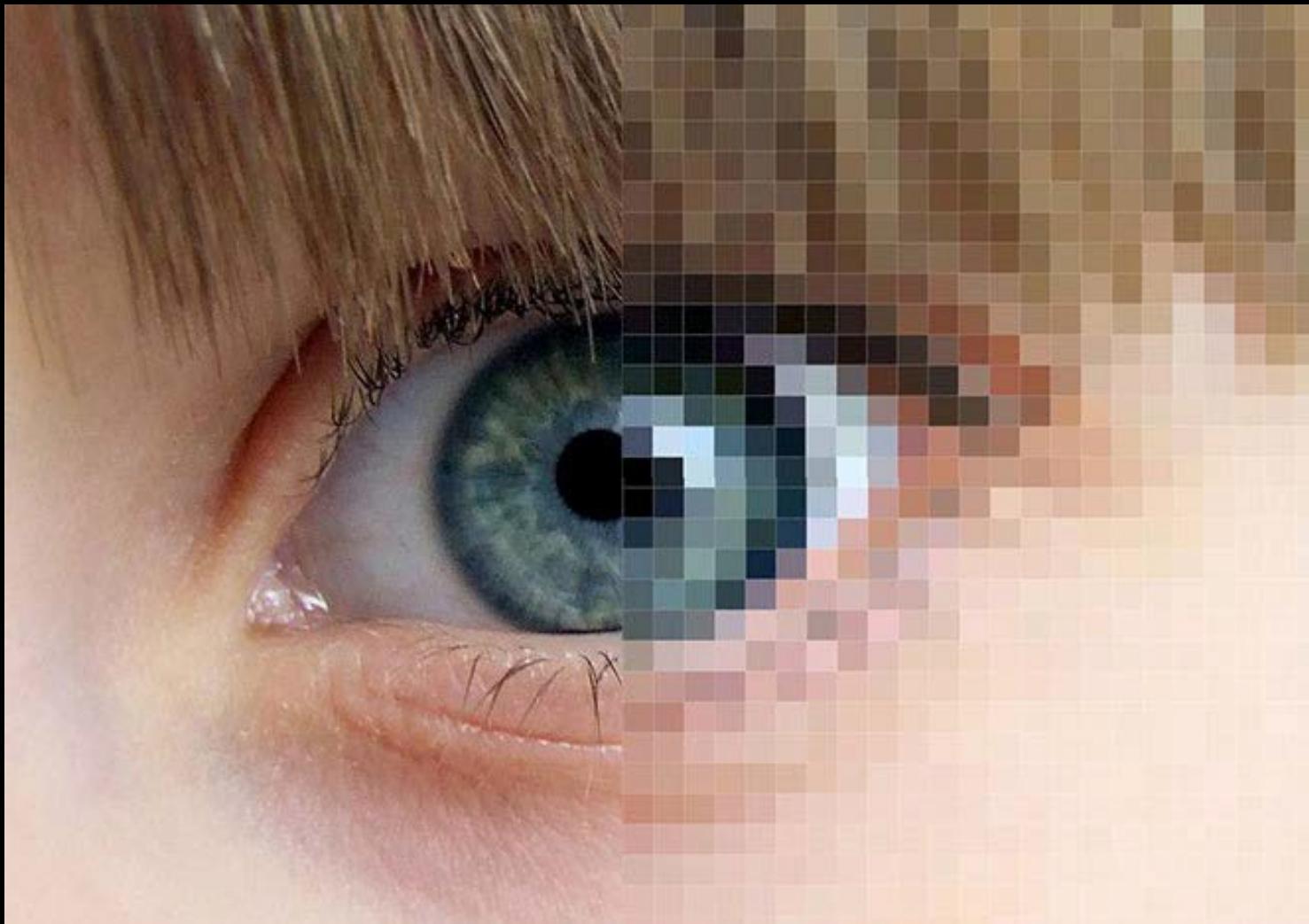
Garden path at Giverny



The house among roses

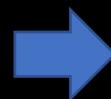


Segmentation with CNNs: image resolution and its effect in segmentation



Segmentation with CNNs: image resolution and its effect in segmentation

Basic definition: Number of pixels in an image



Pixel size: physical size (length and width) covered by one pixel

16 cm



8x8



64x64

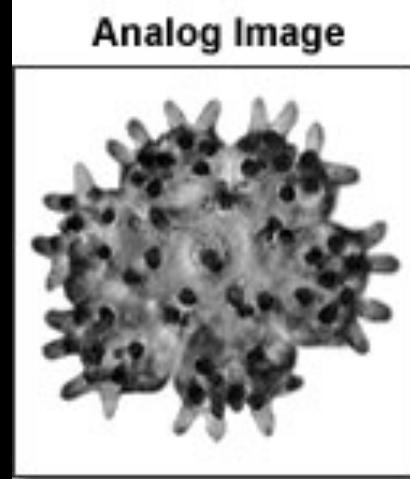


128x128

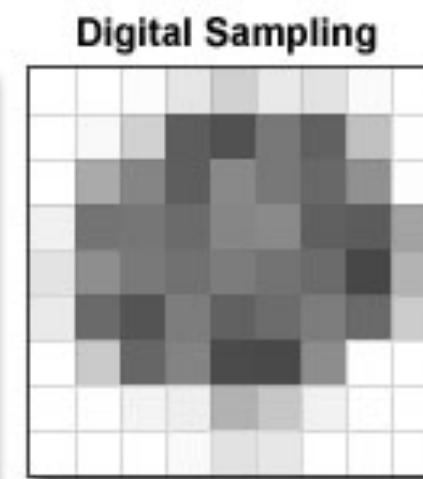


512x512

- The pixel size influence the amount of details for a given field of view.
- Detectors also limit the size of the finest detail that we can acquire



Analog Image

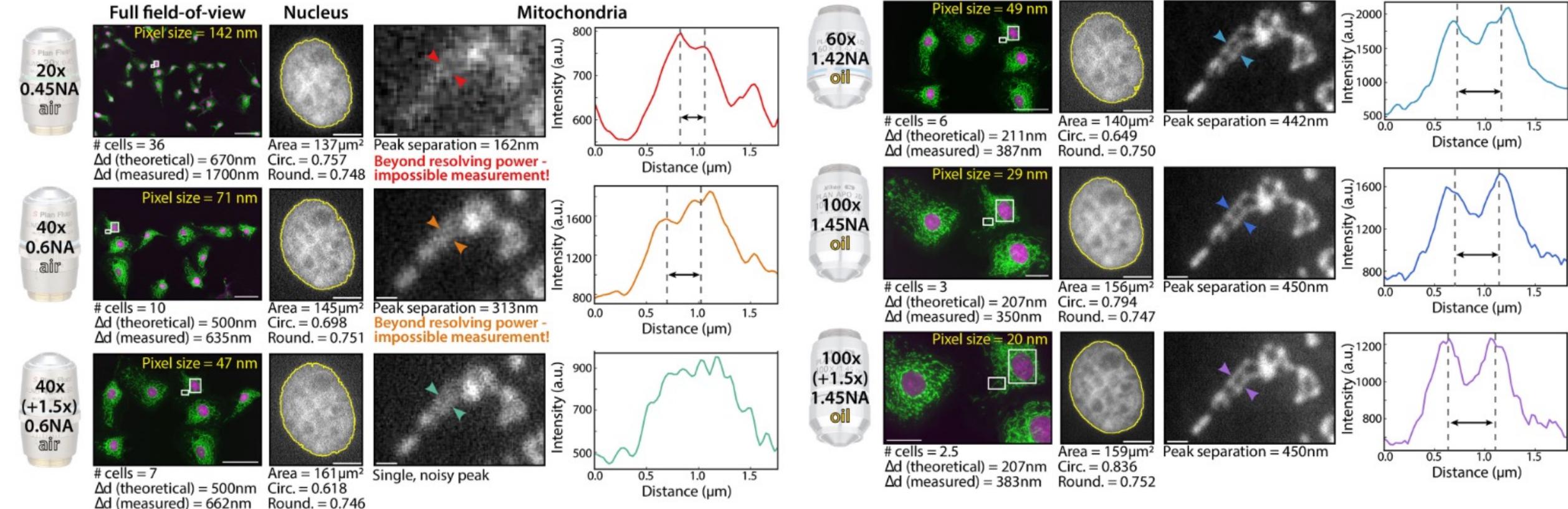


Digital Sampling

| 249 | 244 | 240 | 230 | 209 | 233 | 227 | 251 | 255 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 248 | 245 | 210 | 93 | 81 | 120 | 97 | 193 | 254 |
| 250 | 170 | 133 | 94 | 137 | 120 | 104 | 145 | 253 |
| 241 | 116 | 118 | 107 | 134 | 138 | 96 | 92 | 163 |
| 277 | 142 | 121 | 113 | 124 | 115 | 107 | 71 | 179 |
| 234 | 106 | 84 | 125 | 97 | 108 | 125 | 106 | 204 |
| 241 | 202 | 102 | 132 | 75 | 73 | 141 | 246 | 252 |
| 253 | 252 | 244 | 239 | 178 | 199 | 242 | 250 | 245 |
| 255 | 249 | 244 | 250 | 226 | 231 | 249 | 251 | 253 |

Pixel Quantization

Segmentation with CNNs: image resolution and its effect in quantification

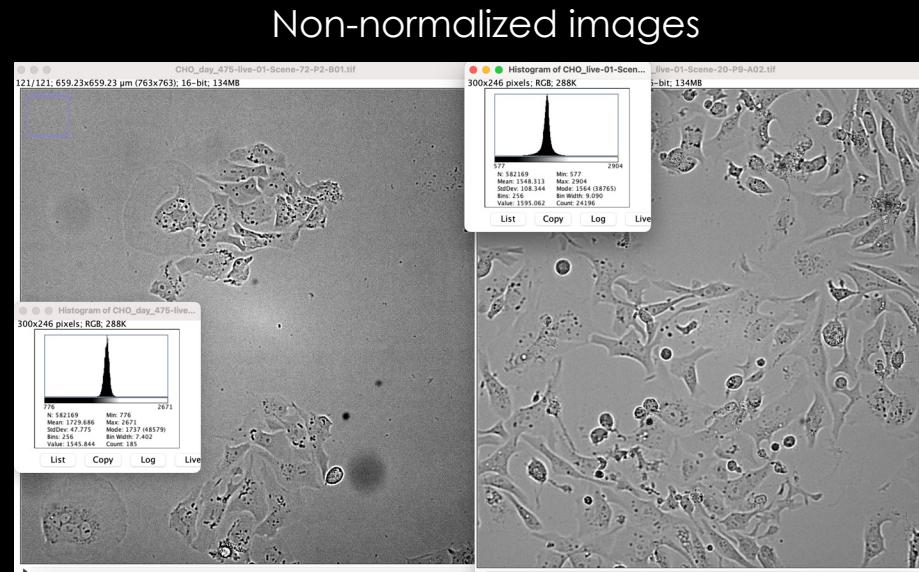


Segmentation with CNNs: image preparation and features

Intensity values vary with the physical properties of the data, the calibration of imaging devices or the natural variability of the sample

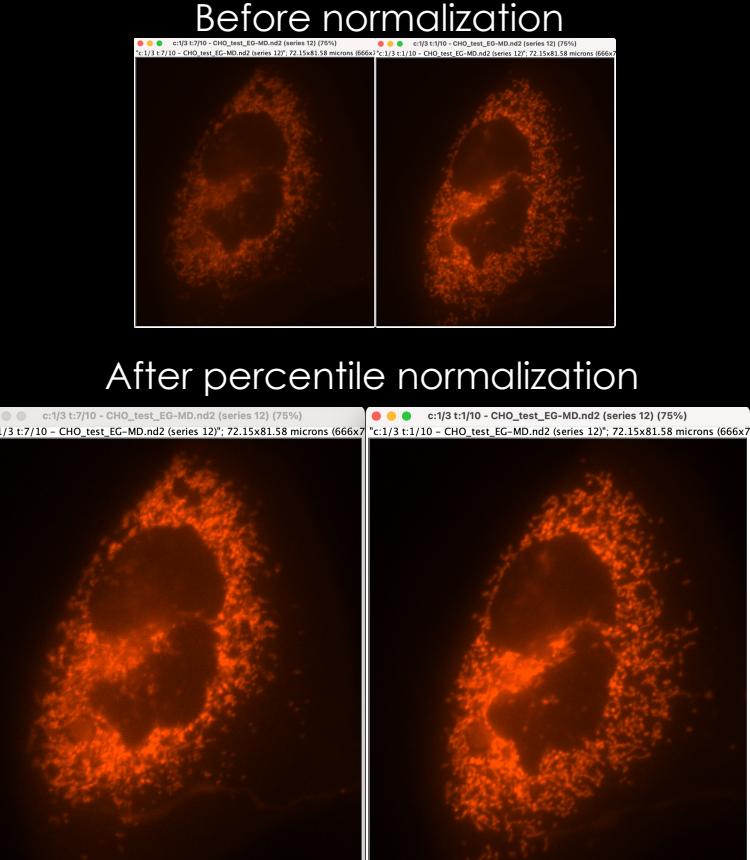
MNIST data: black and white pixels

0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9



Common strategies:

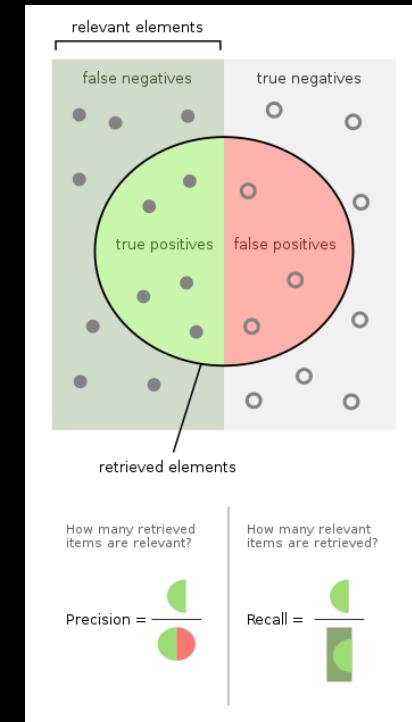
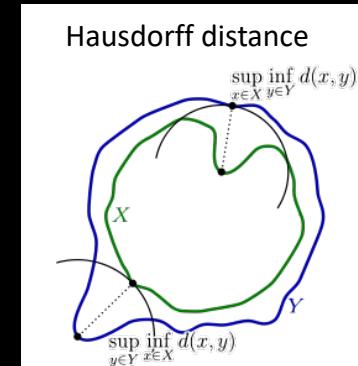
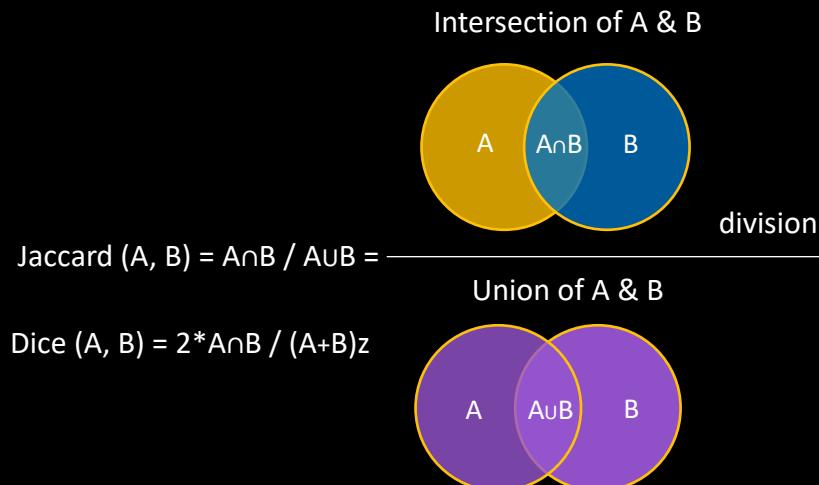
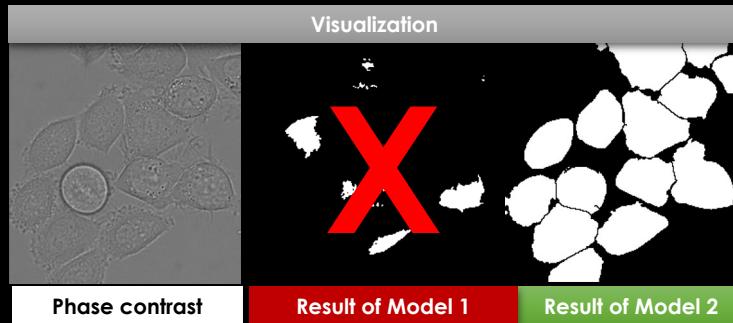
- Intensity projection: Clip the dynamic range of values to the [0, 1] range
- Standardization with the mean and standard deviation
- Percentile projection (common in fluorescence): remove outliers (i.e., noise and artifacts) from the intensity distribution (extremes in the tails) and clip to the [0, 1] range.
- Normalize w.r.t. the entire population (training data)



Evaluation of the model performance → Accuracy

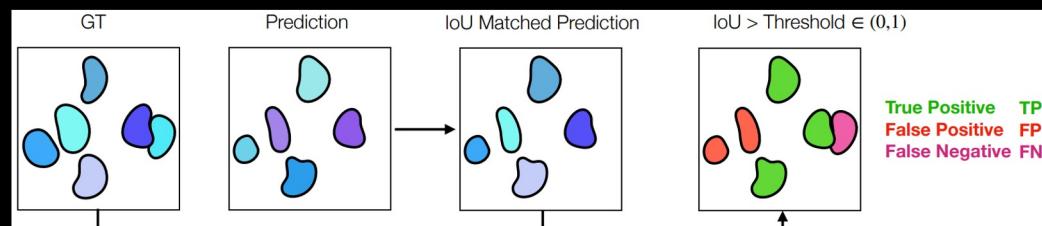


You need to verify that the model is doing precisely what you want



Quantify the accuracy

- Precision, recall, F1 ($= (2 * \text{precision} * \text{recall}) / (\text{precision} + \text{recall})$)
- Jaccard index / Dice coefficient
- Hausdorff distance
- Mean Squared Error (L2)
- Structural similarity index (SSIM)
- Biologically relevant measures (cell densities, fluorescence intensities, diameters)



https://github.com/mawiegert/neubias_academy_stardist
Schmidt, Weigert et al 2018

Biological relevance of the segmentation results



- Segmentation result
- Real object
- ✓ Accuracy (overlap)
- ✗ Length, curvature, diameter

Quantitative evaluation of segmentation and tracking

Computer science

Biological relevance

Practical usability

Jaccard/Dice coefficients

Acyclic Oriented Graph

Precision – Recall – F1

Complete tracks

Morphological measures (size, shape)

Branching correctness

Cell cycle accuracy

Fluorescence intensity

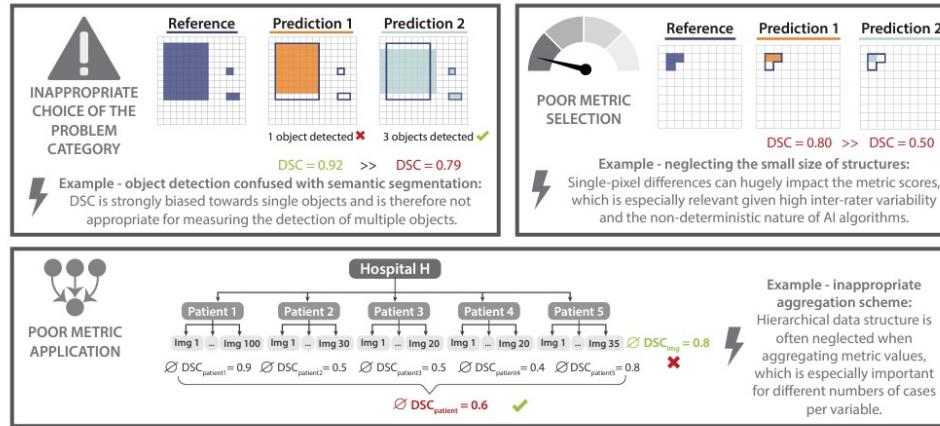
Number of tunable parameters

Generalizability

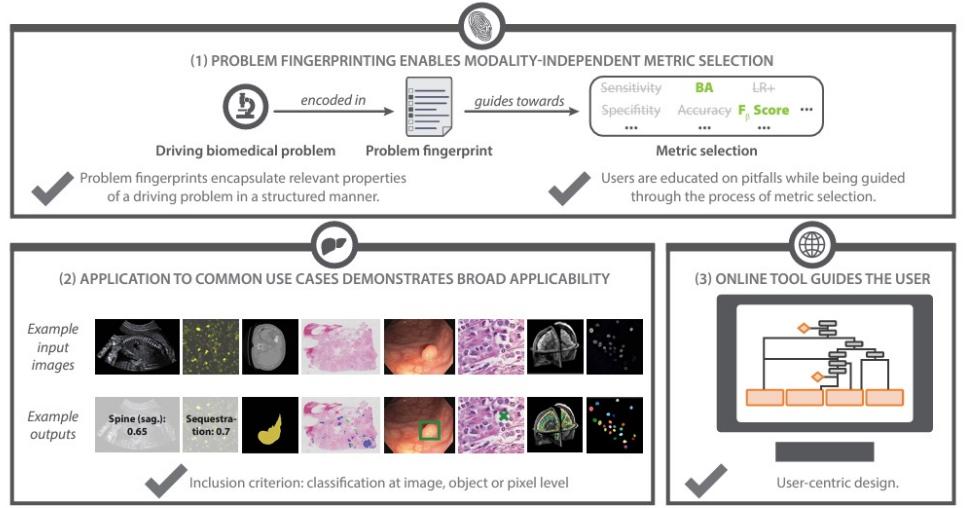
Metrics reloaded: Recommendations for image analysis validation

Lena Maier-Hein, Annika Reinke, Patrick Godau, Minu D. Tizabi, Florian Büttner, Evangelia Christodoulou, Ben Glocker, Fabian Isensee, Jens Kleesiek, Michal Kozubek, Mauricio Reyes, Michael A. Riegler, Manuel Wiesenfarth, A. Emre Kavur, Carole H. Sudre, Michael Baumgartner, Matthias Eisenmann, Doreen Heckmann-Nötzel, A. Tim Rädsch, Laura Acion, Michela Antonelli, Tal Arbel, Spyridon Bakas, Arriel Benis, Matthew Blaschko, M. Jorge Cardoso, Veronika Cheplygina, Beth A. Cimini, Gary S. Collins, Keyvan Farahani, Luciana Ferrer, Adrian Galdran, Bram van Ginneken, Robert Haase, Daniel A. Hashimoto, Michael M. Hoffman, Merel Huisman, Pierre Jannin, Charles E. Kahn, Dagmar Kainmueller, Bernhard Kainz, Alexandros Karargyris, Alan Karthikesalingam, Hannes Kenngott, Florian Kofler, Annette Kopp-Schneider, Anna Kreshuk, Tahsin Kurc, Bennett A. Landman, Geert Litjens, Amin Madani, Klaus Maier-Hein, Anne L. Martel, Peter Mattson, Erik Meijering, Bjoern Menze, Karel G.M. Moons, Henning Müller, Brennan Nichyporuk, Felix Nickel, Jens Petersen, Nasir Rajpoot, Nicola Rieke, Julio Saez-Rodriguez, Clara I. Sánchez, Shravya Shetty, Maarten van Smeden, Ronald M. Summers, Abdel A. Taha, Aleksei Tiulpin, Sotirios A. Tsaftaris, Ben Van Calster, Gaël Varoquaux, Paul F. Jäger

(a) VARIOUS PITFALLS RELATED TO CHOICE OF VALIDATION METRIC



(b) ADDRESSED BY PROBLEM-DRIVEN METRICS RELOADED FRAMEWORK



Lena Maier-Hein, Metrics reloaded: Recommendations for image analysis validation, <https://arxiv.org/abs/2206.01653>, arXiv 2022 (last update June 2023)

| Fingerprint name | Fingerprint illustration | Fingerprint description |
|--|--------------------------|---|
| Image processing category identified by category mapping | | Semantic segmentation (SemS): assignment of one or multiple category labels to each pixel. |
| Domain interest-related properties (selection) | | |
| Particular importance of structure boundaries | | The biomedical application requires exact structure boundaries. Example: segmentation for radiotherapy planning; knowledge of exact structure boundaries is crucial to destroy the tumor while sparing healthy tissue. |
| Particular importance of structure center (e.g., in cells, vessels) | | Important: Overlap-based metrics do not measure shape agreement. In the case of complex shapes (high boundary-to-volume ratio) it is therefore typically advisable to set this property to TRUE. |
| Compensation for annotation imprecisions requested | | The biomedical application requires accurate knowledge of structure centers. Example: cell centers are subsequently used for cell tracking and cell motion characterization, so false center movement should be suppressed. |
| ... | ... | ... |
| Target structure-related properties (selection) | | |
| Small size of structures relative to pixel size | | Structures of the provided class are only a few pixels in size. Example: multiple sclerosis lesions in magnetic resonance imaging (MRI) scans. |
| High variability of structure sizes (within an image and/or across images) | | The target structures vary substantially in size, such that some structures are several times the size of others. Example: polyps in colonoscopy screening, where some polyps are several times the size of others. Counterexample: large organs, such as the liver or the kidneys, which are relatively comparable in size across individuals. |
| ... | ... | ... |
| Data set-related properties (selection) | | |
| Presence of class imbalance | | The class prevalences differ substantially. Example: In a screening application, the positive class (e.g., cancer) may occur extremely rarely. In this case, prevalence-dependent metrics, such as Accuracy, may be extremely misleading. |
| Non-independence of test cases | | The test cases are hierarchically structured, indicating non-independence of test cases. Examples: multiple images of the same patient, hospital or video. |
| ... | ... | ... |
| Algorithm output-related properties (selection) | | |
| Possibility of algorithm output not containing the target structure(s) | | The algorithm may yield outputs in which not all classes are present. |
| ... | ... | ... |

Considerations: The objective

Accuracy versus validity

Example:

High segmentation accuracy but
poor temporal consistency

→ Limit object tracking



- Segmentation
- Real object
- ✓ Fluorescence average value
- ✗ Length, curvature, diameter, shape

Mistaken objective

Example:

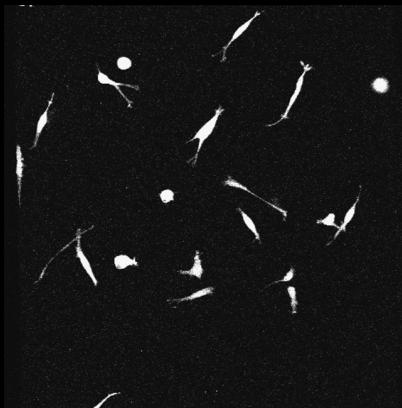
Diagnosis of diabetic retinopathy.

Issues:

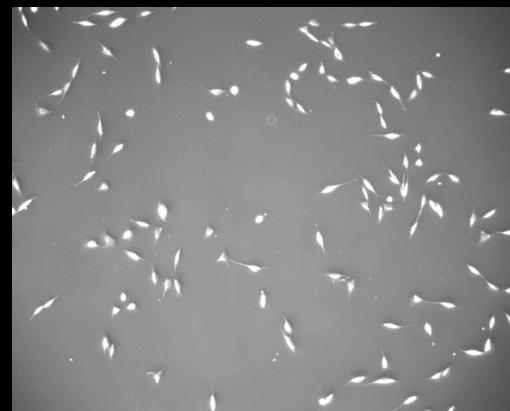
1. Discrepancy among doctors and non-valid majority voting
2. Hidden real objective → “Should this patient see a doctor?”

Considerations: Generalizability

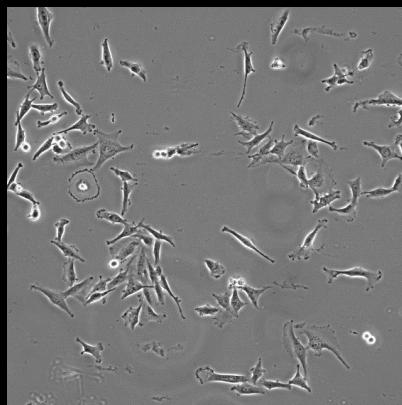
DL models are extremely sensitive to pixel sizes (object size), imaging modalities, morphologies, cell types, fluorescence channels...



FluoC3DLMDA231



PhC-C2DL-PSC



Usiigaci

Generalizability is still an active and hot field of study
with important open questions:

- Is it because we lack enough training data?
- Should we get deeper models?
- Is it possible to have one single model for a specific task regardless the data?

