

Mitosis Detection in Breast Cancer Histology Images with Multi Column Deep Neural Networks

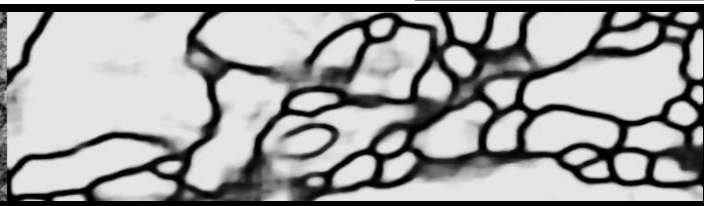
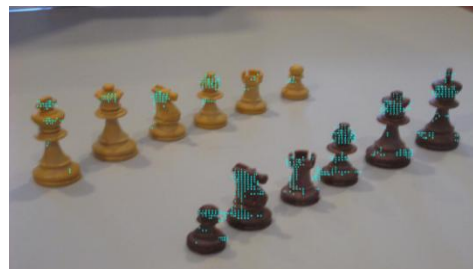
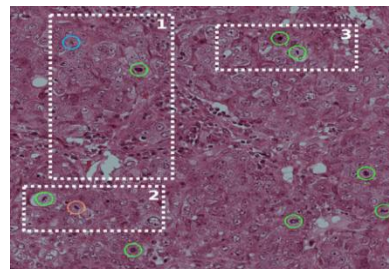
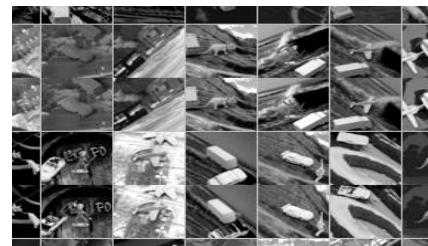
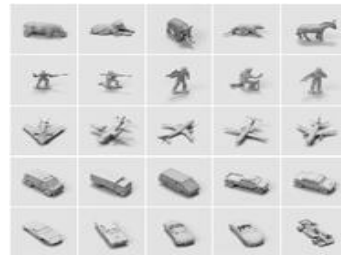
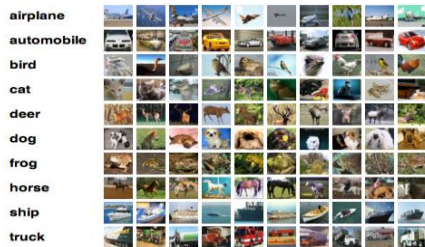
Dan C. Cireşan and Alessandro Giusti

IDSIA, Lugano, Switzerland
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DNN for Visual Pattern Recognition

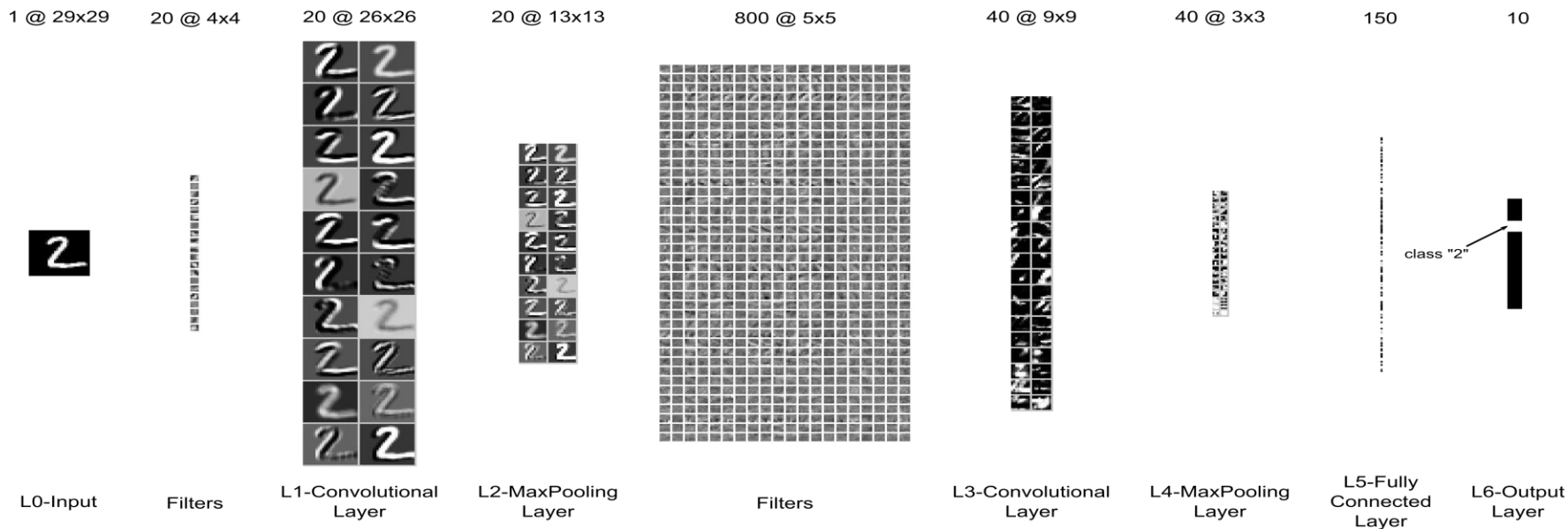
- One of the first to have a DNN implemented on GPU (CUDA), 2009
- We applied DNN on a plethora of pattern recognition tasks



Why mitosis detection?

- Mitosis detection is a challenging visual pattern recognition problem
- No histology or medicine background
- **ICPR2012 & MICCAI2013 competitions:**
 - 2012 ICPR Competition: 50 images, 300 mitosis; 17 teams
 - 2013 MICCAI Competition: ~600 images, 1157 mitosis; 14 teams

Deep, Convolutional Neural Network





MITOSIS DETECTION IN BREAST CANCER HISTOLOGICAL IMAGES

IPAL UMI CNRS - TRIBVN - Pitié-Salpêtrière Hospital - The Ohio State University

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Mitosis Detection in Breast Cancer Histological Images (MITOS dataset)

An ICPR 2012 Contest



We propose a contest of mitosis detection in images of H&E stained slides of breast cancer. Mitotic count is an important parameter for the prognosis of breast cancer. However, mitosis detection is a challenging problem and has not been addressed well in the literature. Indeed, mitosis detection is very challenging since mitosis appear in image as small objects with a large variety of shapes, and they can thus be confused with some other objects or artefacts present in the image.

We add a further dimension to the contest by using two different slide scanners having different resolution to produce RGB images and a multi-spectral microscope producing images in 10 different spectral bands and 17 layers Z-stack.



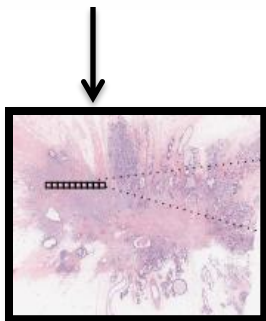
USER LOGIN

Username *

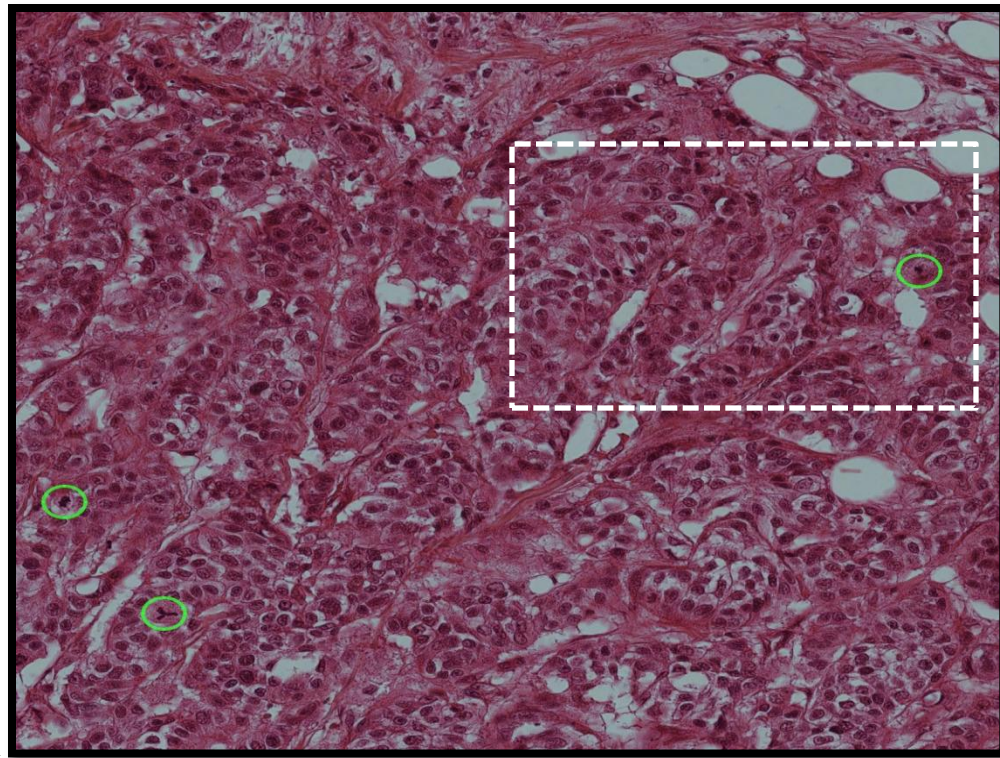
Password *

[Request new password](#)

Data Description



2048x2048 px (0.5 x 0.5 mm)



Method

- We use a **powerful pixel classifier** (a Deep Convolutional Neural Network) to detect pixels close to mitosis centroids
- Input: **raw pixel values** in a window (no features, no preprocessing)
- Output: **probability** of central pixel being close to a mitosis centroid

Network Architecture

Layer Type	Maps and neurons	Filter size	Weights	Connections
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Training samples & time

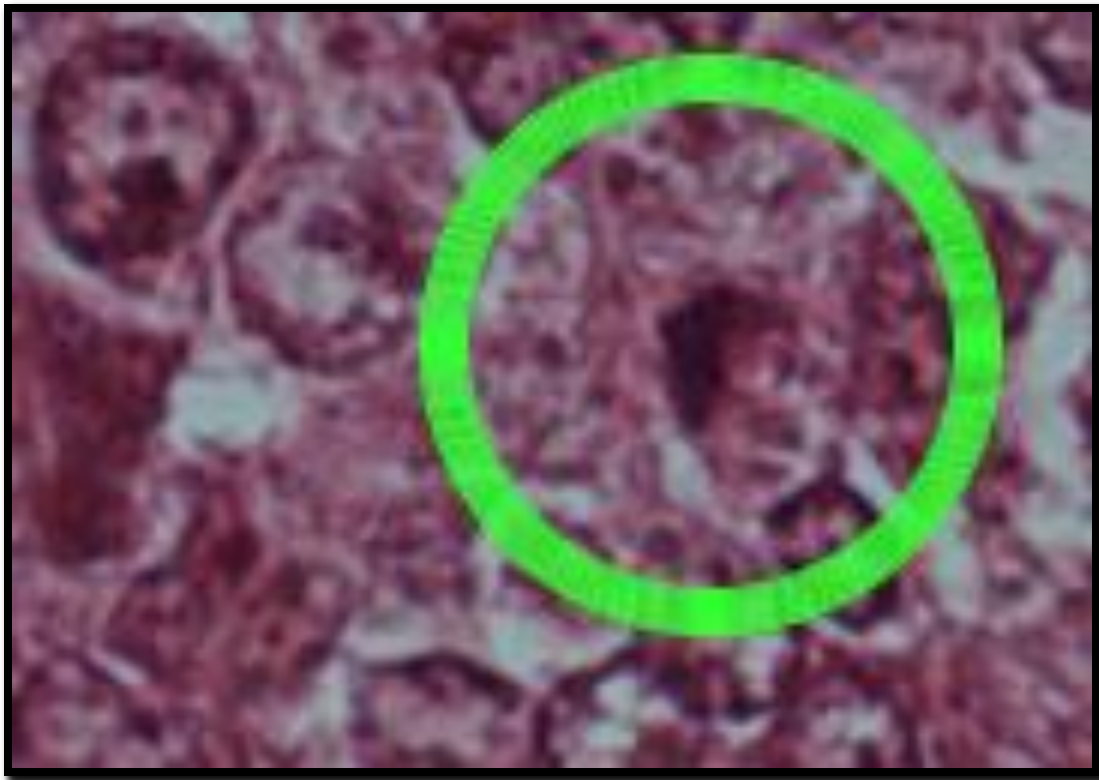
66K positive training samples
(all pixels closer than 10 px to a mitosis)
2M negative training samples

ICPR 2012

→ **5 months** training time for up to
7 epochs on a **CPU**

Or up to **3 days** on a **GPU**

Approach Overview

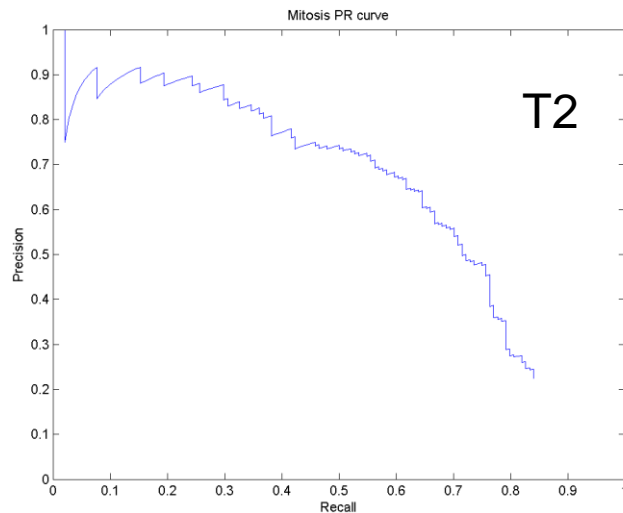
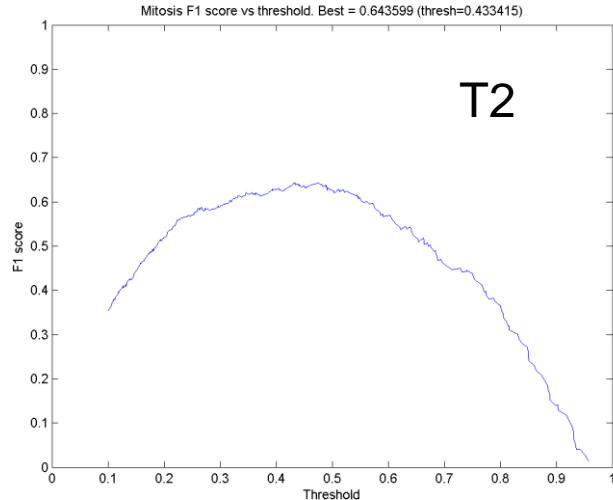


Data and nets

- Training set (263 images with ground truth, coming from 12 patients)
 - We split the training set in two sets T1 (174 images) and T2 (89 images)
- Initially we trained nets on T1 and validated on T2
- Then we trained nets on T1+T2 and applied them to T3 (our submissions)
- Evaluation set (295 images without ground truth, coming from other 11 patients)
 - Used exclusively for testing
 - Denoted as T3 (ground truth known only by the organizers)

Results for net n10

- Trained on T1. Results on the validation set (T2) with 8 variations
- Ground truth is used to decide on which threshold to use when training on T1+T2
- T2: (max F1 ~ 0.64 , F1 at 0.4 ~ 0.6) T3: F1 at 0.4 0.505
- We either overfitted on T2, or T2 and T3 are quite different (or both)



Our submissions

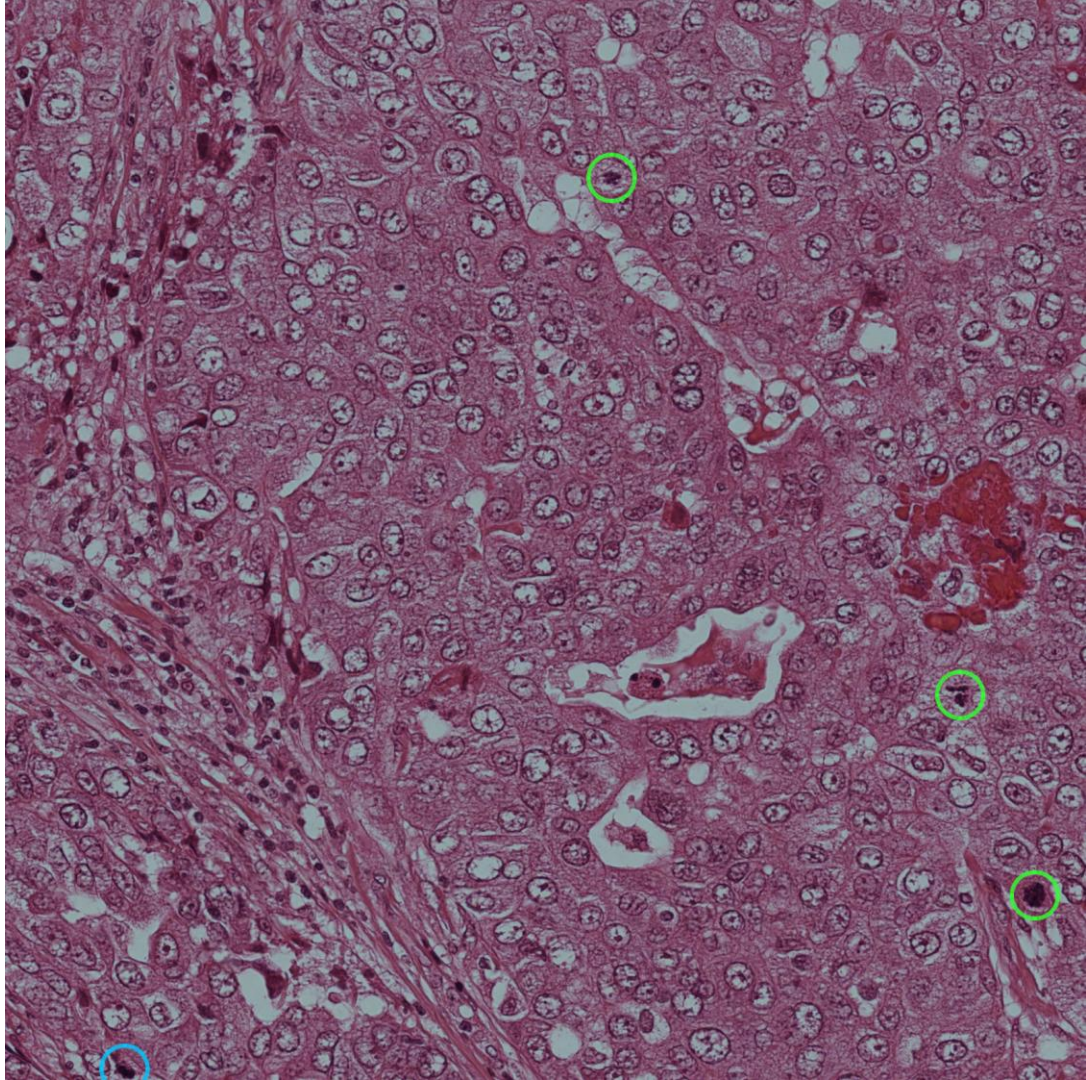
- $n_{10e06} + n_{30e05} + n_{31e02}$, 8 variations, T1+T2
 - $t=0.45 \rightarrow \text{F1-score} = \mathbf{0.593}$
 - $t=0.35 \rightarrow \text{F1-score} = \mathbf{0.460}$
 - $t=0.5 \rightarrow \text{F1-score} = \mathbf{0.611}$
- n_{10e06} , 8 variations, T1, $t=0.4 \rightarrow \text{F1-score} = \mathbf{0.505}$

Results overview on the evaluation dataset

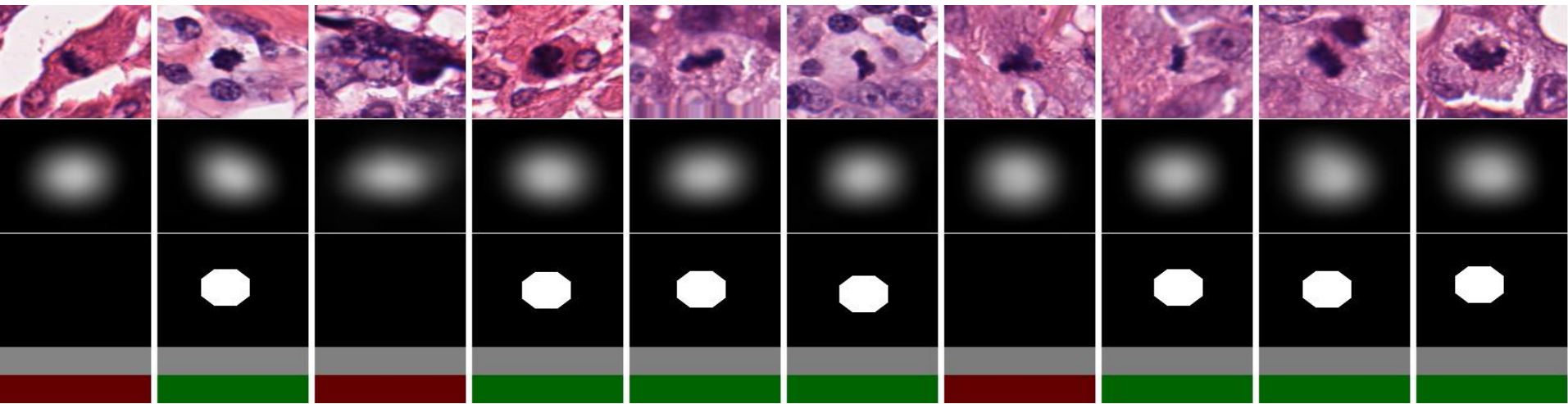
Green: True Positives

Red: False Positives

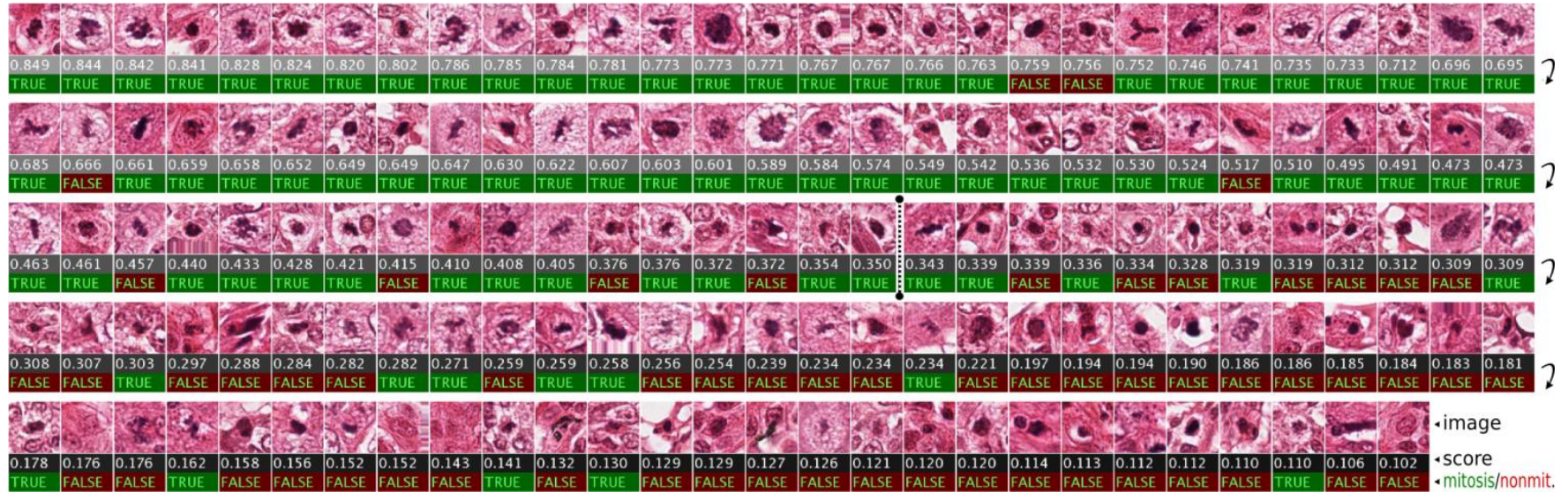
Cyan: False Negatives



n10 on validation data (T2)

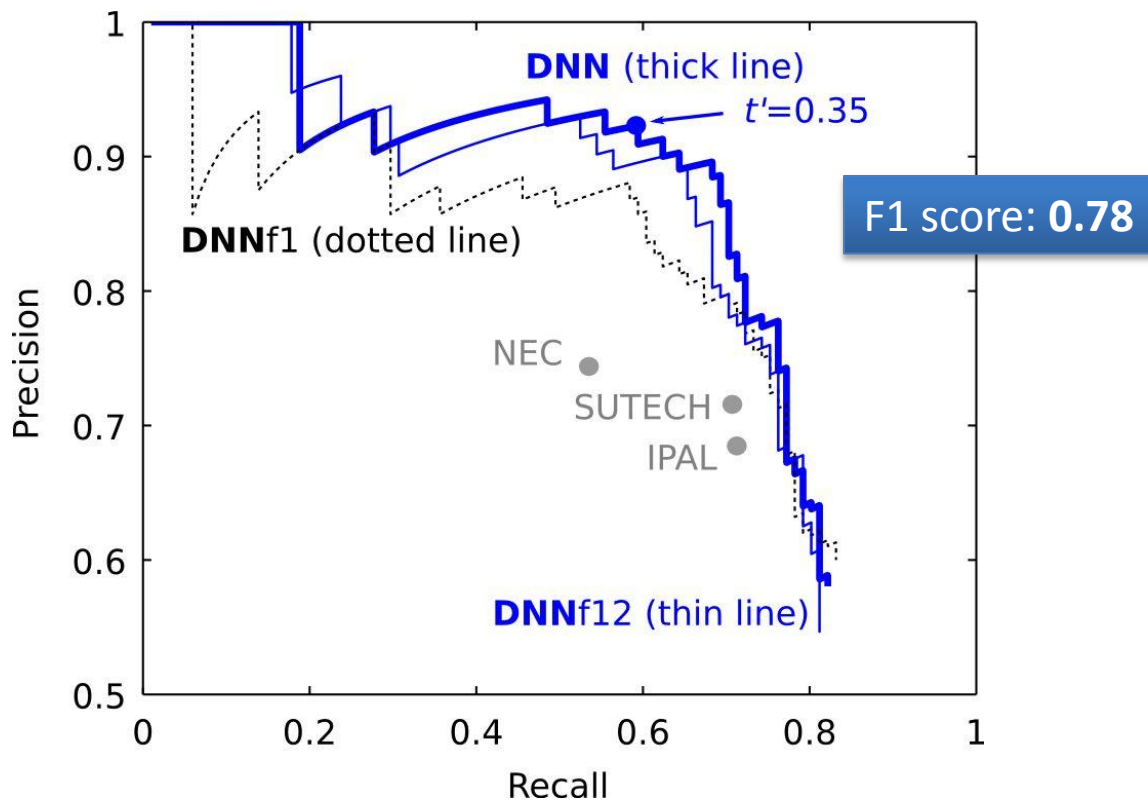


Detection results



method	precision	recall	F_1	score	method	precision	recall	F_1	score
DNN	0.88	0.70	0.782		NUS	0.63	0.40	0.490	
DNNf12	0.85	0.68	0.758		ISIK [19]	0.28	0.68	0.397	
DNNf1	0.78	0.72	0.751		ETH-HEILDERBERG [18]	0.14	0.80	0.374	
RAE [7]	0.69	0.74	0.716		OKAN-IRISA-LIAMA	0.78	0.22	0.343	
SUTECH	0.70	0.72	0.709		IITG	0.17	0.46	0.255	
NEC [12]	0.74	0.59	0.659		DREXEL	0.14	0.21	0.172	
UTRECHT [20]	0.51	0.68	0.583		BII	0.10	0.32	0.156	
WARWICK [10]	0.46	0.57	0.513		QATAR	0.00	0.94	0.005	

Quantitative Results



Assessment of Mitosis Detection Algorithms 2013 - MICCAI Grand Challenge



Assessment of Mitosis Detection Algorithms 2013

AMIDA13 | MICCAI Grand Challenge

<http://amida13.isi.uu.nl/>

Home

Background

Dataset

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- more training data
 - 2012 ICPR Competition
 - 50 images, 300 mitosis, 17 teams
 - 2013 MICCAI Competition
 - ~600 images, 1157 mitosis, 14 teams
- test data is more difficult

User login

Username *

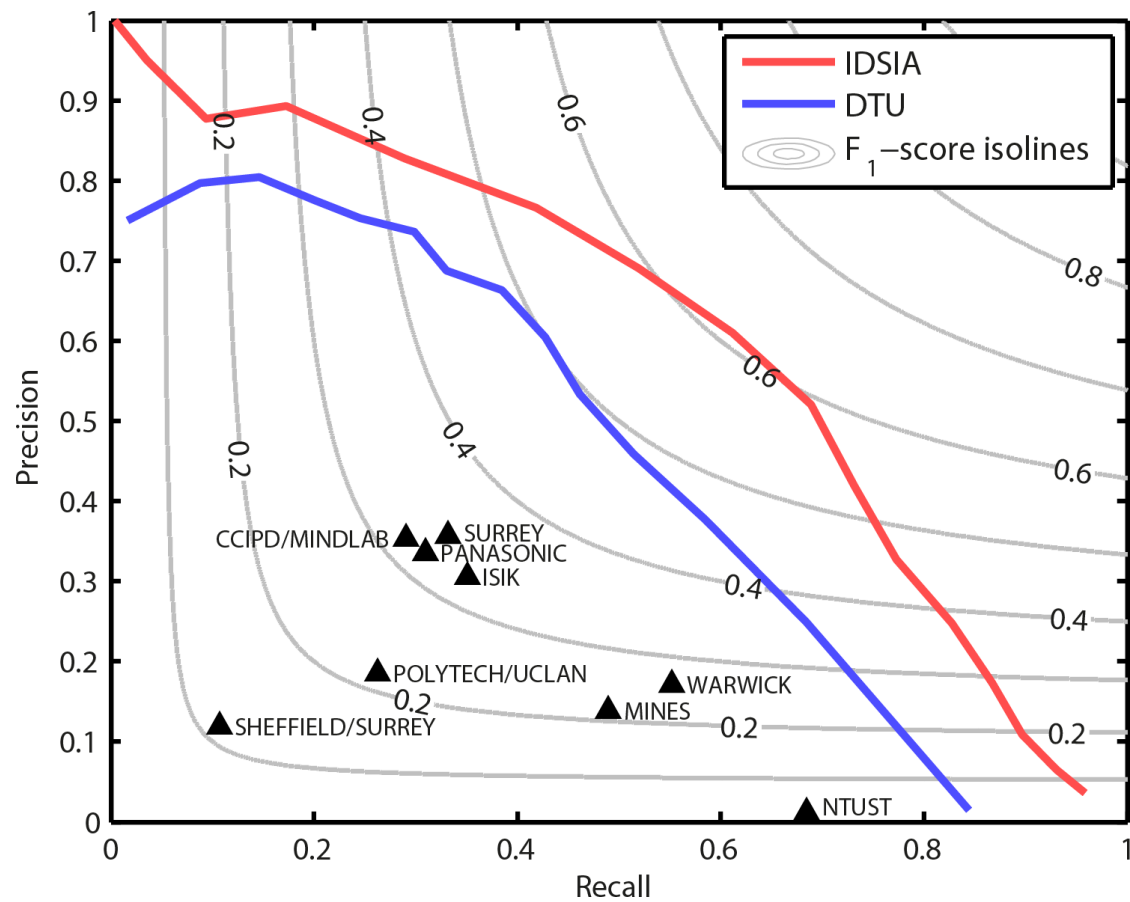
Password *

- [Create new account](#)
- [Request new password](#)

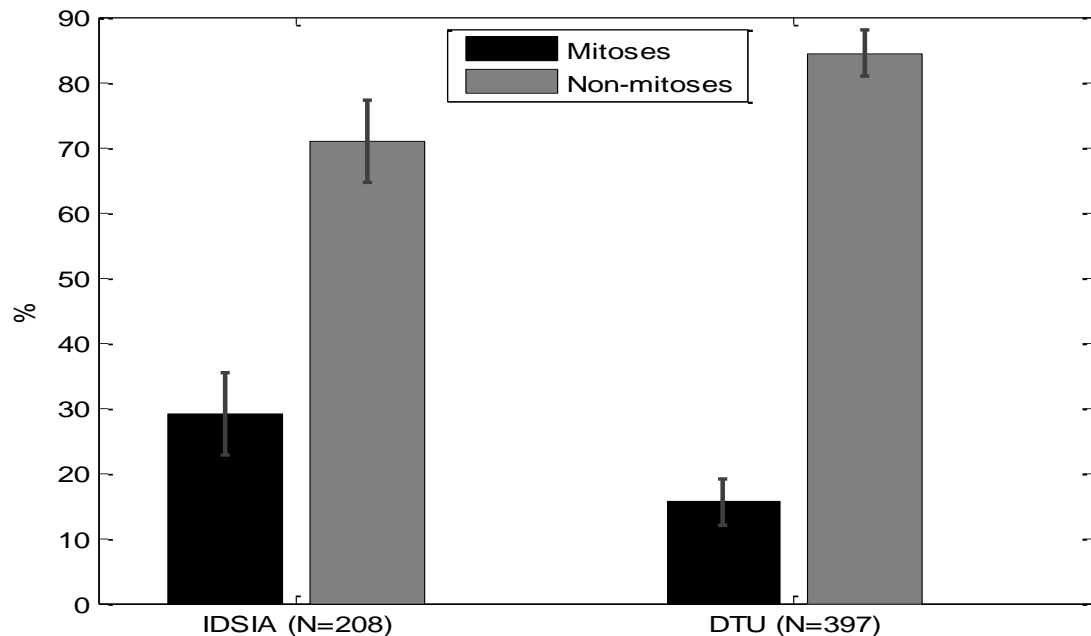
Log in

Updates

Results



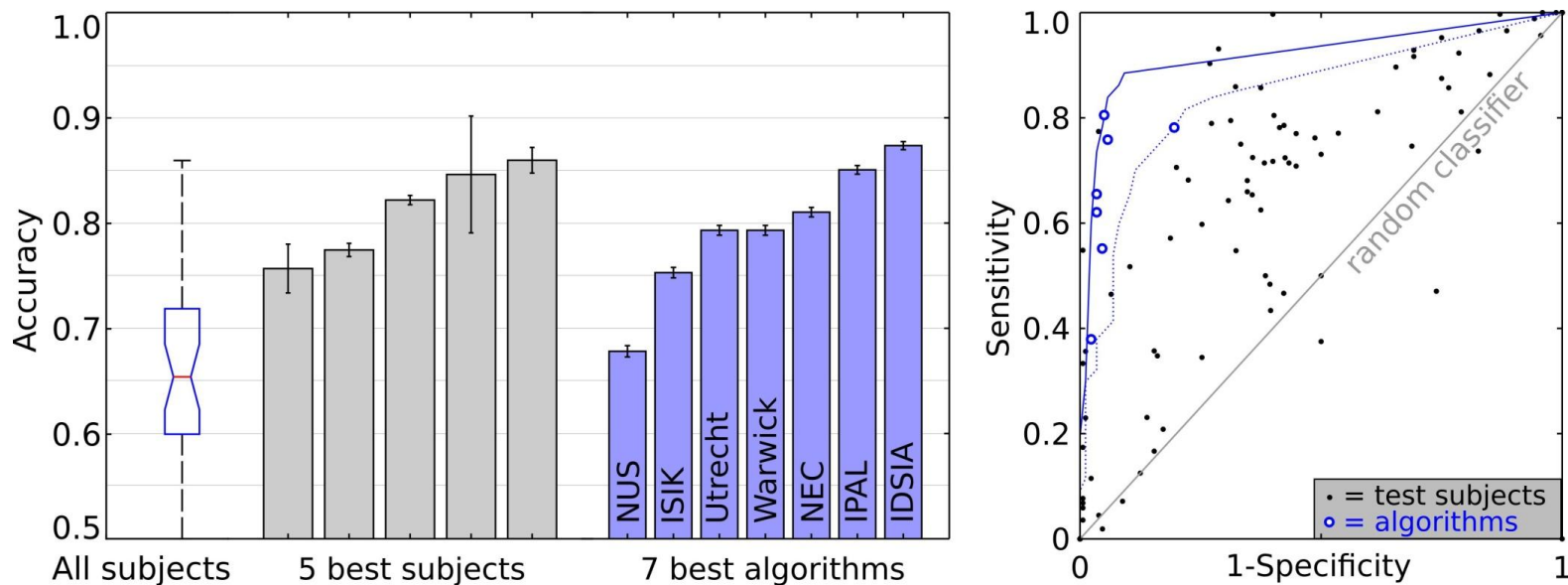
Reannotation experiment



histologists
reannotated 30% of
all our “False
Positives” as actual
mitoses they missed
during the original
annotation

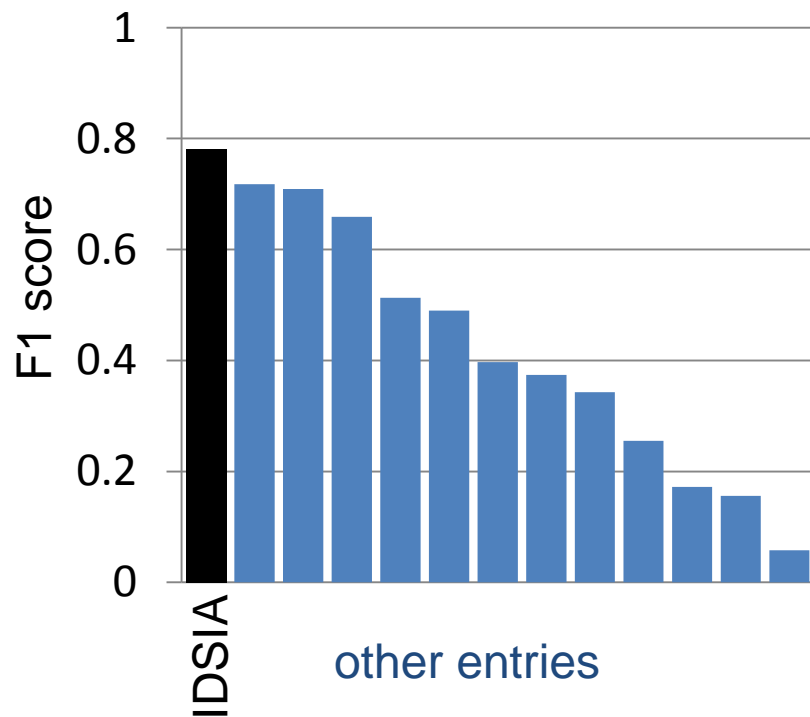
How do you compare with machines?

<http://bit.ly/YUYQFG>

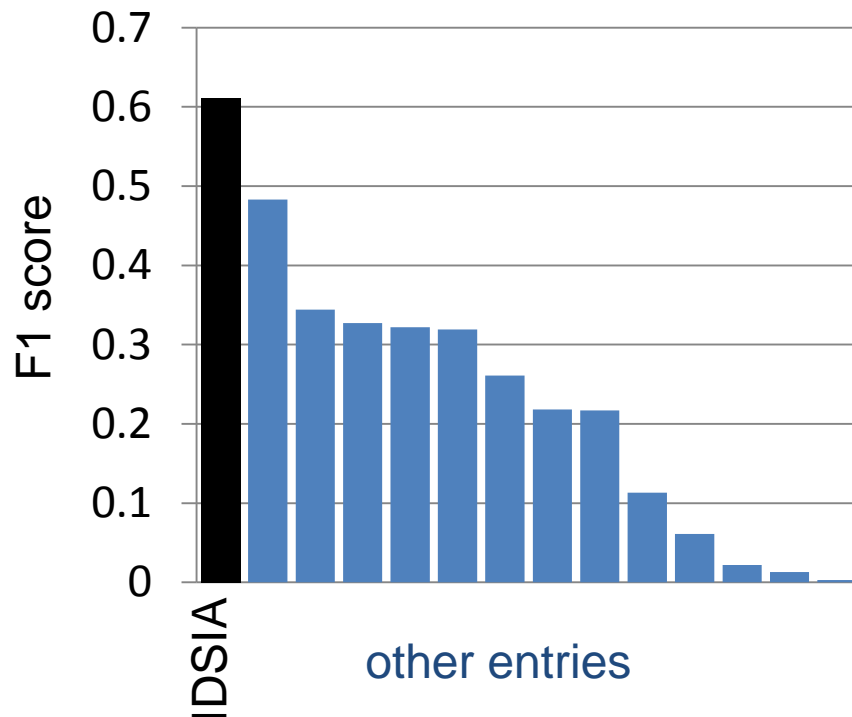


Results of Mitosis Detection Competitions

ICPR 2012



MICCAI 2013



Conclusions

- No need to extract handcrafted features: the network learns powerful features by itself
- Big deep nets combining CNN and other ideas are now state of the art for many image classification, detection and segmentation tasks
- Our DNN won six international competitions
- DNN can be used for various applications: automotive, biomedicine, detection of defects, document processing, image processing, etc.
- **DNN are already better and much faster than humans on many difficult problems**
- GPUs are essential for training DNN. Testing can be done on CPU.
- More info: www.idsia.ch/~ciresan dan.ciresan@gmail.com



Looking for new projects

- Industry
- Academic
 - Unrelated fields: biomedicine, psychology, finance, literature, history
 - Vision for robotics

Other projects

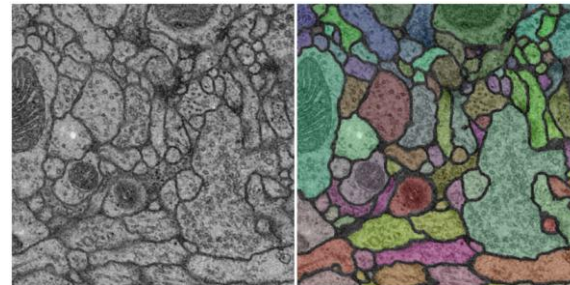
Neural Networks for Segmenting Neuronal Structures in Electron Microscopy Stacks – ISBI 2012

Training data:

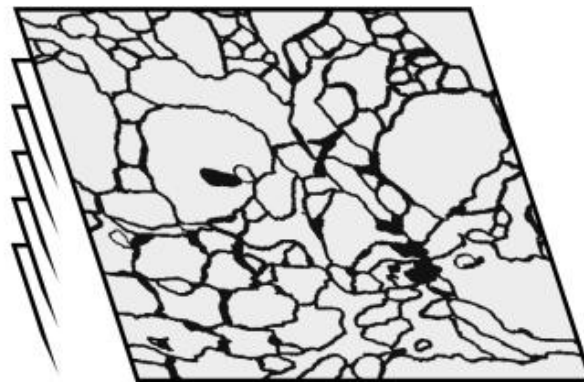
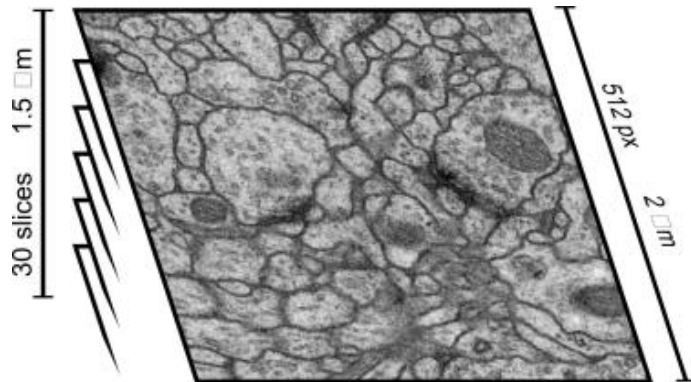
30 labeled 512x512 slices

Test data:

30 unlabeled 512x512 slices



CONNECTOMICS

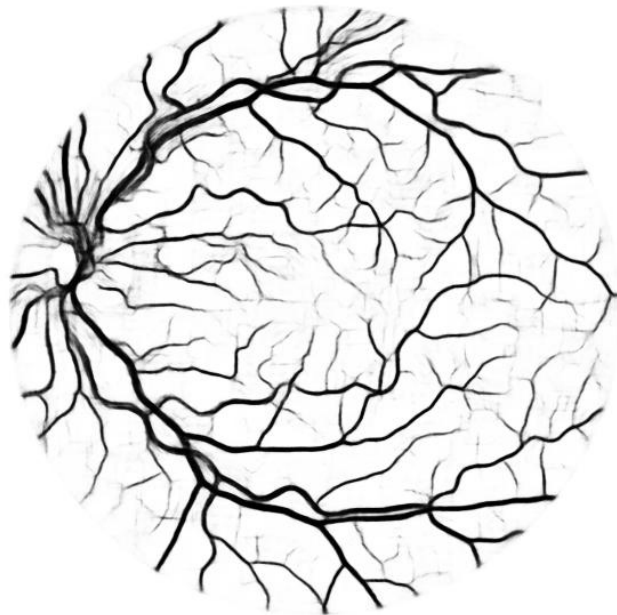


Retina vessel segmentation

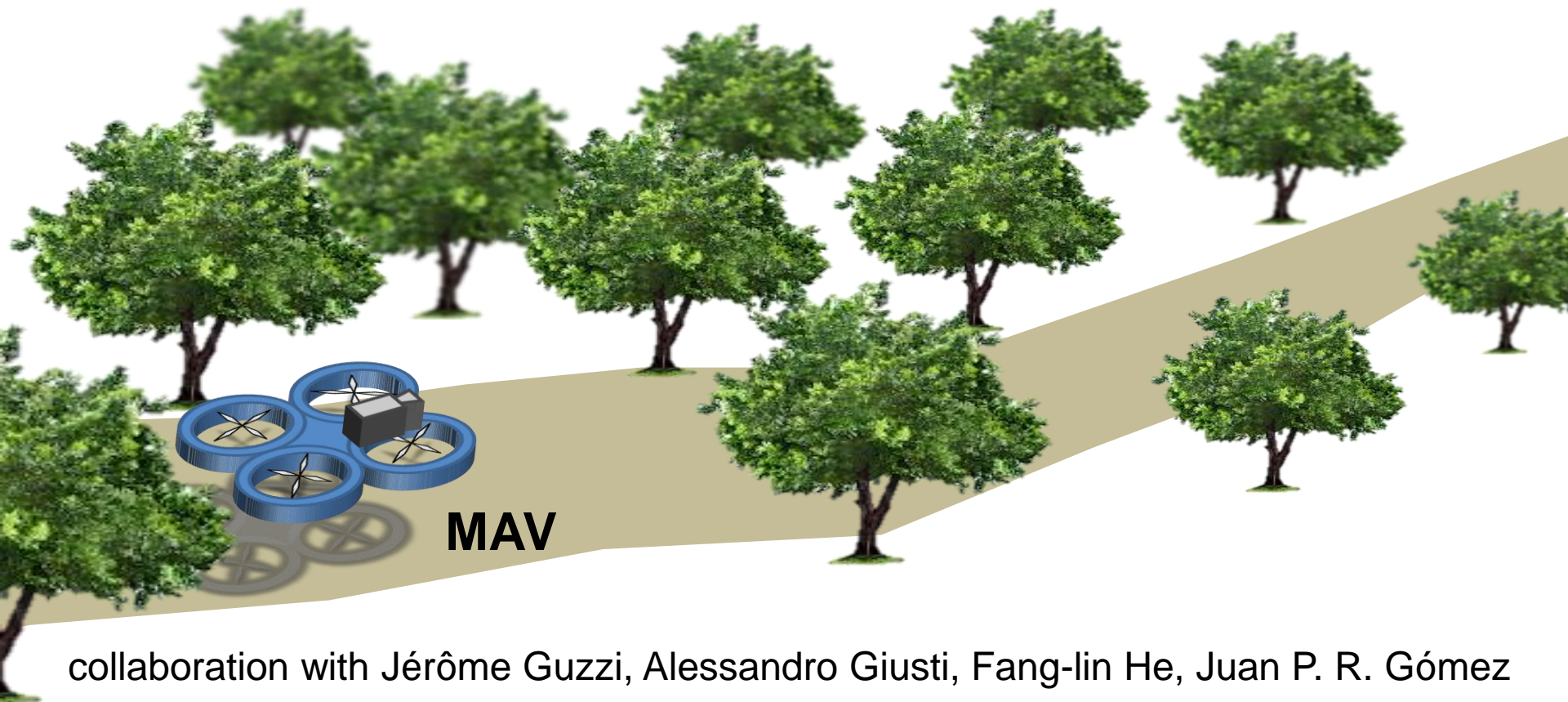
- challenging problem
- clinical relevance (e.g. for diagnosing glaucoma)
- state of the art results for DRIVE and STARE datasets
- better than a second human observer



DNN
→



Trail Following Problem



collaboration with Jérôme Guzzi, Alessandro Giusti, Fang-lin He, Juan P. R. Gómez