



Deep Learning for Life Science



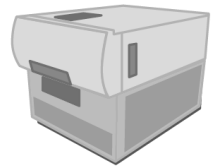
Hossein Azizpour

Assistant Professor in Machine Learning
Robotics, Perception, and Learning (RPL)

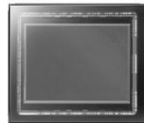
KTH

The time is right!

necessary technological developments come together



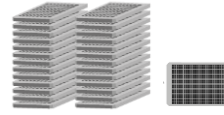
high throughput confocal



CMOS



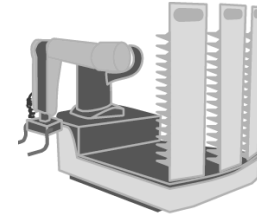
Protein & chemical labels



miniaturization & high throughput



tissue slide scanners



automation



SSDs, network storage

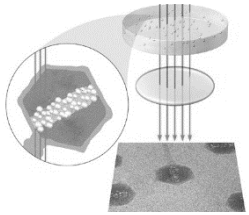
More sensitive labels and sensors

Higher throughput data creation

Increased storage capacity

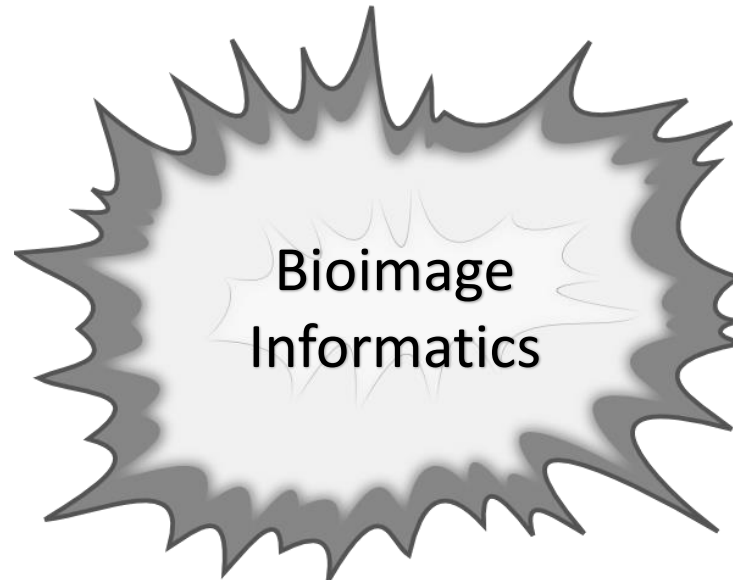


Cloud computing

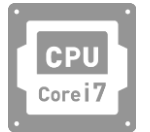


cryo-EM

More advanced microscopy techniques

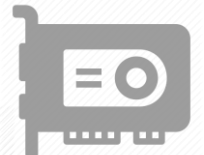


Faster computing

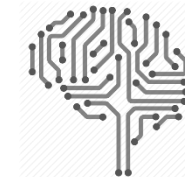


Faster CPUs

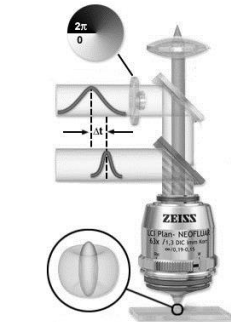
Better algorithms



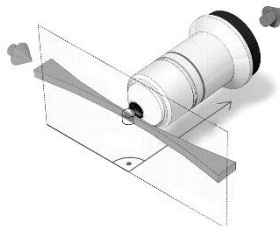
GPUs



deep learning



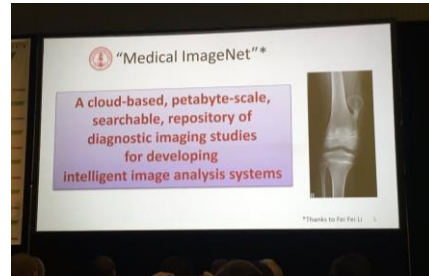
super resolution



light sheet

A New Era

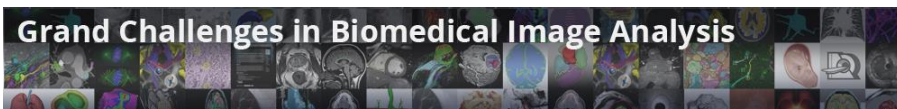
of large publicly available data and benchmarks



powered by Sage Bionetworks



Year(s)	Challenge	Task
2009-2010	DIADEM	Neuron morphology
2012	PTC	Particle detection in time-lapse microscopy
2012	SNEMI23	Neurite segmentation in 2D
2012,2014	MITOS	Cell mitosis detection in histopathology
2012,2014	DM3D	3D deconvolution microscopy
2013-2015	CTC	Cell segmentation and tracking
2013	SMLM	Single-molecule localization
2013	SNEMI3D	Neurite segmentation in 3D
2013	AMIDA	Cell mitosis detection in histopathology
2014,2015	OCCIS	Overlapping cell segmentation in cancer
2014	MITOS-ATYPIA	Mitosis detection and cancer scoring
2015	GLAS	Gland segmentation in histopathology
2015	NCC	Nucleus counting in multichannel micro.
2015-2016	BigNeuron	Large-scale 3D neuron reconstruction
2016-2017	CAMELYON	Cancer metastasis detection
2017	DREAM	Breast cancer detection
2017	CYTO	Cell atlas protein localization



A New Era

Excitement surrounding bioimage informatics



FOCUS ON BIOIMAGE INFORMATICS **REVIEW**

Biological imaging software tools

Kevin W Elceiri¹, Michael R Berthold², Ilya G Goldberg³, Luis Ibáñez⁴, B S Manjunath⁵, Maryann E Martone⁶, Robert F Murphy⁷, Hanchuan Peng⁸, Anne L Plant⁹, Badrinath Roysam¹⁰, Nico Stuurman¹¹, Jason R Swedlow¹², Pavel Tomancak¹³ & Anne E Carpenter¹⁴

Few technologies are more widespread in modern biological laboratories than imaging.

BIOINFORMATICS **EDITORIAL**

Vol. 28 no. 8 2012, doi:10.1093/bioinformatics/bts488

Editorial Advance Access publication March 15, 2012

Bioimage informatics: a new category in *Bioinformatics*

Enric Alcázar¹ and Jonathan D. Wren⁴

¹Department of Computer Science, University of Virginia, Charlottesville, VA 22904, USA, ²Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridgeshire, UK, ³Department of Biology, University of Virginia, Charlottesville, VA 22904, USA, ⁴Department of Medical Research, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma, USA

OPEN ACCESS Freely available online

PLOS COMPUTATIONAL BIOLOGY

Chapter 17: Bioimage Informatics for Systems Pharmacology

Hai Li, Zheng Yin, Guangxu Jin, Hong Zhao, Stephen T. C. Wong*

Center for Modeling Cancer Development, Department of Systems Medicine and Bioengineering, The Methodist Hospital Research Institute, Weill Medical College of Cornell University, Houston, Texas, United States of America

FOCUS ON BIOIMAGE INFORMATICS **COMMENTARY**

Why bioimage informatics matters

Gene Myers

Driven by the importance of spatial and physical factors in cellular processes and the size and complexity of modern image data, computational analysis of biological imagery has become a vital emerging sub-discipline of bioinformatics and computer vision.

July 2012 | volume 9 | number 7

nature methods

www.nature.com/naturemethods Techniques for life scientists and chemists

PERSPECTIVE

Imaging the future of bioimage analysis

Erik Meijering¹, Anne E Carpenter², Hanchuan Peng³, Fred A Hamprecht⁴ & Jean-Christophe Olivo-Marin⁵

1. Introduction

The old adage that a picture is worth a thousand words certainly applies to the field of bioimage analysis. The field is now expanding to include the analysis of large amounts of cell images with approaches in image analysis, computer vision, and machine learning. This is a natural extension of the field of image analysis, which has been traditionally used for the analysis of individual images. The field of bioimage analysis is now expanding to include the analysis of large amounts of cell images with approaches in image analysis, computer vision, and machine learning. This is a natural extension of the field of image analysis, which has been traditionally used for the analysis of individual images.

Leading Edge Essay

Computer Vision in Cell Biology

Gaudenz Danuser^{1,*}

¹Harvard Medical School, 240 Longwood Avenue, Boston, MA 02140, USA

*Correspondence: gaudenz.danuser@hms.harvard.edu
DOI: 10.1016/j.cel.2011.11.001

Computer vision refers to the theory and implementation of artificial systems that extract information from images to understand their content. Although computers are widely used by cell biologists for visualization and measurement, interpretation of image content, i.e., the selection of events of interest and the definition of what they mean in terms of cellular mechanisms, is mostly done manually.

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

LESIONS LEARNT

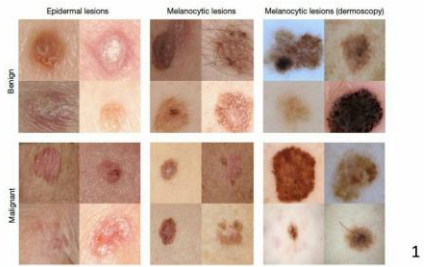
Artificial intelligence powers detection of skin cancer from images **PAGES 36 & 115**

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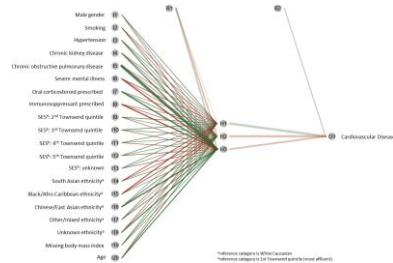
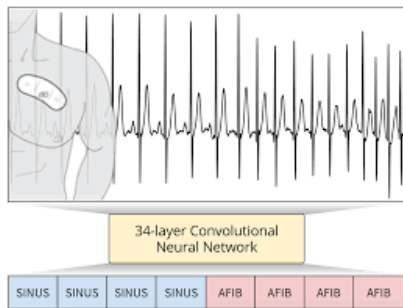
A New Era of AI-assisted medical advances



21 Board Certified Stanford Dermatologists
129,450 images of 2,032 diseases
1.41 million AI training images



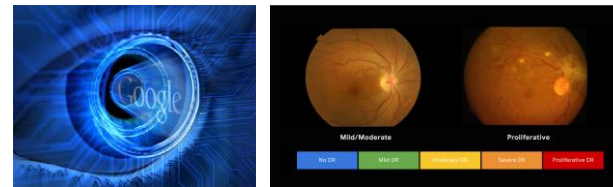
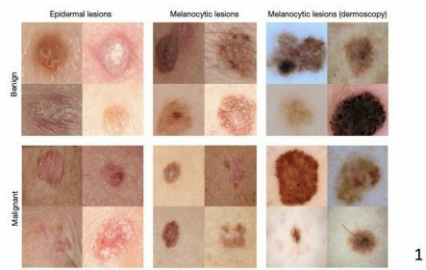
Accuracy



A New Era of AI-assisted medical advances

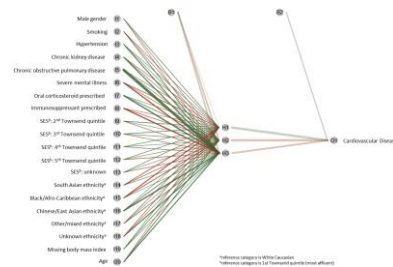
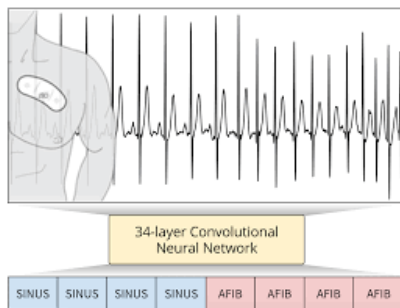


21 Board Certified Stanford Dermatologists
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Lack of specialists

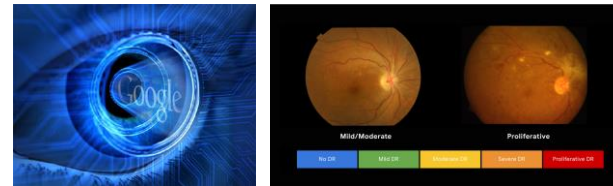
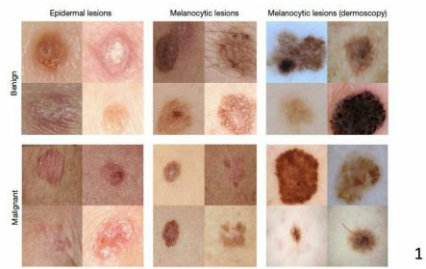
Accuracy



A New Era of AI-assisted medical advances

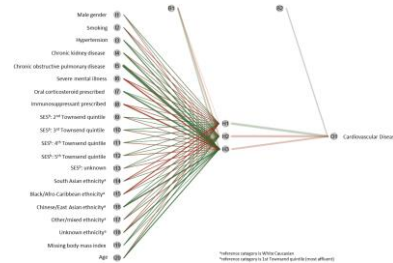
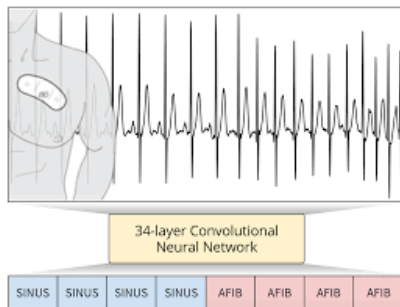


21 Board Certified Stanford Dermatologists
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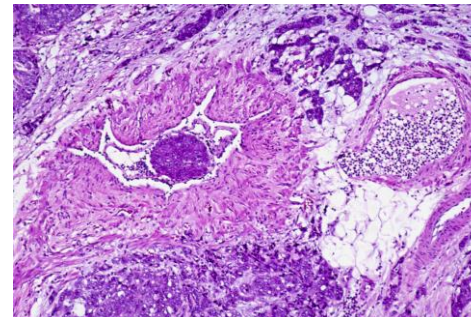


Lack of specialists

Accuracy



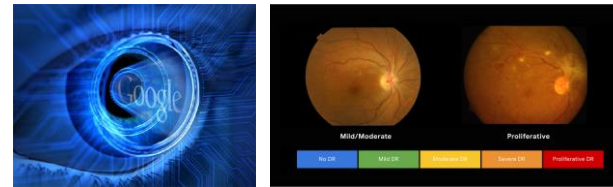
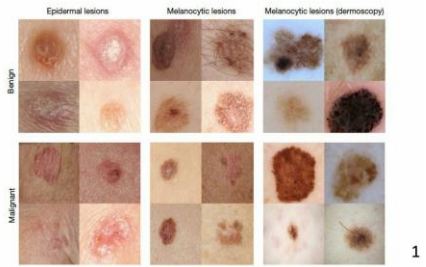
Efficiency



A New Era of AI-assisted medical advances

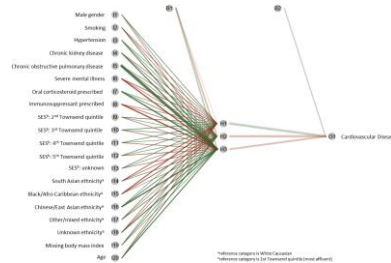
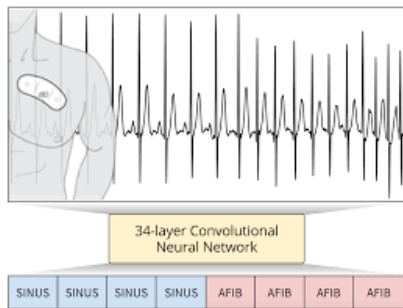


21 Board Certified Stanford Dermatologists
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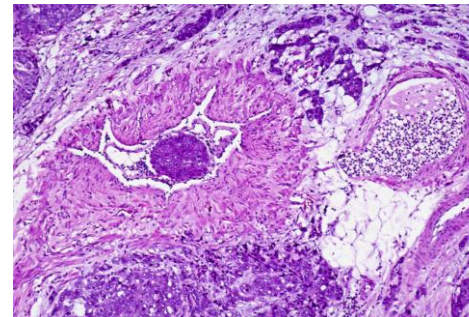


Lack of specialists

Accuracy



Efficiency



Cheaper



A New Era

General Life Science



SciLifeLab

verily

AstraZeneca

THE HUMAN PROTEIN ATLAS

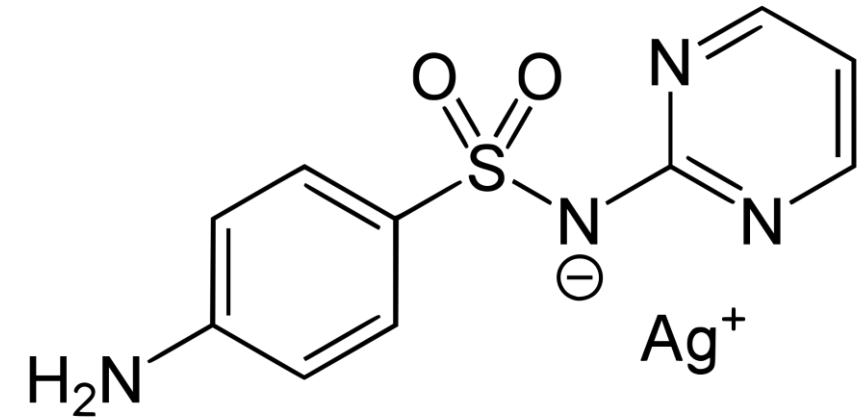
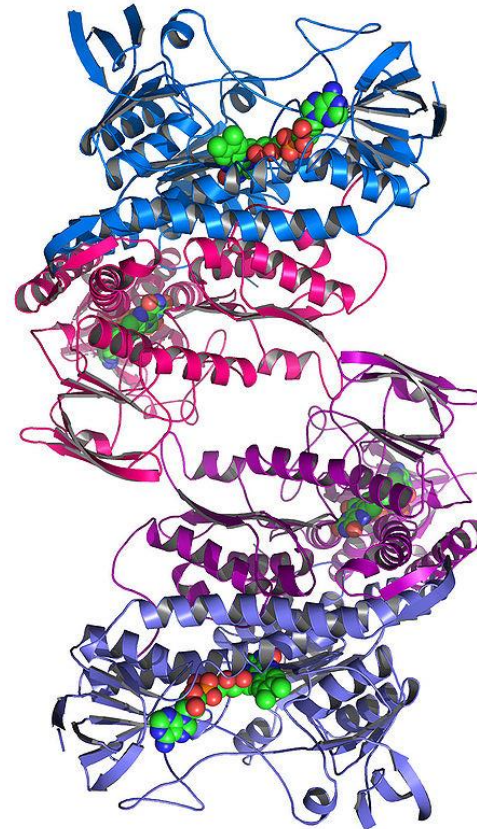
ABOUT & HELP

A Tissue-Based Map of the Human Proteome

Here, we summarize our current knowledge regarding the human proteome mainly achieved through antibody-based methods combined with transcriptomics analysis across all major tissues and organs of the human body. A large number of lists can be accessed with direct links to gene-specific images of the corresponding proteins in the different tissues and organs.

[Read more](#)

TISSUE ATLAS SUBCELL ATLAS CELL LINE ATLAS CANCER ATLAS

A screenshot of the 'The Human Protein Atlas' website. The main heading is 'THE HUMAN PROTEIN ATLAS' with 'ABOUT & HELP' below it. The central focus is 'A Tissue-Based Map of the Human Proteome'. A paragraph describes the project: 'Here, we summarize our current knowledge regarding the human proteome mainly achieved through antibody-based methods combined with transcriptomics analysis across all major tissues and organs of the human body. A large number of lists can be accessed with direct links to gene-specific images of the corresponding proteins in the different tissues and organs.' Below this is a 'Read more' link. At the bottom, there are four categories: 'TISSUE ATLAS', 'SUBCELL ATLAS', 'CELL LINE ATLAS', and 'CANCER ATLAS', each with a representative image.

Contents



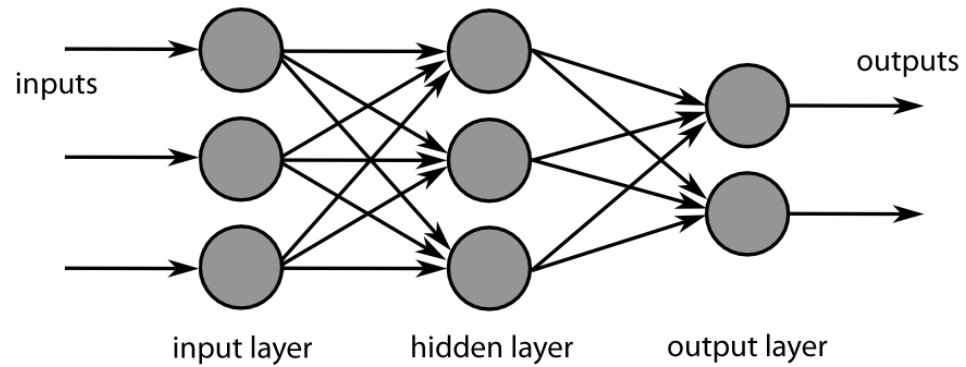
- Problem Definition
- Opportunities and challenges
- An example pipeline
- Domain Adaptation
- Uncertainty Estimation
- Future Directions

Contents



- **Problem Definition**
- Opportunities and challenges
- An example pipeline
- Domain Adaptation
- Uncertainty Estimation
- Future Directions

Deep Learning for Medical Science



Deep Learning for Medical Science

Under-supervised Learning

$D \sim P(X,Y)$ and $P(X)$ $P(Y|X)$ or $P(Z|X)$

weakly supervised learning

semi-supervised learning

Un/self Supervised Learning

$D \sim P(X)$ $P(X), P(Z|X), P(X|Z)$

clustering

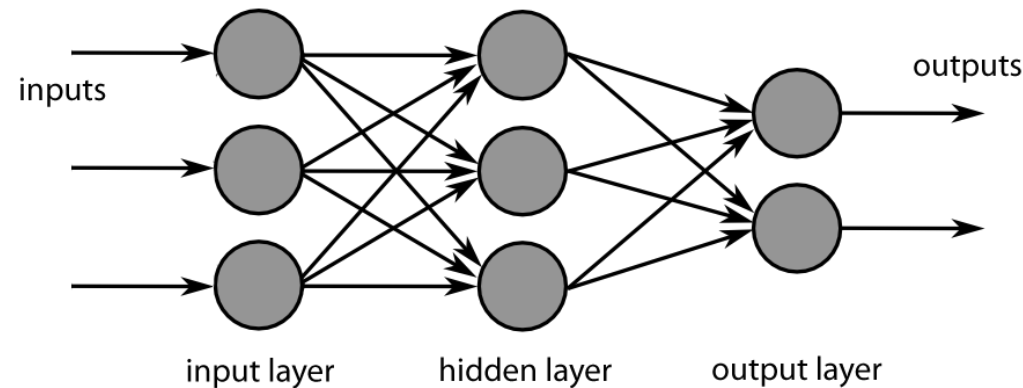
dimensionality reduction

Supervised Learning

$D \sim P(X,Y)$ $P(Y|X)$

classification

regression



Discriminative Models

Generative Models

Deep Learning for Medical Science



Prognosis

Risk Estimation

Diagnosis



Novel Biomarker

Patient Care

New Treatments

Personalized Medicine

Contents



- Problem Definition
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Opportunities



- Large amount of data is available (stored somewhere, hopefully digitized)
 - High-content screening
 - Digital pathology
 - Radiology
 - Drug discovery
 - Genomics
 - Clinical data
 - ...
- Repetitive routine tasks
- Shortage of specialists, outsourcing diagnosis/prognosis to different countries
- Training procedure for new specialists
- Improved and/or consistent accuracy
- Efficient diagnosis process
- Interesting scientific challenges
- Private and public Investments
- Last but not least, direct impact on human lives

Challenges



- Reliability
 - Interpretability
 - Uncertainty
- Recall is extremely important, precision also very important
- Public scrutiny for automated systems and AI in general
- Data standardization
- Different imaging equipment with different internal parameters and operator settings
- Multi-modal data
- Non-Euclidean data
- Bias (regional, temporal, etc.). Fair machine learning.
- Annotation cost (specialists' time are precious/expensive)
- Ambiguous definitions → Disagreement among specialists
- Privacy Issues with data collection
- Reverse engineering networks
- Inherently noisy labels
- Deep learning is data-hungry

Challenges



- **Reliability**
 - Interpretability
 - **Uncertainty** ✓
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- **Different imaging equipment with different internal parameters and operator settings**
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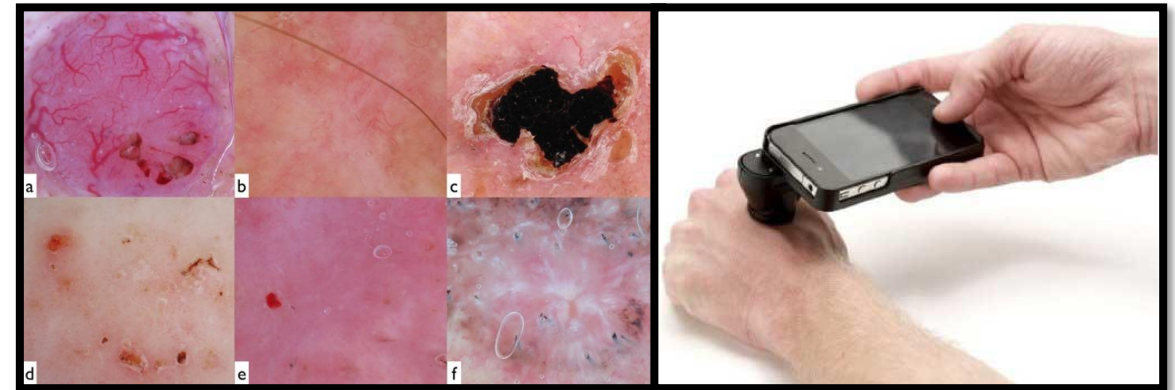
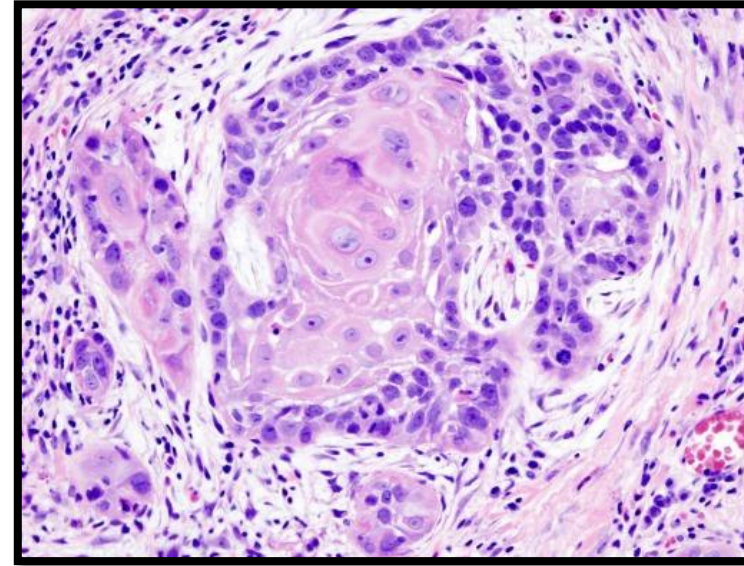
Contents



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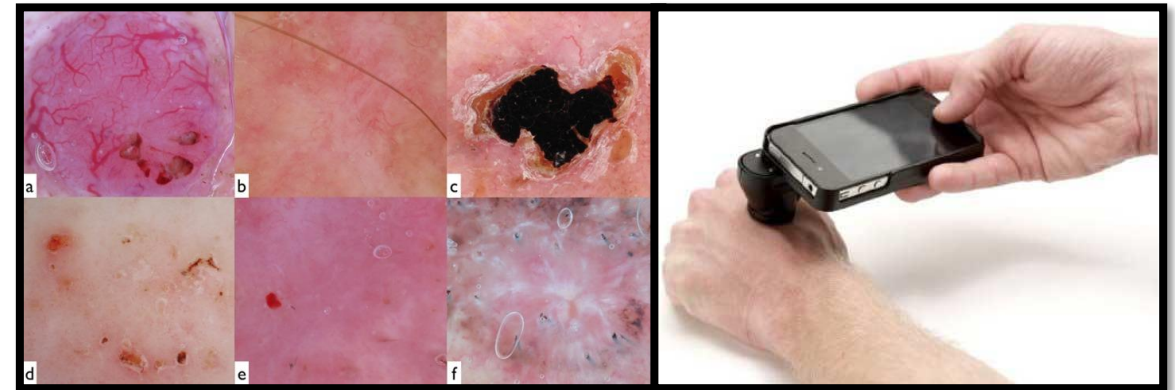
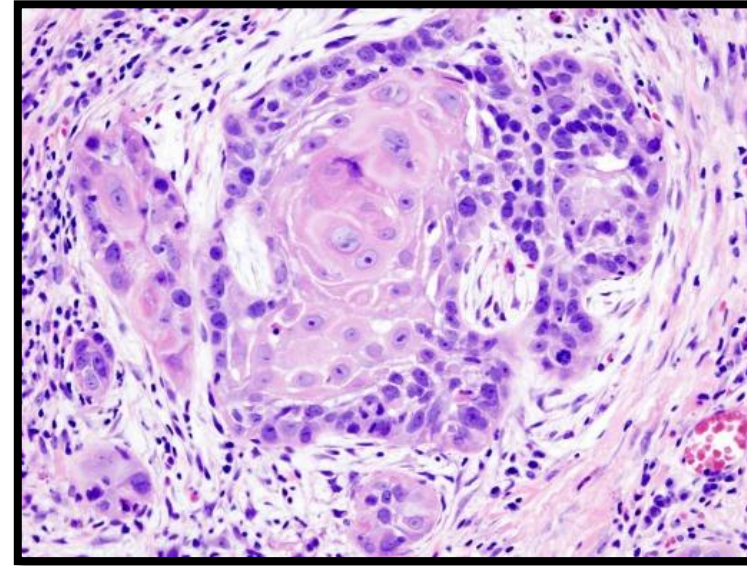
Medical Projects

- Histopathology
- Radiology
- Standard camera



Medical Projects

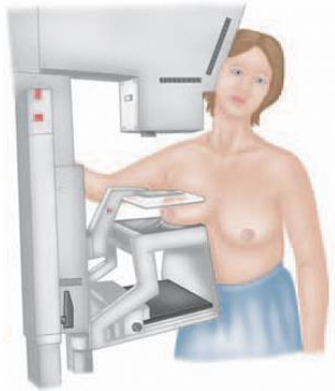
- Histopathology
- **Radiology** ✓
- Standard camera



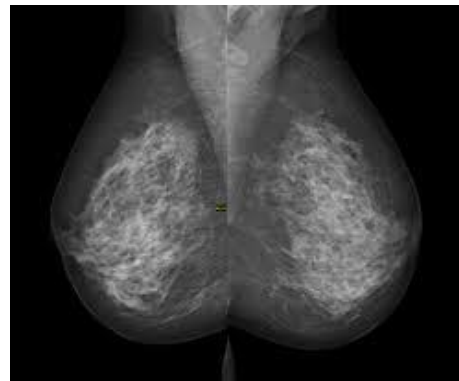
Digital mammographic screening for breast cancer



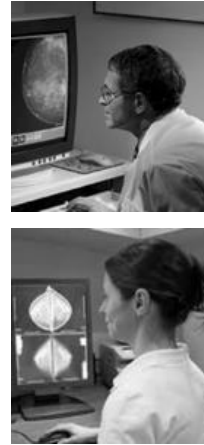
Current screening in Sweden



Women invited for screening*



Digital mammograms acquired from multiple angles



Two radiologists review case



Discussion and decision



Healthy



Recall

1. Additional imaging
2. Physical exam
3. Tissue sample



Cancer diagnosis

It is estimated that mammography-based screening **reduces breast cancer mortality by around 30%**

*All women in Sweden between 40 and 74 are invited for screening every 18 to 24 months.

Critical shortage of radiologists



SVENSKA DAGBLADET

Start Näringsliv Kultur Ledare ≡ Meny

Debatt

”Akut personalbrist hotar mammografin”

Landstingen klarar inte själva att lösa dilemmat med att landets mammografienheter dräneras på personal, samtidigt som belastningen ökar. Nu krävs konkret handling för att trygga mammografiverksamheten, skriver Ulrika Årehed Kågström och Jan Zedenius, Cancerfonden.

© 11 okt, 2016

Spara artikel



f 313 delningar



Gratis i en månad!

Få full tillgång till SvD digital.

Prova nu



Foto: Lars Pehrson

Limitations in Computer aided detection (CAD)



Radiology

Can Computer-aided Detection Be Detrimental to Mammographic Interpretation?¹

Liene E. Philpotts, MD

REVIEW AND COMMENTARY ■ CONTROVERSIES

Mammographic interpretation is one of the most difficult tasks in all of radiology. Reading mammograms can be more of an art than a science. Breast parenchymal patterns are not stable between patients, between left and right breasts, and even within the same breast from year to year in the same patient. Positioning, particularly in the mediolateral oblique projection, and the amount of compression applied are variable from examination to examination. Breast cancer has a varied appearance on mammograms, from the obvious spiculated masses, to very subtle asymmetries noted on only one view, to faint calcifications seen only with full digital resolution or a magnifying glass. The large volume of cases requiring interpretation in many practices is also daunting, given the number of women in the population for whom yearly screening mammography is recommended. Task repetition and fatigue combine to make missing the subtle signs of breast cancer a very real possibility, but one that can have serious consequences.

Given these difficulties, it is not surprising that approximately 20% of cancers are known to be missed at mammography (1-3). Some of this is because of the reduced sensitivity of mammography in the detection of lesions in dense breast tissues. But even if a lesion is visible on the images, the combination of the variable presentation of breast cancer on mammograms, as stated above, as well as the interpreting radiologist's threshold for both detecting and deciding to act on (ie, recall) such lesions, affects the reading. Accuracy in mammographic interpretation depends on many factors, of which experience and volume of studies read

seems obvious that this difficult task could likely be made less error prone with the help of computer programs. However, how much is art and how much is science? How can a computer be expected to operate in a very imperfect system (ie, variable mammograms and differing breast cancer patterns) at a level that would be clinically relevant (ie, not missing any or many cancers) without causing more problems (eg, many false-positive results)? It is a lot to ask, even of a computer.

CAD Studies and How They Differ

The literature about CAD is somewhat confusing and varies in both modeling and validity of results. There are some important differences in the CAD studies that have been published. While that does not negate the results, it does throw into question the validity of some studies. Results of some of the early studies, which were performed more by using retrospective analyses or computer modeling, suggested that CAD can achieve the main task for it was intended—that is, increasing cancer detection (1-7). Such studies showed an increase, or potential increase, in the cancer detection rates for radiologists with the use of CAD. There was initially a great deal of excitement over the concept of CAD and the results of these early studies.

However, much of the early literature was based on retrospective studies. That is, CAD was applied to mammograms with known cancers, and the images were reviewed to determine if CAD marked the cancers. Such studies were performed in an artificial study environment. This is known as the "laboratory effect"

Published online
10.1146/radiol.2531090609
Radiology 2009; 253:17-22

¹From the Department of Diagnostic Radiology, Yale University School of Medicine, New Haven, Conn. Received April 20, 2009; revision requested April 29; revision received June 11; final version accepted June 11. Address correspondence to the author, 333 Cedar St, PO Box

Limitations of CAD

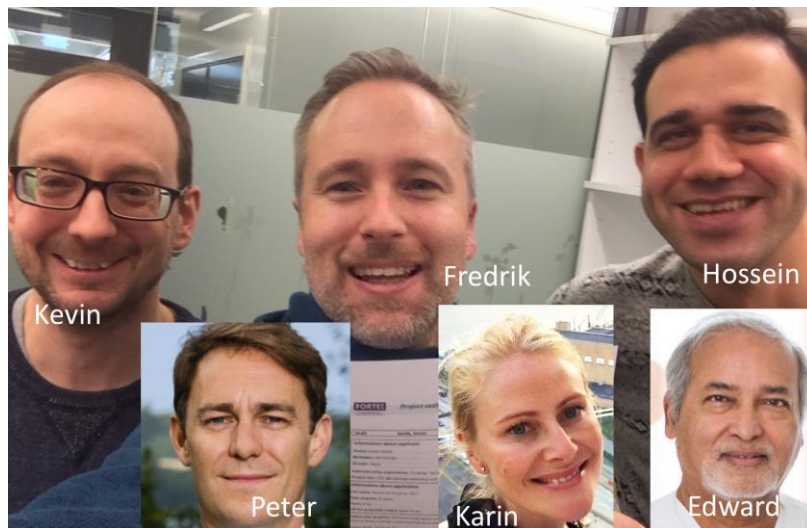
Clinical success depends on CAD having a high sensitivity, a reasonable specificity, and the reader taking appropriate action when interpreting the CAD prompts. All of these features work in conjunction, and all need to be optimized for the system to be valuable. Because mammography is an imperfect system, particularly in the detection of many of the more subtle cancers in denser breast tissues, to have reasonable sensitivity, the false-positive rate of CAD prompts must be high; thus, the specificity is low. Thus, the balance is not easy to achieve.



Difficult cases result in unacceptably high FP rate

MammoAI

mammoAI



UCSF

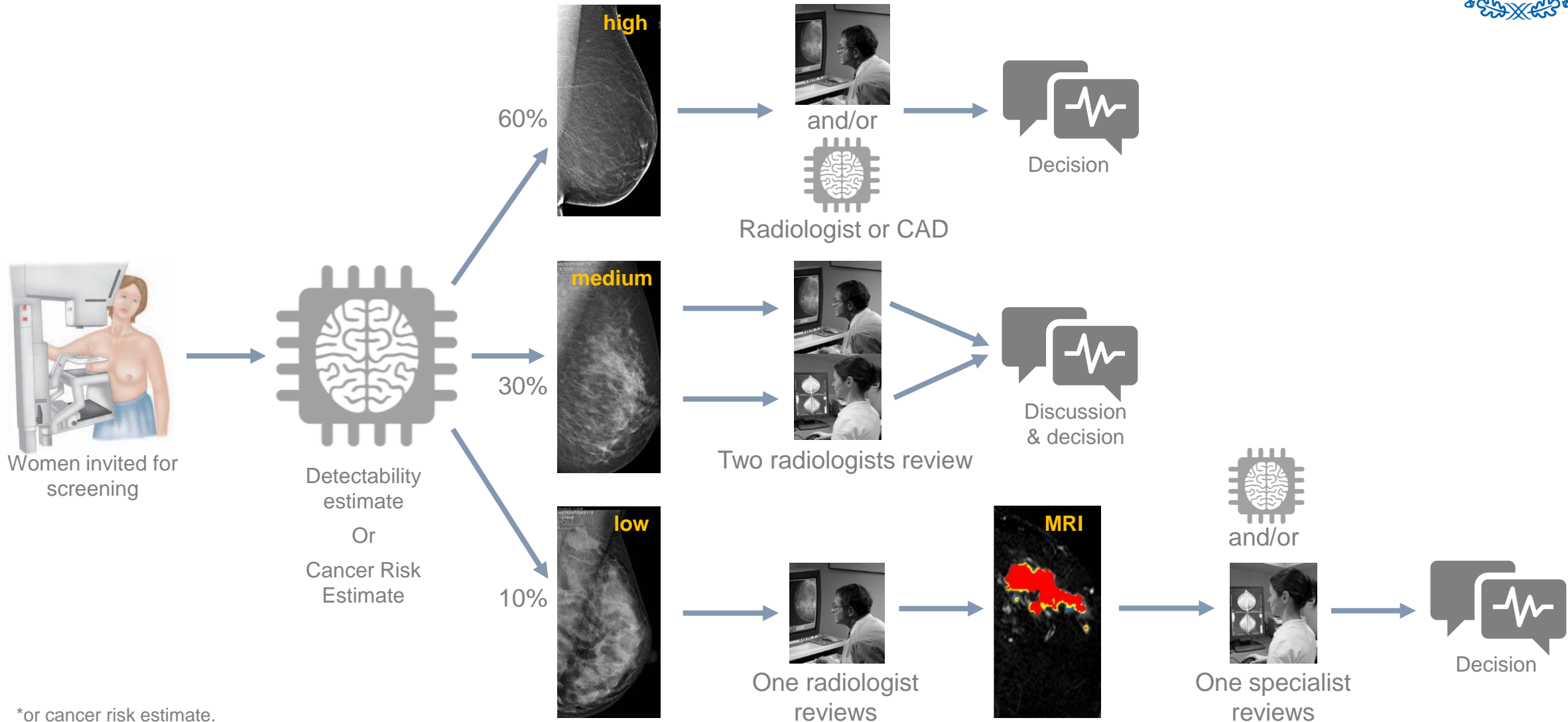


KAROLINSKA
UNIVERSITETSSJUKHUSET



SECTRA

Optimized Workflow



*or cancer risk estimate.

Massive dataset:

every mammogram in Stockholms län (2008 – 2015)



Screening: 241,149 exams
Clinical: 57,752 exams



Screening register:
~400,000 women (entire SLL)



Cancer register:
~9,000 women (entire SLL)



mammoAI

Total: ~2,400,000 images
Cancer: ~20,000 images



INbreast

Total: 410 images
Cancer: 360 images



CBIS-DDSM

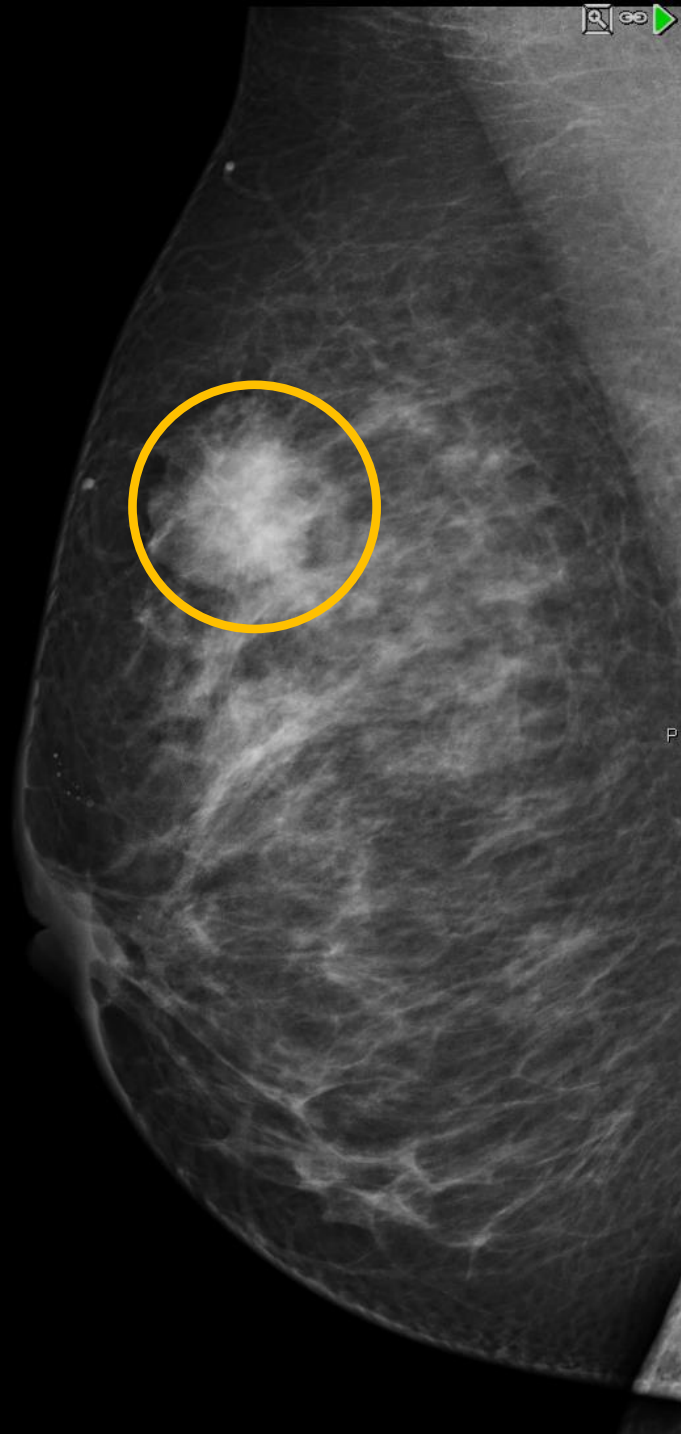
Total: 4,067 images
Cancer: 855 images

Deep Learning for Mammography



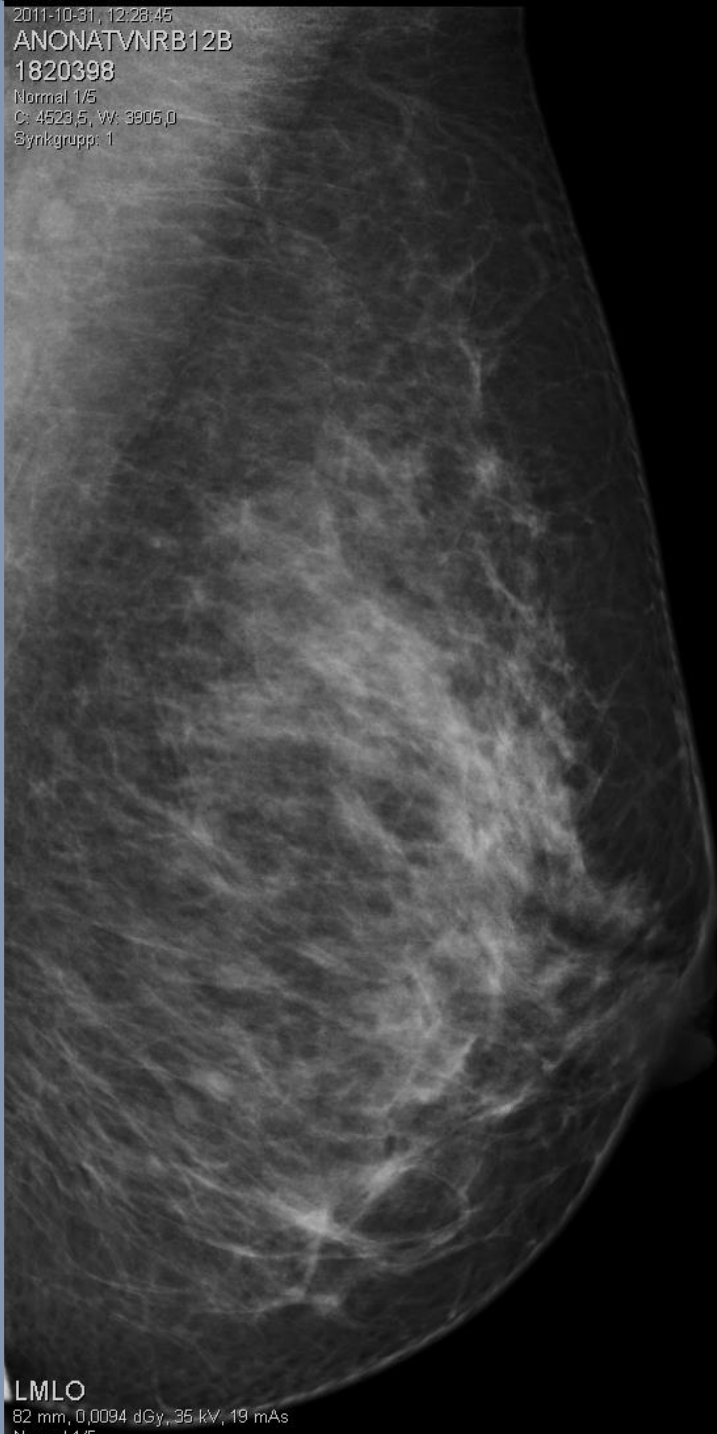
Tumor Detection Network (CAD)
and Risk Estimation

**Right
MLO**



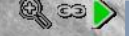
2011-10-31, 12:28:45
ANONATVNRB12B
1820398
Normal 1/5
C: 4523.5, W: 3905.0
Synkgrupp: 1

**Left
MLO**



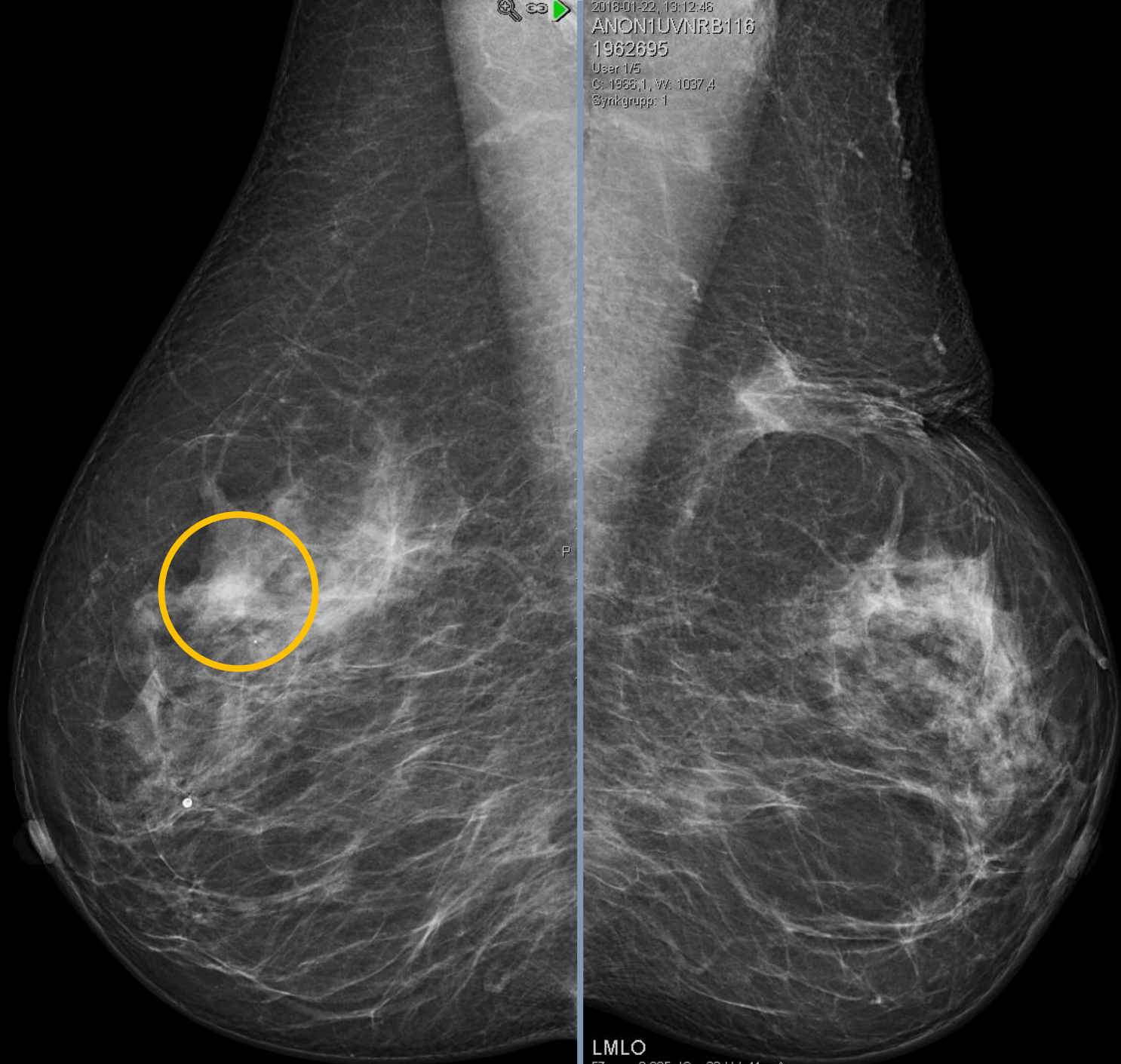
LMLO
82 mm, 0.0094 dGy, 35 kV, 19 mAs
Normal 1/5

**Right
MLO**

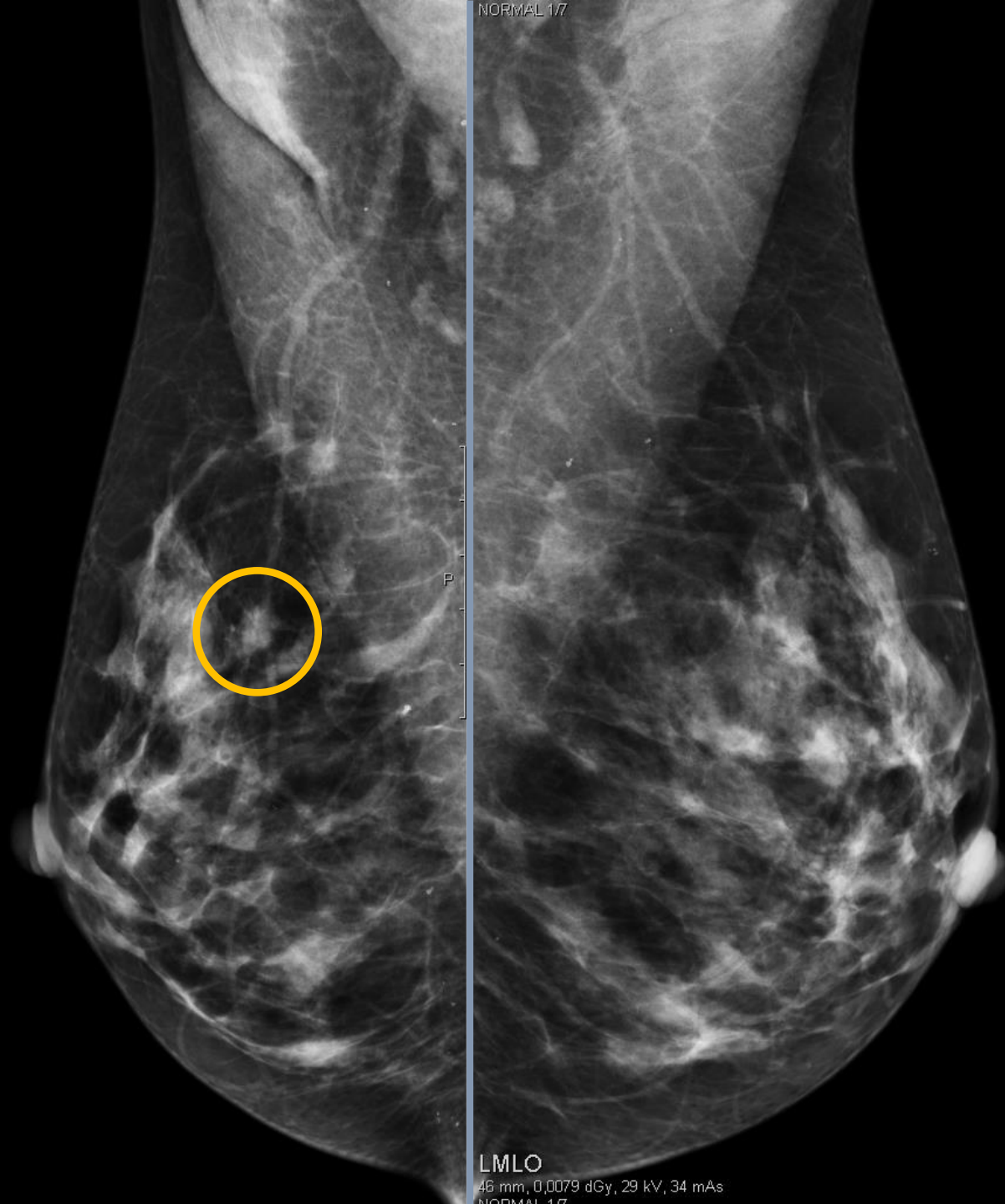


2016-01-22, 13:12:46
ANON1UVNRB116
1962695
User 1/5
C: 1966,1, W: 1097,4
Bynkrupp: 1

**Left
MLO**



**Right
MLO**



**Left
MLO**

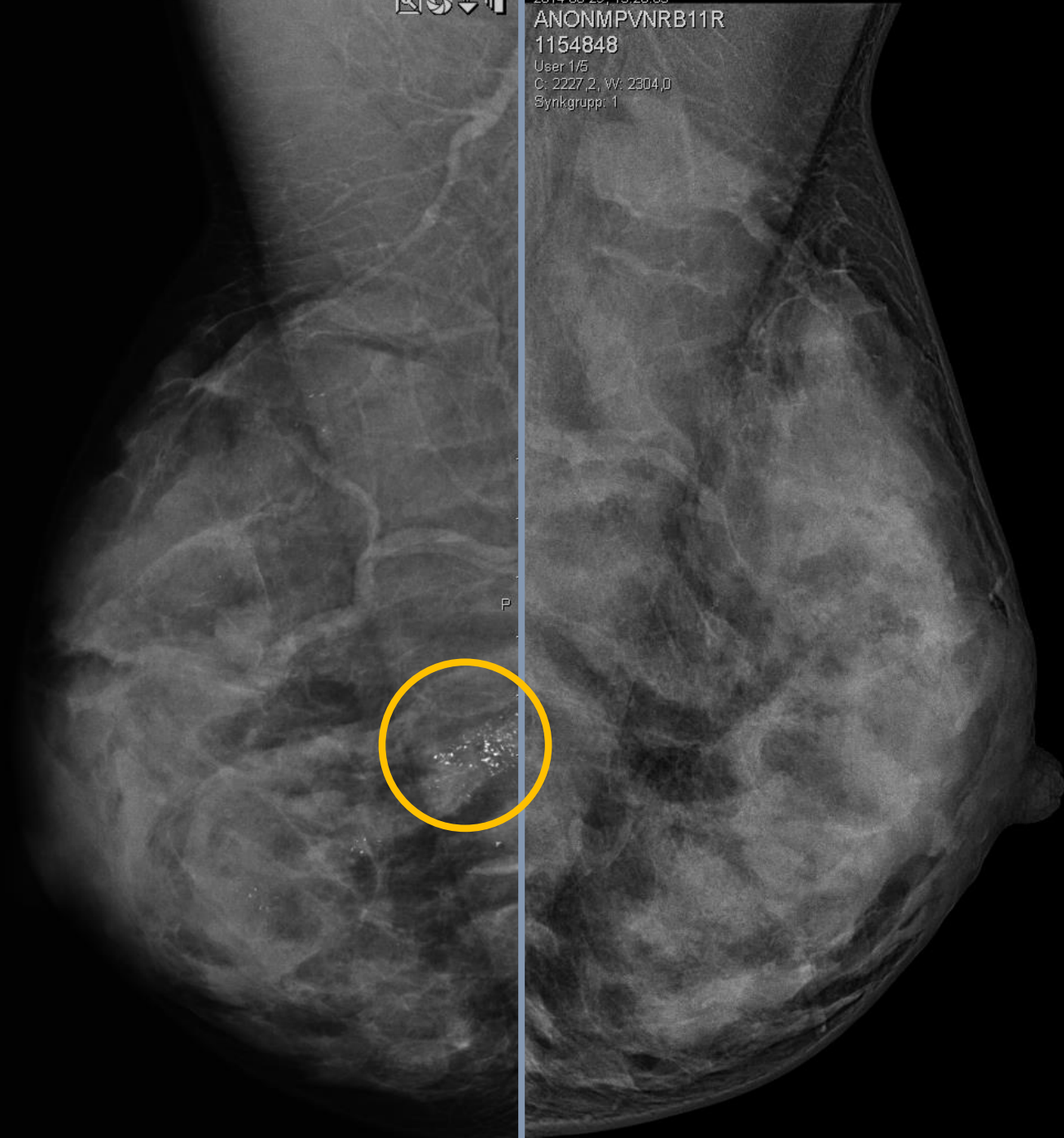
LMLO
46 mm, 0.0079 dGy, 29 kV, 34 mAs
NORMAL 17

**Right
MLO**



2014-08-29, 13:28:05
ANONMPVNRB11R
1154848
User: 1/5
C: 2227.2, W: 2304.0
Synkgrupp: 1

**Left
MLO**

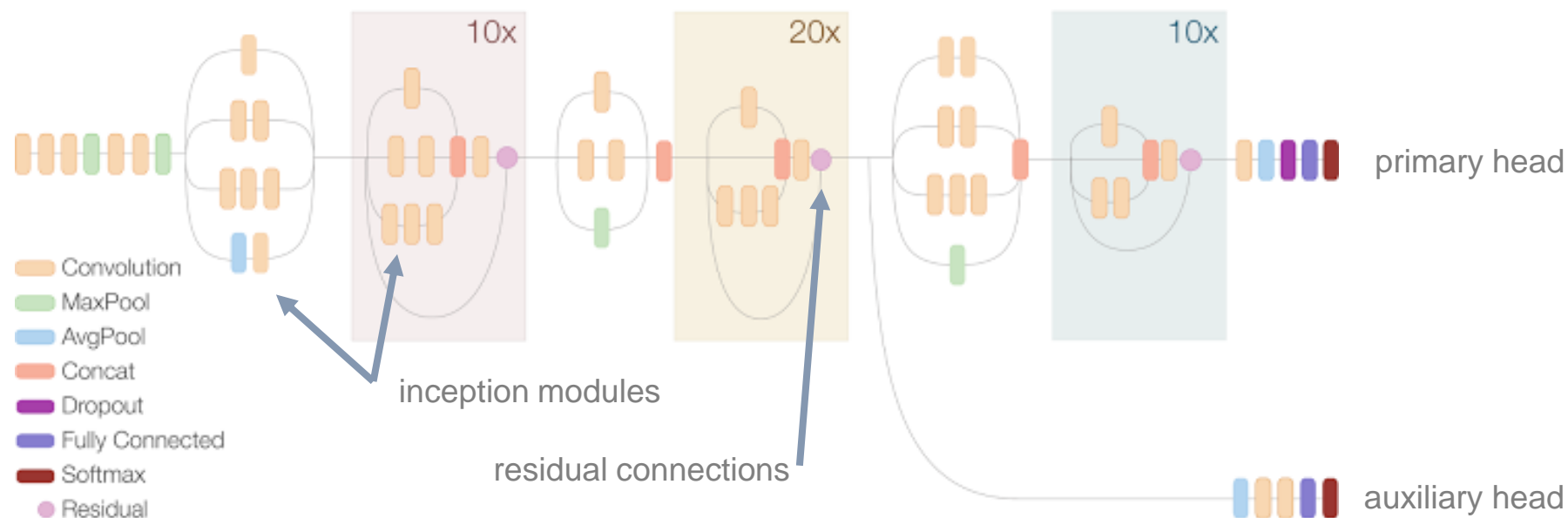
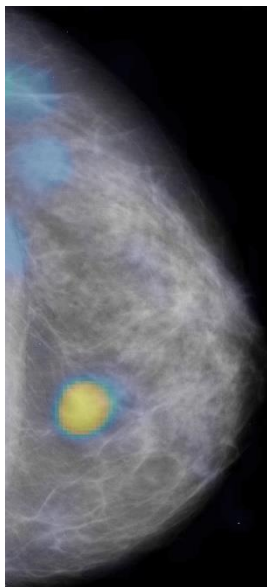


P

1 MLO

Tumor detection

Based on state-of-the-art **Inception-ResNet¹** architecture



¹ Szegedy, Christian, et al. "Inception-v4, inception-resnet and the impact of residual connections on learning." arXiv preprint arXiv:1602.07261 (2016).

Training the network

Modified the pretrained network (ImageNet) so it is **fully convolutional**

First, trained the network to localize tumors using existing annotated datasets (semi-supervised learning)



Dream

Total: 500 images
Cancer: 32 images



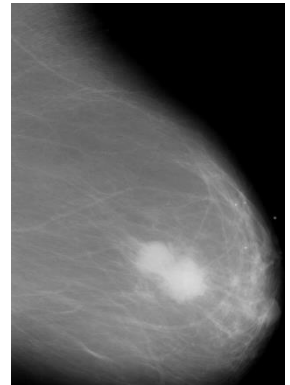
CBIS-DDSM

Total: 4,067 images
Cancer: 855 images



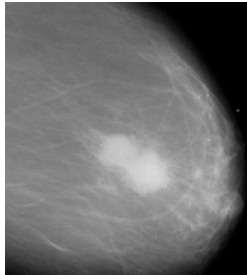
INbreast

Total: 410 images
Cancer: 360 images

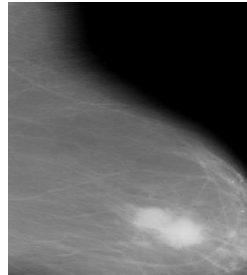


Data augmentation – generated n

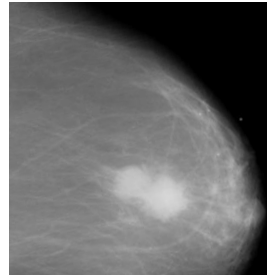
ing examples from a few thousand



random crops



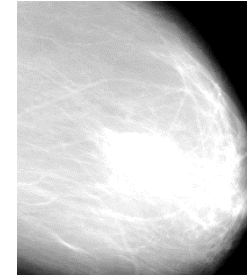
aspect ratio



rotation

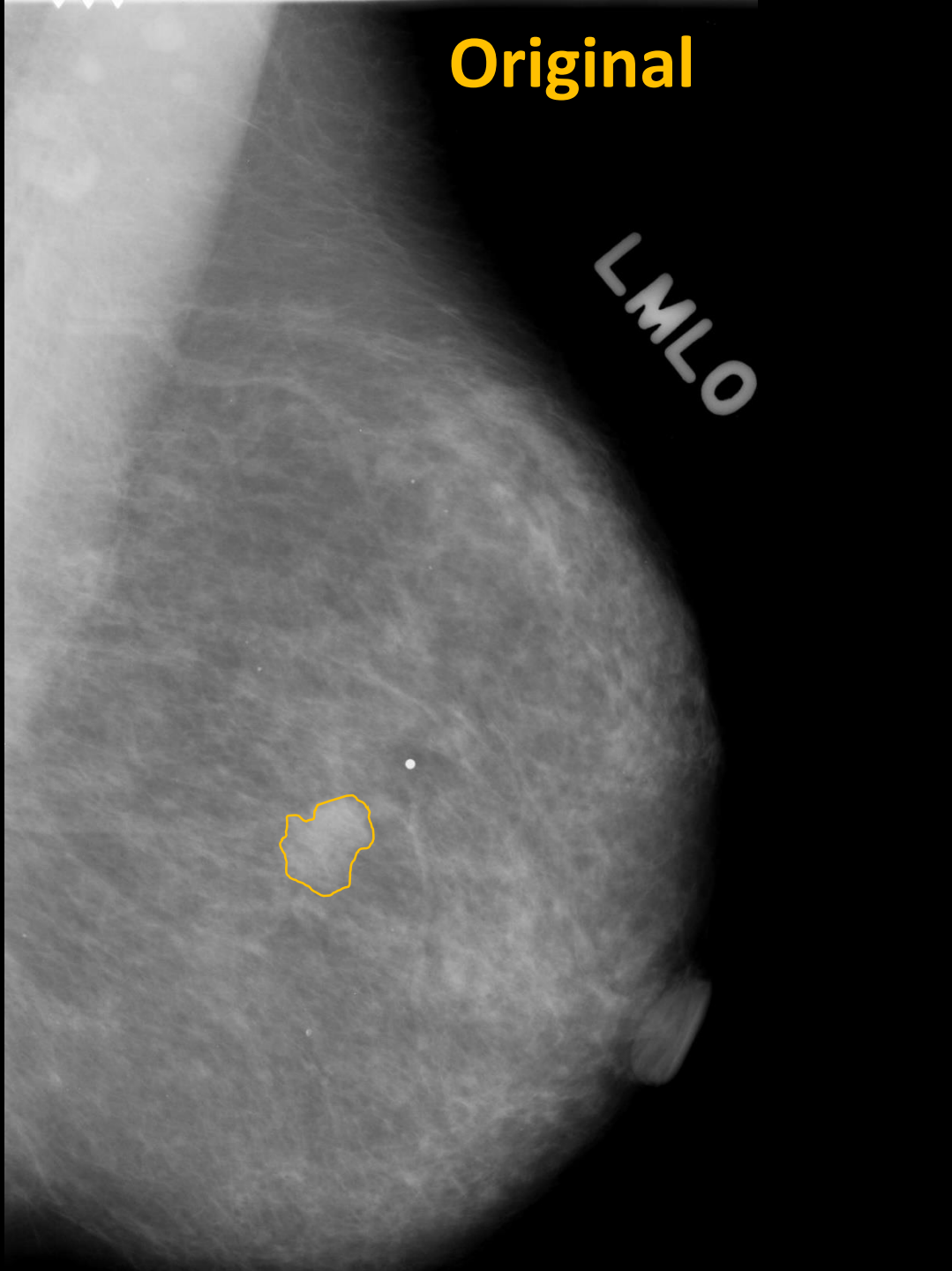


contrast

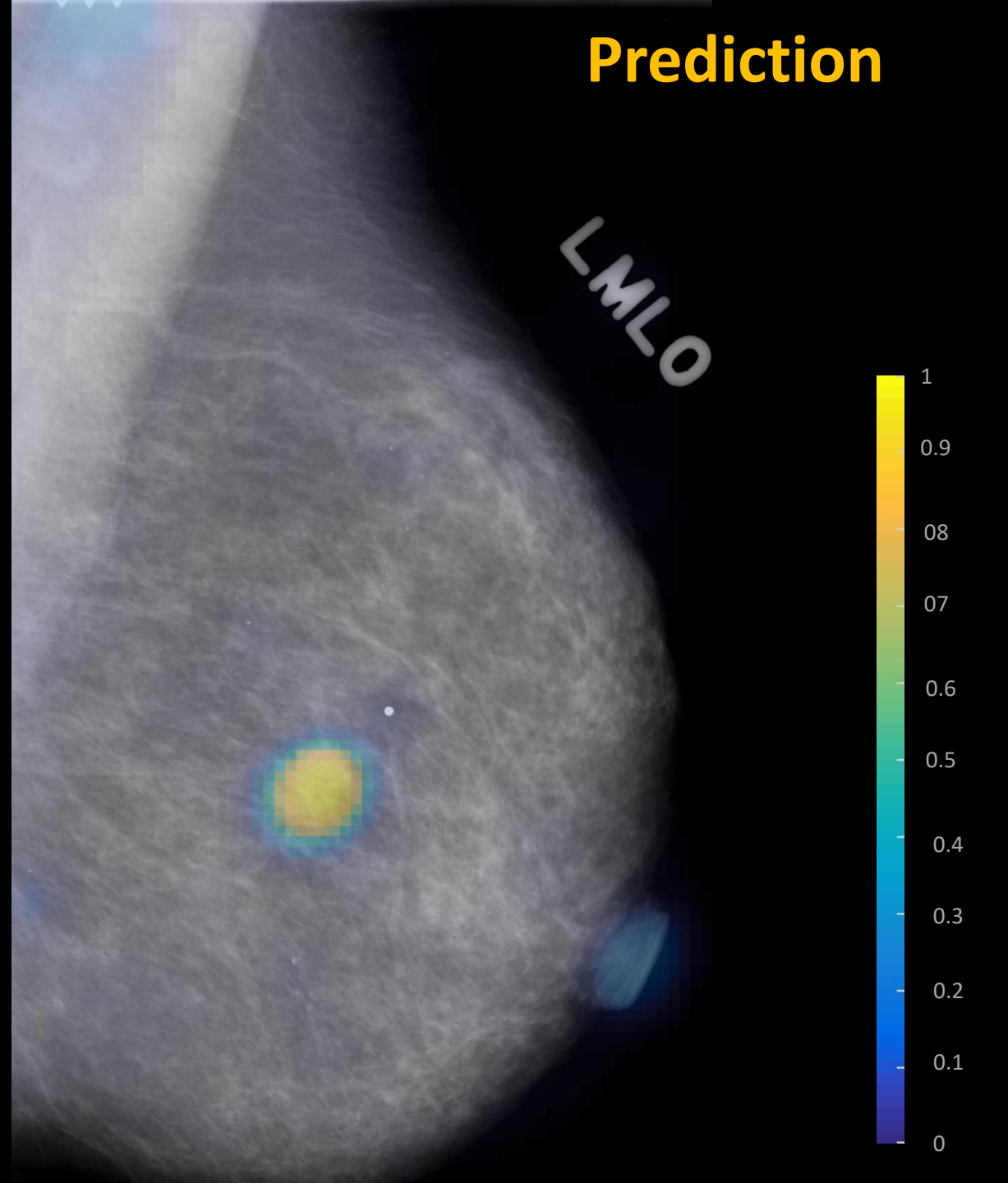


brightness

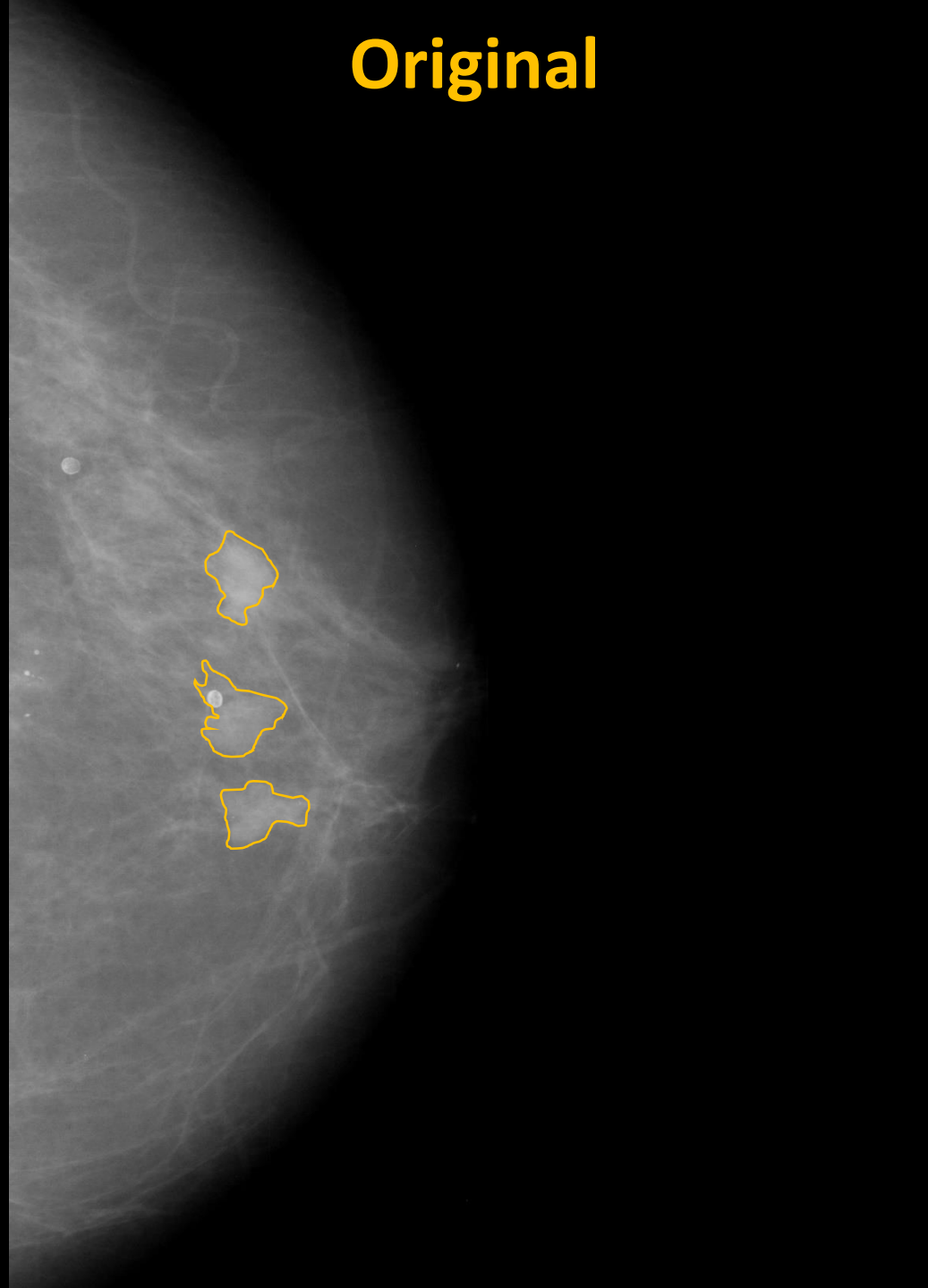
Original



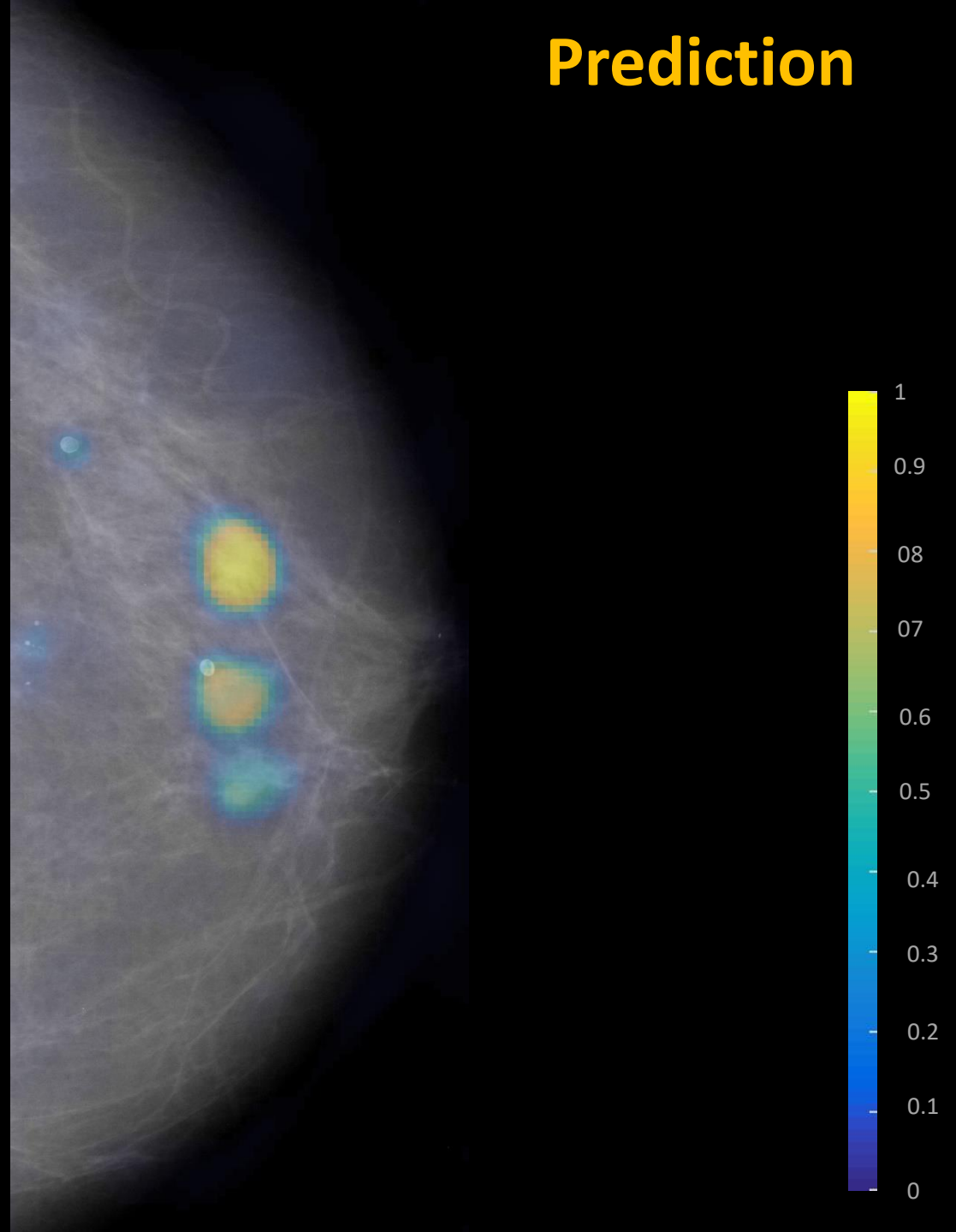
Prediction



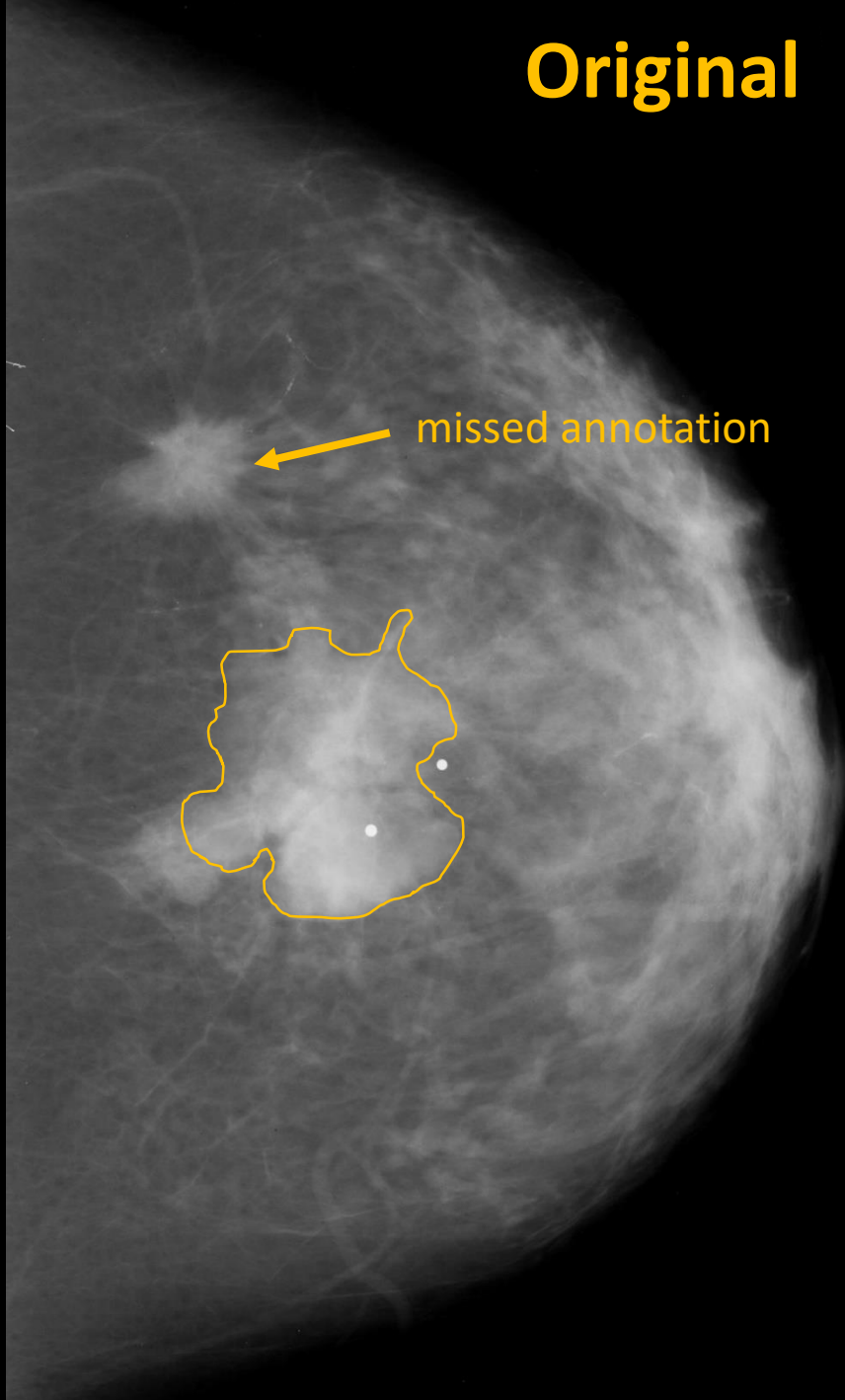
Original



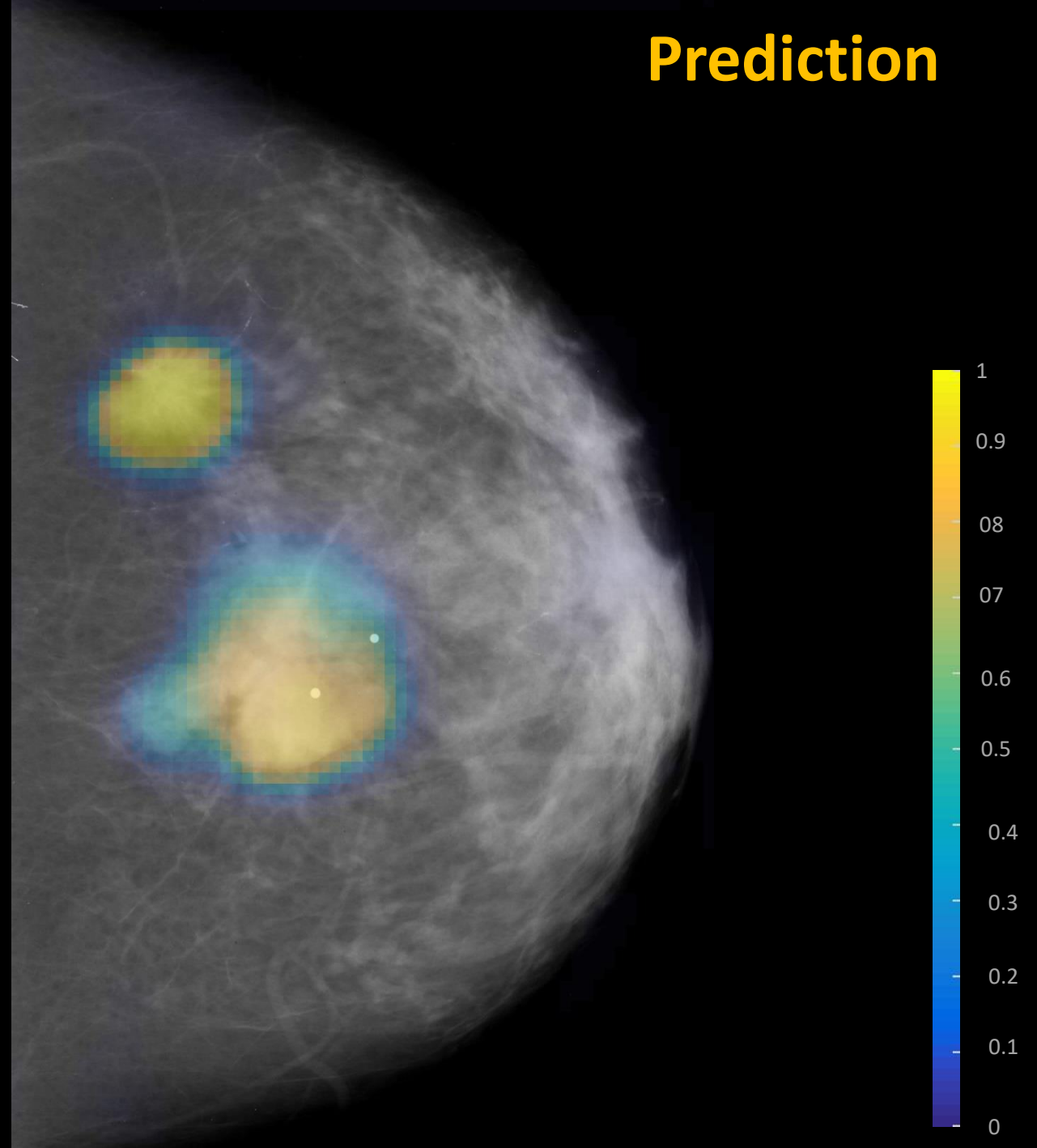
Prediction



Original



Prediction



Risk Estimation

- Risk: risk of a woman developing cancer at some point in future
- Positive set: prior and contra-lateral mammograms

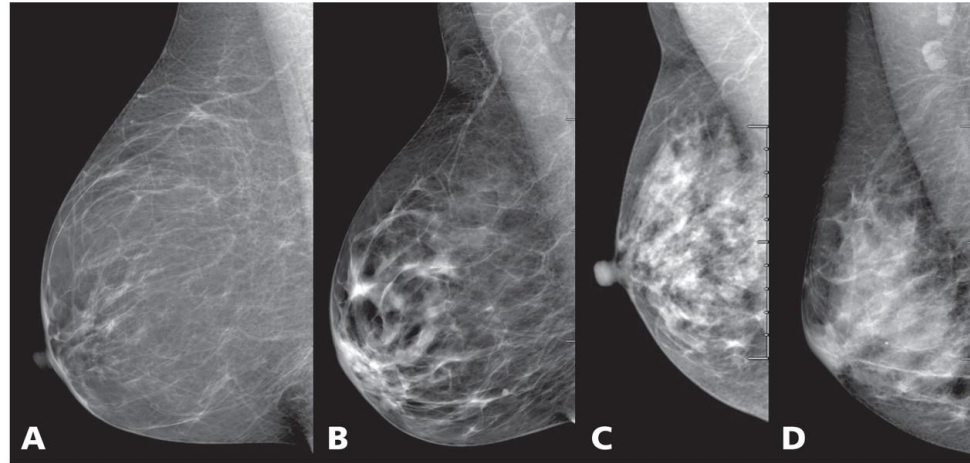


Figure 1 Representations of the 4 Breast Imaging Reporting and Data System (BI-RADS) breast density qualitative and quantitative assessments. A) BI-RADS 1: almost entirely fat; B) BI-RADS 2: scattered fibroglandular densities; C) BI-RADS 3: heterogeneously dense; and D) BI-RADS 4: extremely dense.

Method	AUC	Odds Ratio (95% CI)
Deep Learning Risk	64%	5.32 (2.39-9.69)
Mammographic Density Risk	57%	1.96 (1.23-3.11)

Contents



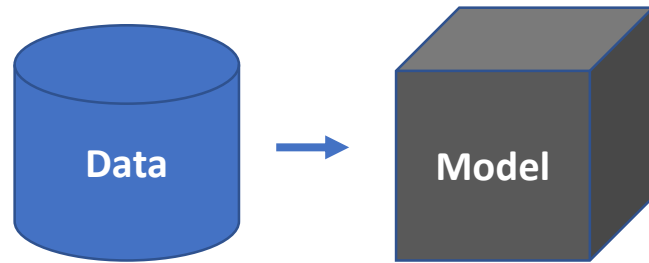
- Problem Definition
- Opportunities and challenges
- An example pipeline
- **Domain Adaptation**
- Uncertainty Estimation
- Future Directions

Knowledge Transfer

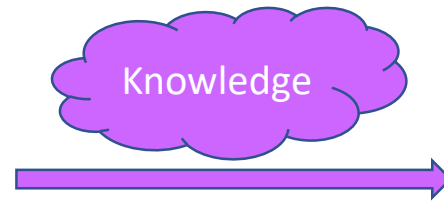


SOURCE

$$D_s \sim P_s(X, Y) \quad M_s \equiv P_s(Y_s|X) \text{ or } P(X, Y_s)$$

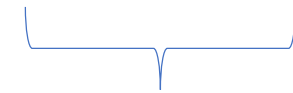
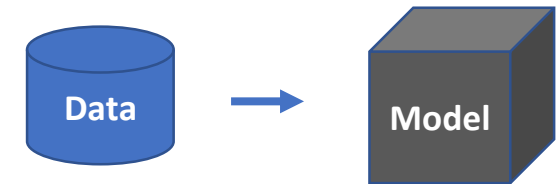


Rich/large



TARGET

$$D_t \sim P_t(X, Y) \quad M_t \equiv P_t(Y_t|X) \text{ or } P(X, Y_t)$$



small/noisy

Transfer Learning

- when $Y_s \neq Y_t$ or $P_s(Y_s|X)$

Human detection

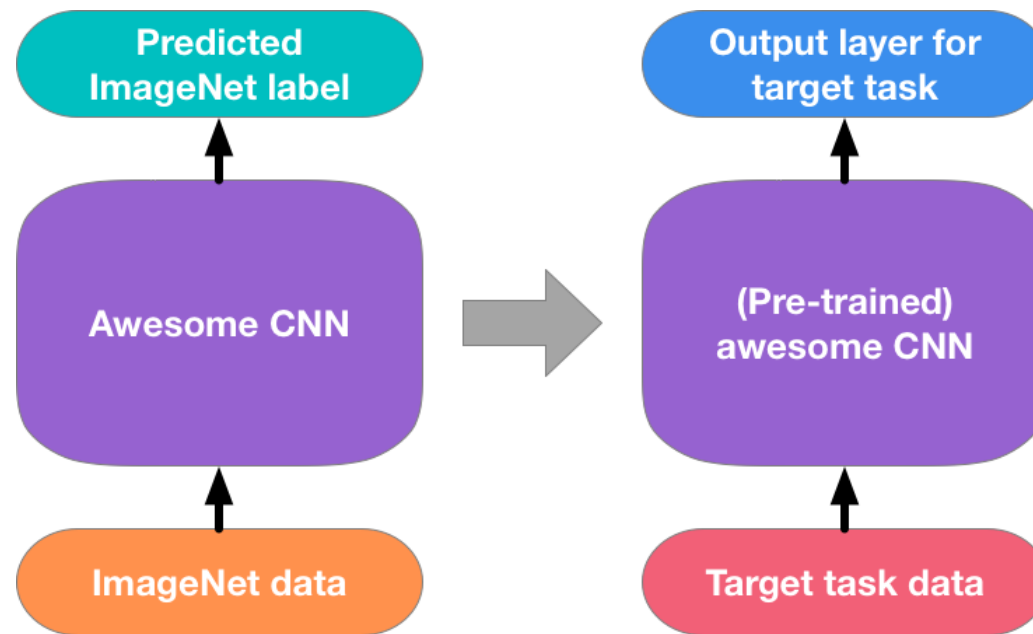


Horse detection

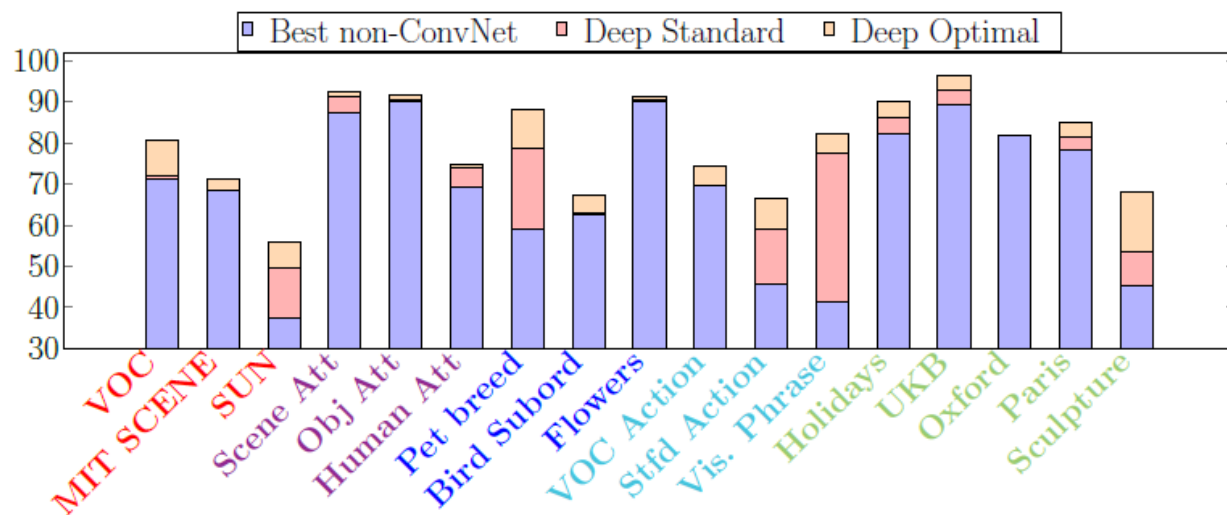


Deep Transfer Learning

- Fine tuning is the most common way

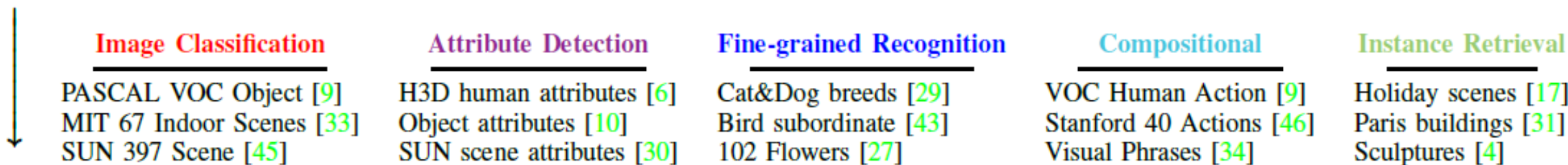


Deep Transfer Learning



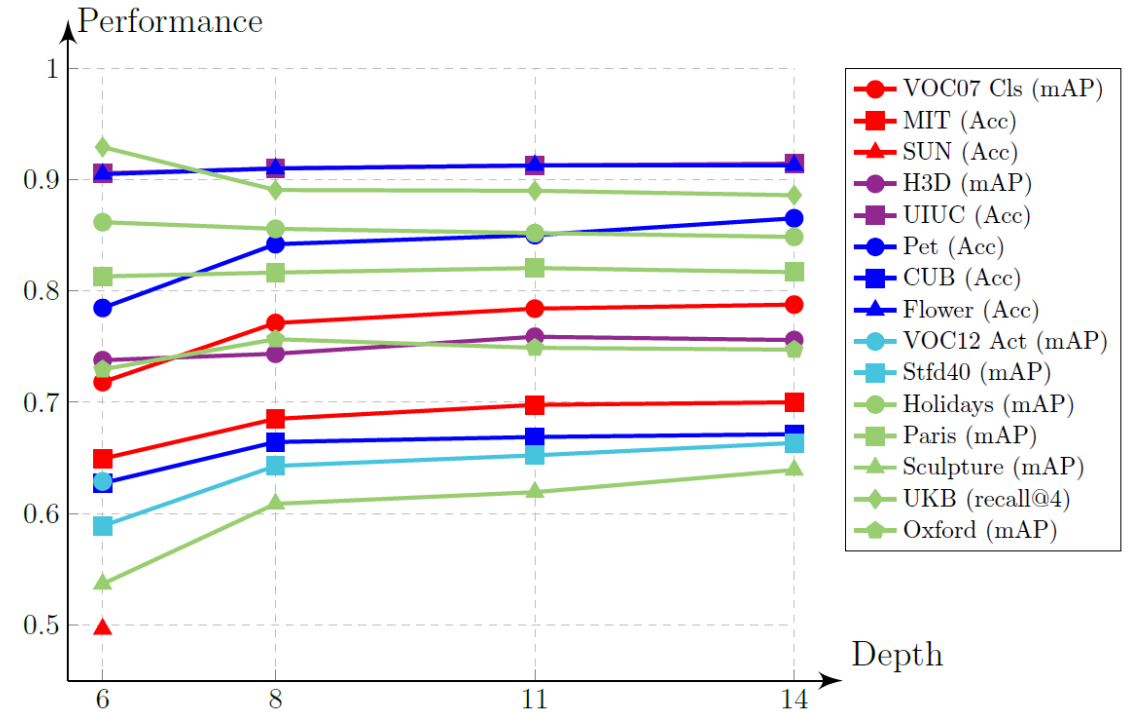
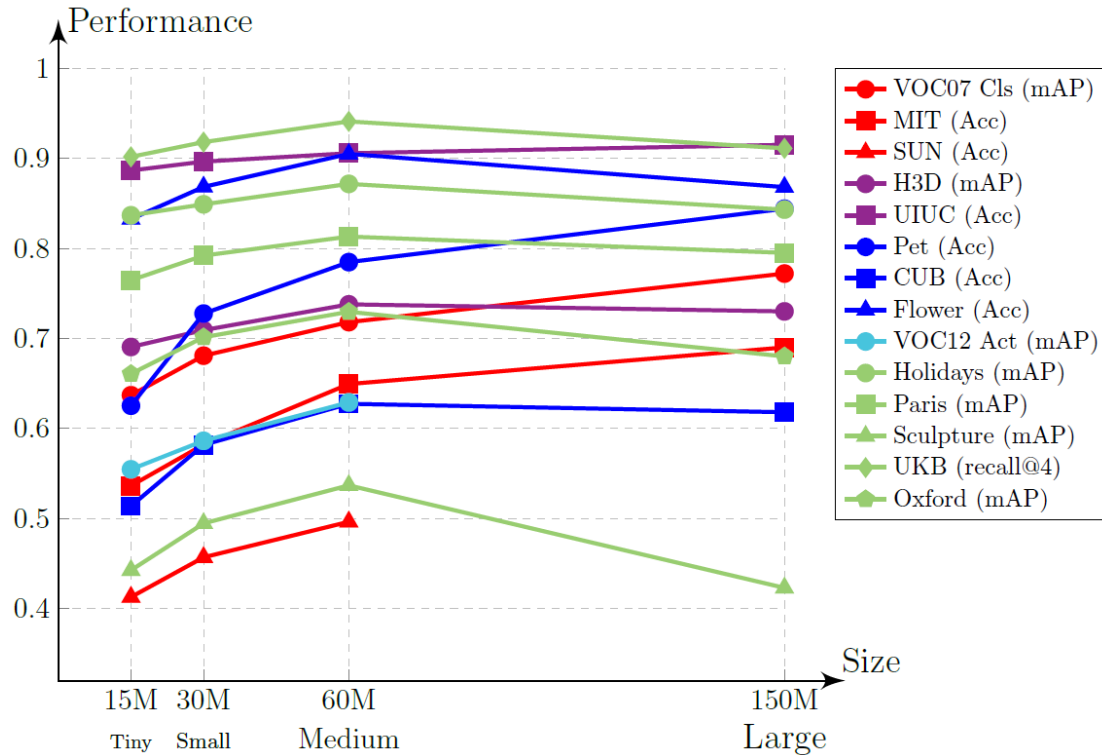
Factor	Target task			
	Source task ImageNet	...	FineGrained recognition	...
Early stopping	————— Don't do it —————		—————	
Network depth	————— As deep as possible —————		—————	
Network width	————— Wider —————	————— Moderately wide —————		—————
Diversity/Density	————— More classes better than more images per class —————			
Fine-tuning	————— Yes, more improvement with more labelled data —————			
Dim. reduction	————— Original dim —————	————— Reduced dim —————		—————
Rep. layer	————— Later layers —————	————— Earlier layers —————		—————

Increasing distance from ImageNet →



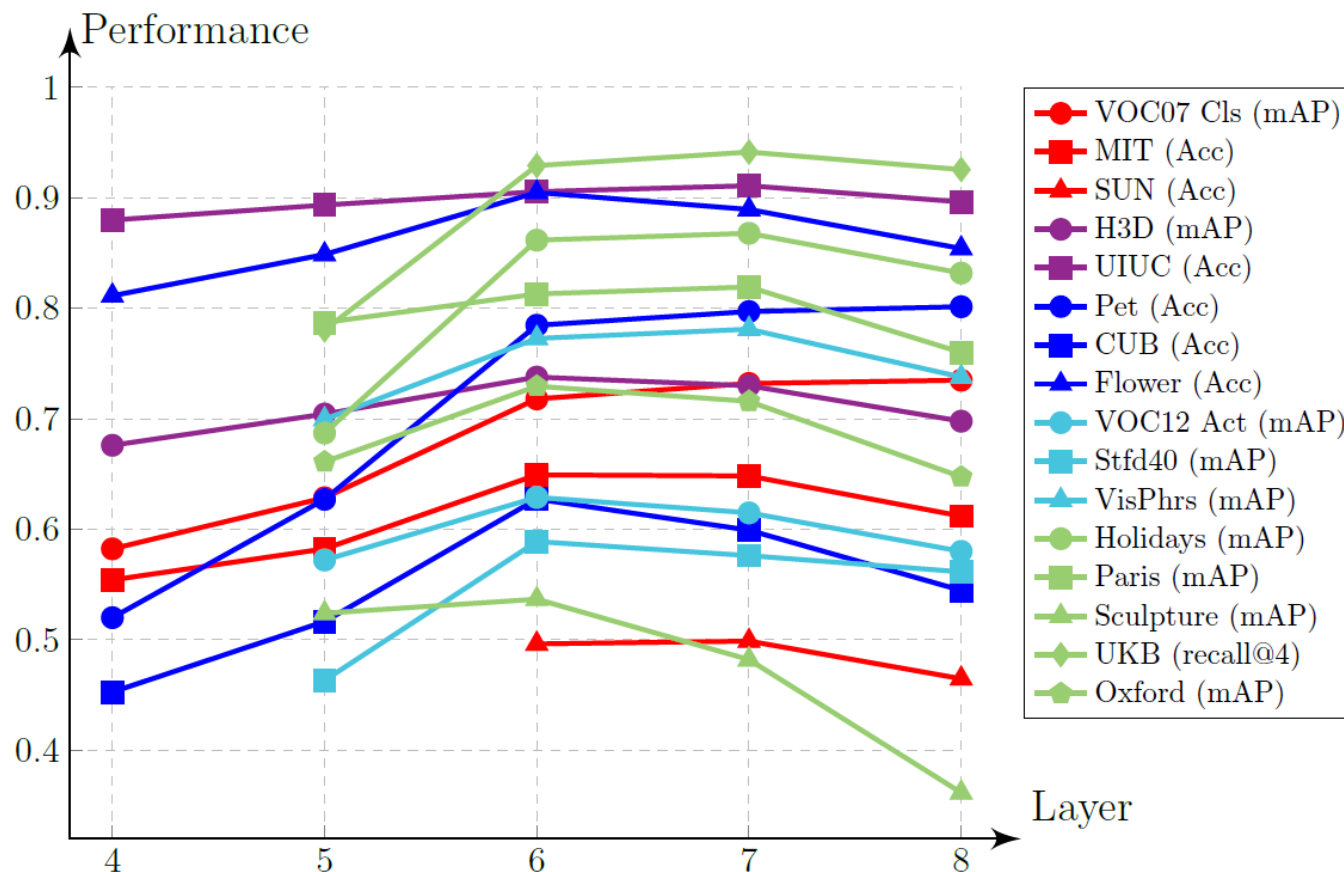
Deep Transfer Learning

Width vs Depth



Deep Transfer Learning

Which Layer?



Deep Transfer Learning



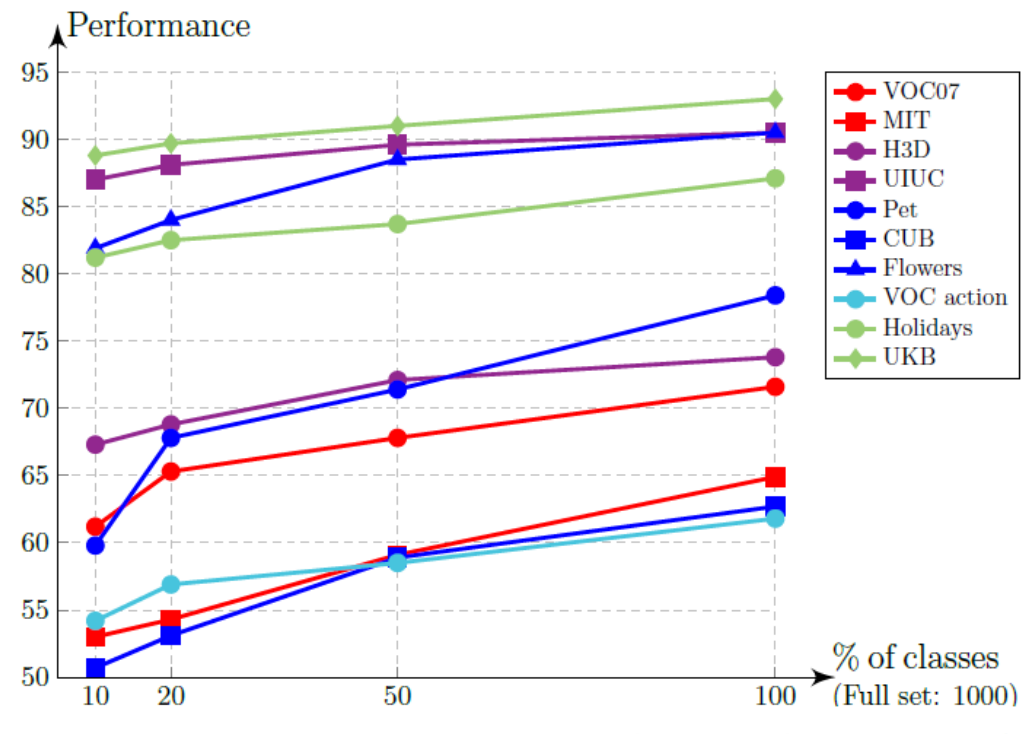
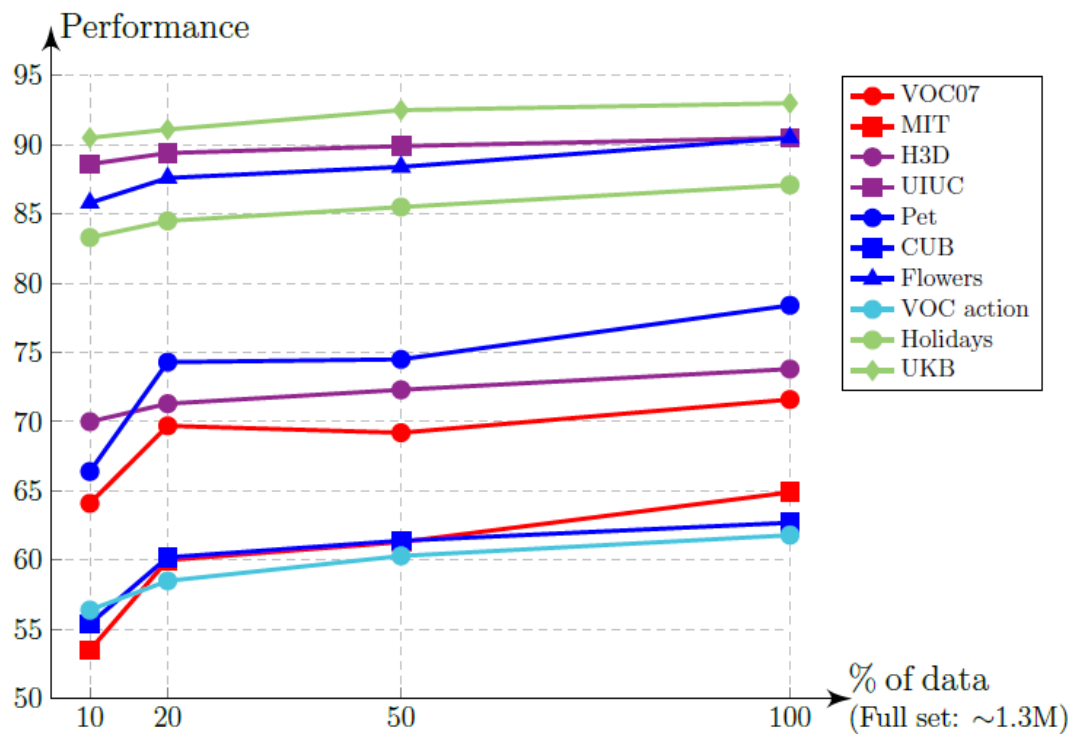
Multiple Representations

Source task	Image Classification			Attribute Detection		Fine-grained Recognition			Compositional	Instance Retrieval		
	VOC07	MIT	SUN	H3D	UIUC	Pet	CUB	Flower	Stanf. Act40	Oxf.	Scul.	UKB
ImageNet	71.6	64.9	49.6	73.8	90.4	78.4	62.7	90.5	58.9	71.2	52.0	93.0
Places	68.5	69.3	55.7	68.0	88.8	49.9	42.2	82.4	53.0	70.0	44.2	88.7
Hybrid	72.7	69.6	56.0	72.6	90.2	72.4	58.3	89.4	58.2	72.3	52.3	92.2
Concat	73.8	70.8	56.2	74.2	90.4	75.6	60.3	90.2	59.6	72.1	54.0	93.2

[Azizpour et al. Factors of Transferability for a Generic ConvNet Representation, PAMI 2016]

Deep Transfer Learning

Diversity vs Density



Deep Transfer Learning



Optimizing Transferability Factors are Important!

	Image Classification			Attribute Detection			Fine-grained Recognition			Compositional			Instance Retrieval				
	VOC07	MIT	SUN	SunAtt	UIUC	H3D	Pet	CUB	Flower	VOCa.	Act40	Phrase	Holid.	UKB	Oxf.	Paris	Scul.
non-ConvNet	[38] 71.1	[25] 68.5	[44] 37.5	[30] 87.5	[42] 90.2	[50] 69.1	[29] 59.2	[12] 62.7	[20] 90.2	[28] 69.6	[46] 45.7	[34] 41.5	[40] 82.2	[51] 89.4	[40] 81.7	[40] 78.2	[4] 45.4
Deep Standard	71.8	64.9	49.6	91.4	90.6	73.8	78.5	62.8	90.5	69.2	58.9	77.3	86.2	93.0	73.0	81.3	53.7
Deep Optimized ⁴	80.7	71.3	56.0	92.5	91.5	74.6	88.1	67.1	91.3	74.3	66.4	82.3	90.0	96.3	79.0	85.1	67.9
Err. Reduction	32%	18%	13%	13%	10%	4%	45%	12%	8%	17%	18%	22%	28%	47%	22%	20%	31%
Source Task	ImgNet	Hybrid	Hybrid	Hybrid	ImgNet	ImgNet	ImgNet	ImgNet	ImgNet	ImgNet	ImgNet	ImgNet	Hybrid	ImgNet	ImgNet	ImgNet	ImgNet
Network Width	Medium	Medium	Medium	Medium	Large	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium
Network Depth	16	8	8	8	8	16	16	16	16	16	16	16	8	8	16	16	16
Rep. Layer	last	last	last	last	2nd last	2nd last	2nd last	3rd last	3rd last	3rd last	3rd last	3rd last	3rd last	4th last	4th last	4th last	4th last
PCA	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	✓	✓	✓	✓	✓
Pooling	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	✗	1 × 1	1 × 1	2 × 2	2 × 2	3 × 3

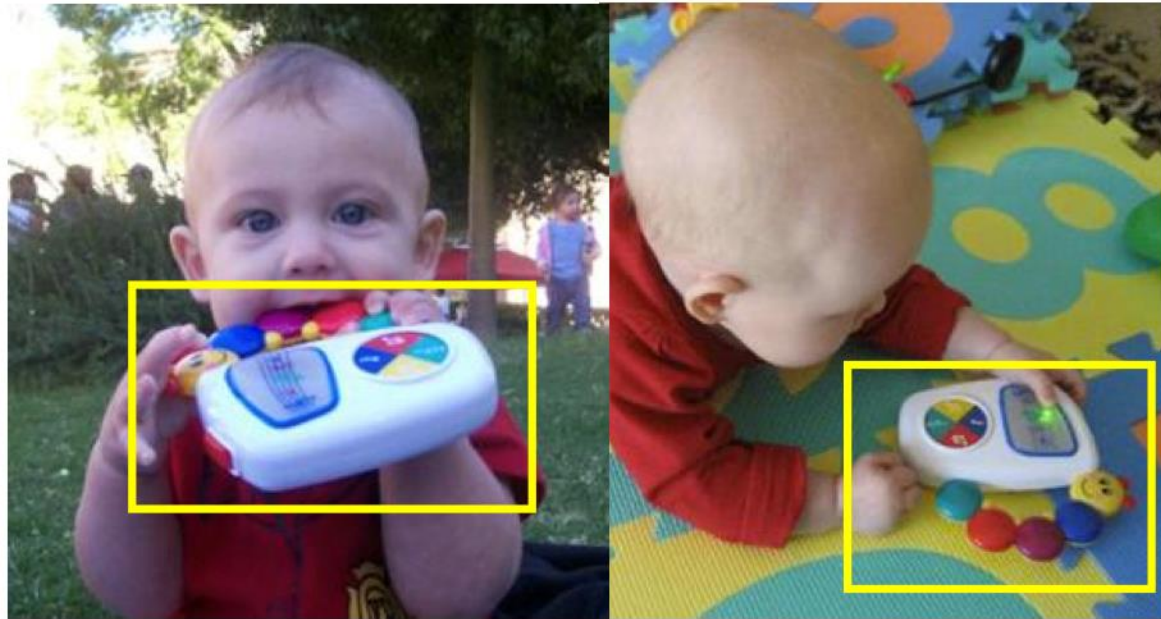
[Azizpour et al. Factors of Transferability for a Generic ConvNet Representation, PAMI 2016]

Domain Adaptation

- when $P_s(X) \neq P_t(X)$



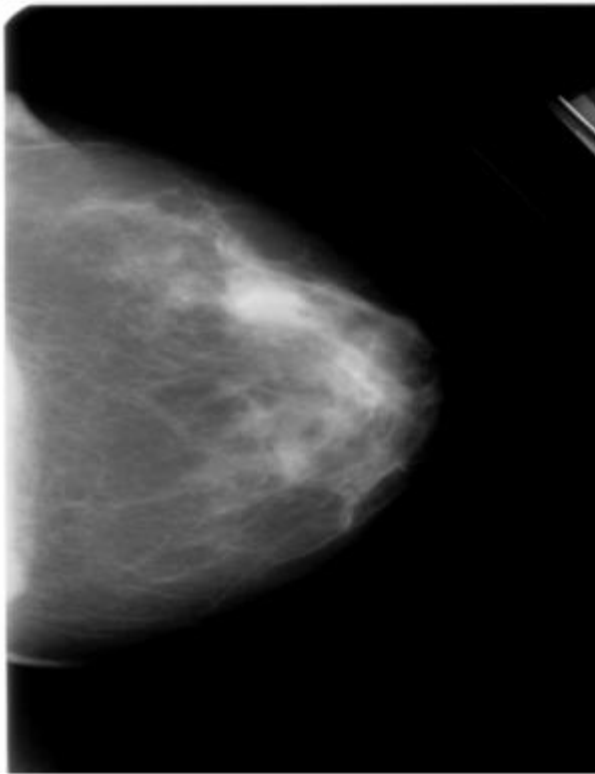
amazon.com



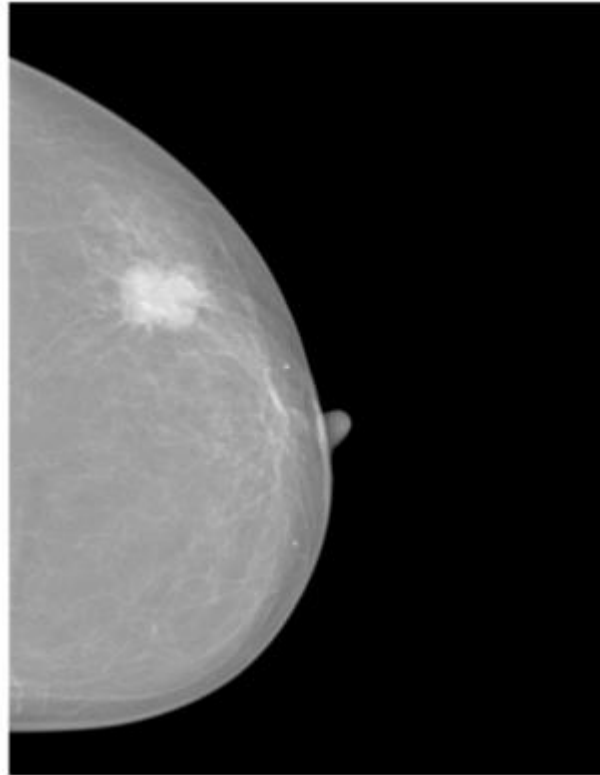
consumer images

Domain Adaptation

DDSM



INBREAST



DREAM



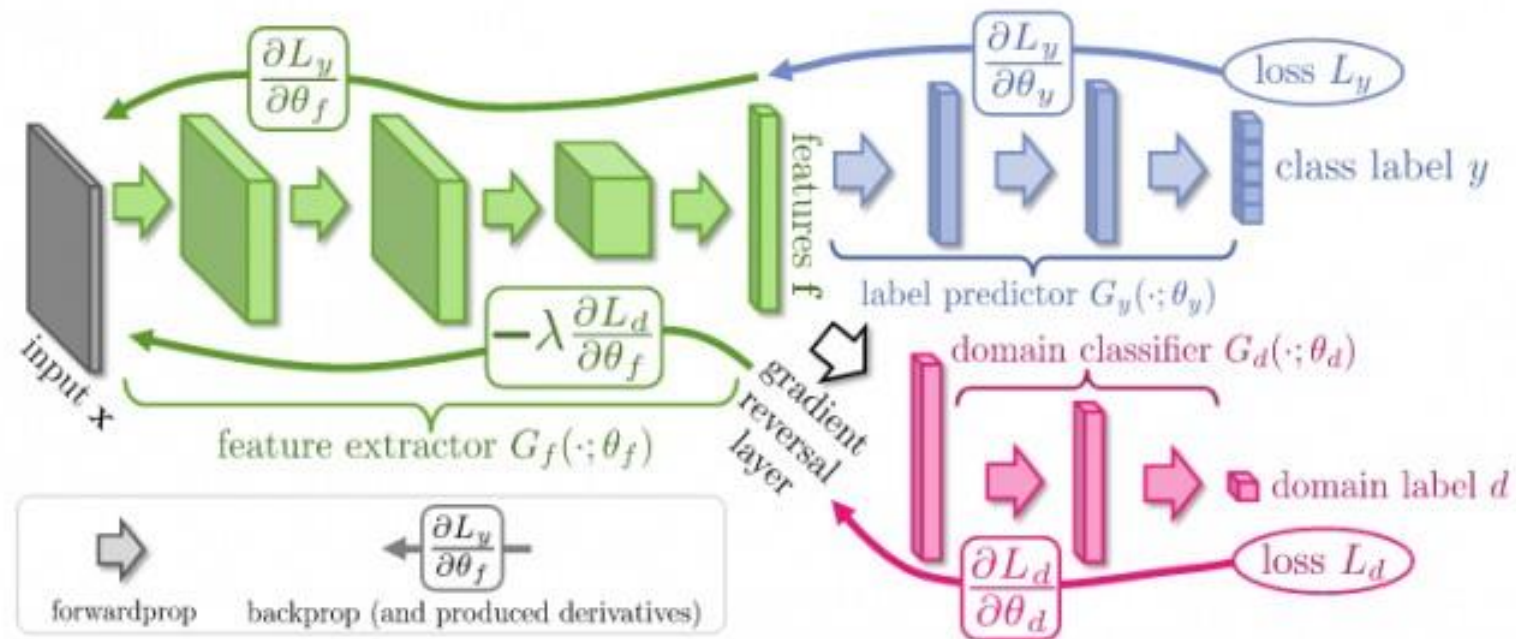
Domain Adaptation

There is usually the assumption that samples drawn from $P_s(X)$ have a corresponding sample in $P_t(X)$.

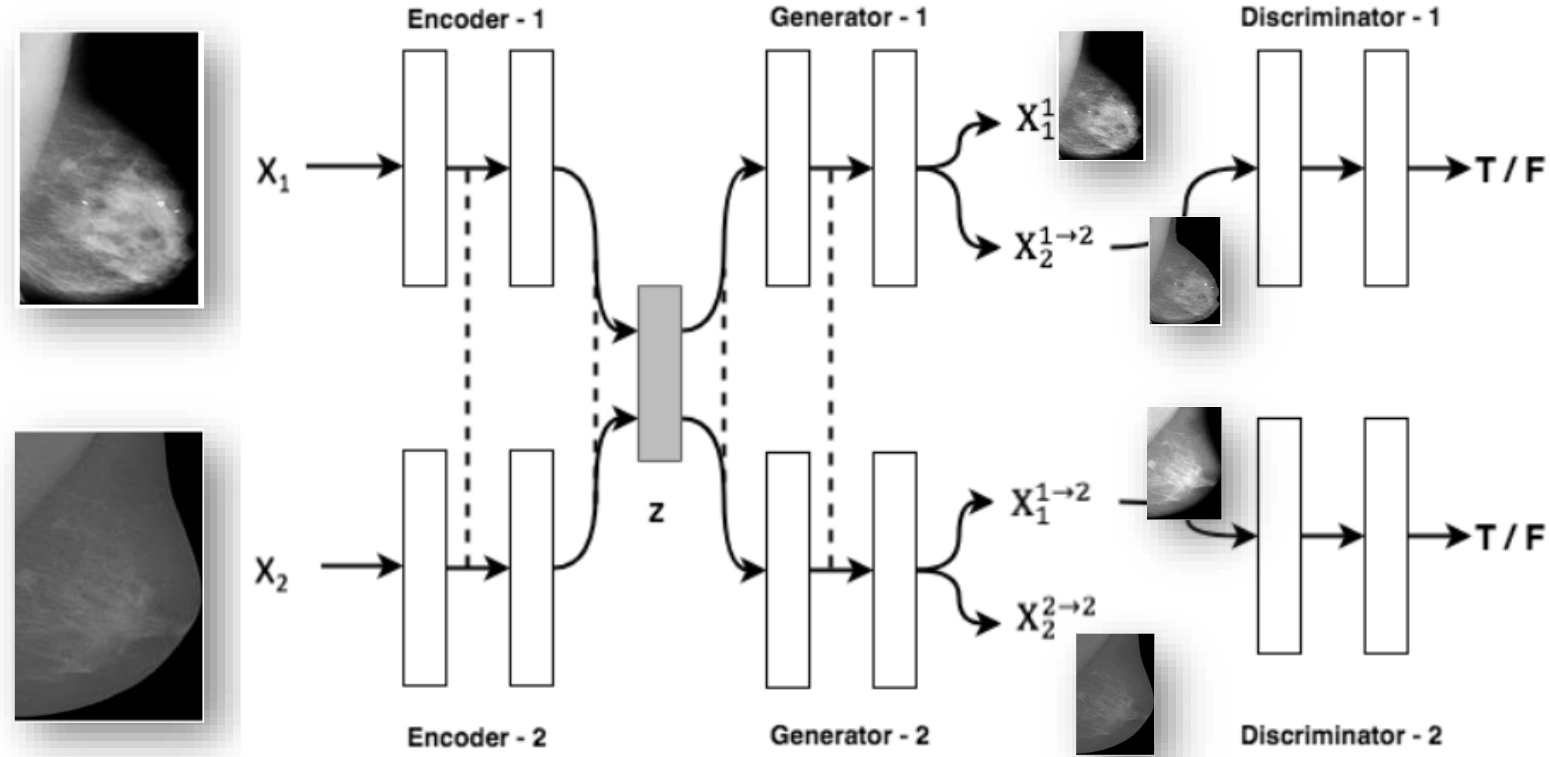
- Supervised Domain Adaptation
- Unsupervised Domain Adaptation

- Directly adapting the model parameters [Rozantsev et al. 2017]
- Learning a common embedding space [Ganin et al 2015, 2016]
- Adapting in the input domain [Bousmalis et al. 2016 Liu et al 2017]

Domain Adaptation



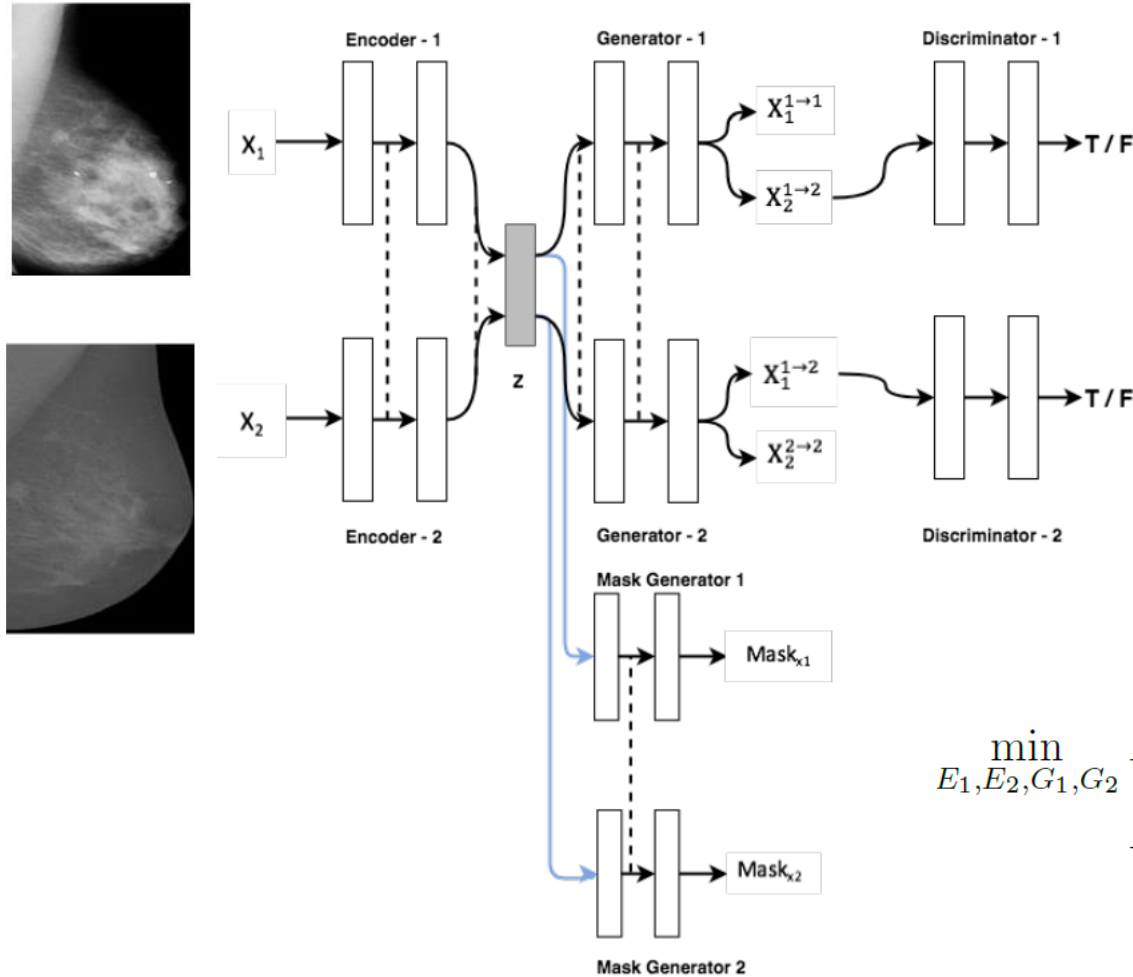
Domain Adaptation



$$\min_{E_1, E_2, G_1, G_2} L_{VAE_1}(E_1, G_1) + L_{CC_1}(E_1, G_1, E_2, G_2) + V_{LSGAN}(E_1, G_1)$$

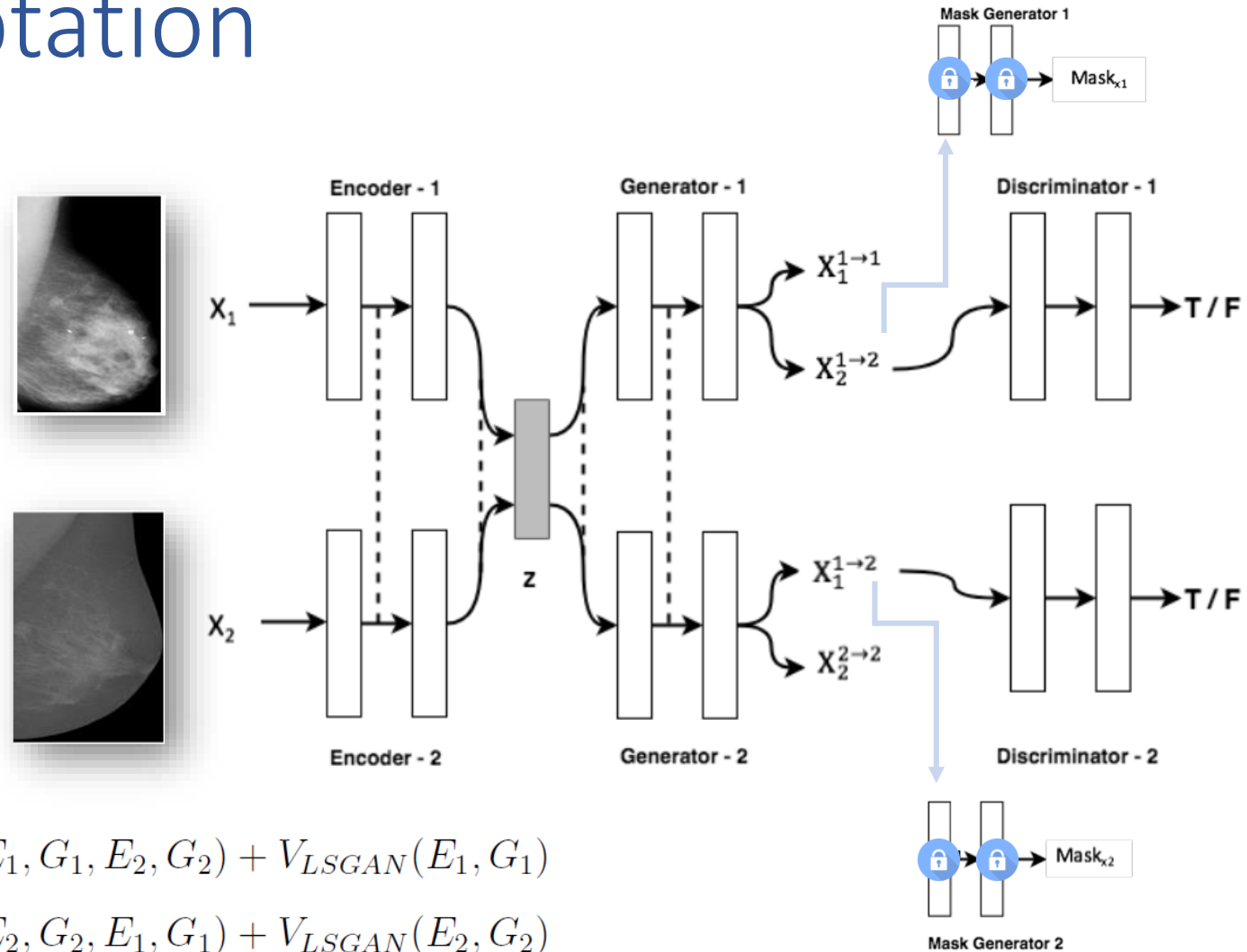
$$L_{VAE_2}(E_2, G_2) + L_{CC_2}(E_2, G_2, E_1, G_1) + V_{LSGAN}(E_2, G_2)$$

Domain Adaptation



$$\begin{aligned}
 \min_{E_1, E_2, G_1, G_2} & L_{VAE_1}(E_1, G_1) + L_{CC_1}(E_1, G_1, E_2, G_2) + V_{LSGAN}(G_1) \\
 & L_{VAE_2}(E_2, G_2) + L_{CC_2}(E_2, G_2, E_1, G_1) + V_{LSGAN}(G_2) \\
 & + L_{label}(E_1, Mask_{G_1}) + L_{label}(E_2, Mask_{G_2})
 \end{aligned}$$

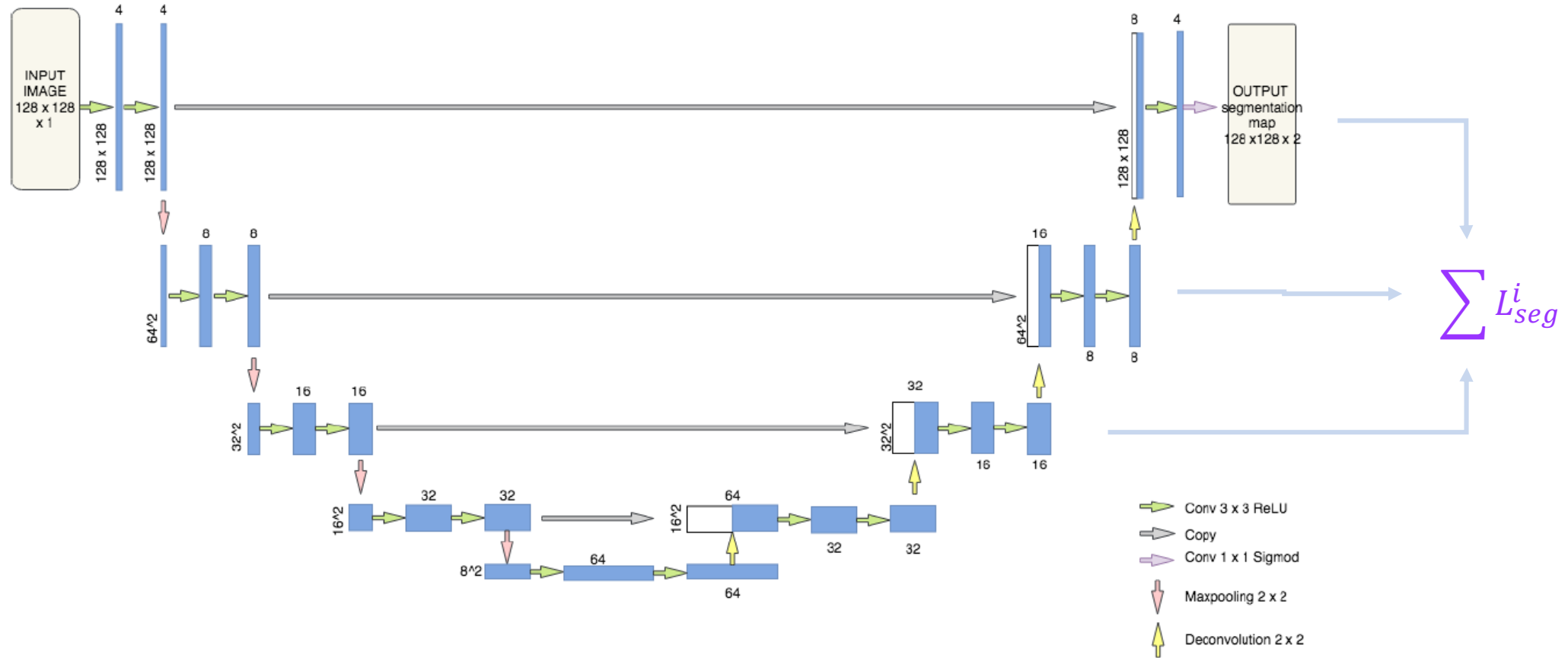
Domain Adaptation



$$\begin{aligned}
 \min_{E_1, E_2, G_1, G_2} & L_{VAE_1}(E_1, G_1) + L_{CC_1}(E_1, G_1, E_2, G_2) + V_{LSGAN}(E_1, G_1) \\
 & L_{VAE_2}(E_2, G_2) + L_{CC_2}(E_2, G_2, E_1, G_1) + V_{LSGAN}(E_2, G_2) \\
 & + L_{seg}(E_2, G_1) + L_{seg}(E_1, G_2)
 \end{aligned}$$

[Tao Wang, Adapting multiple datasets for better mammography tumor detection, KTH 2018]

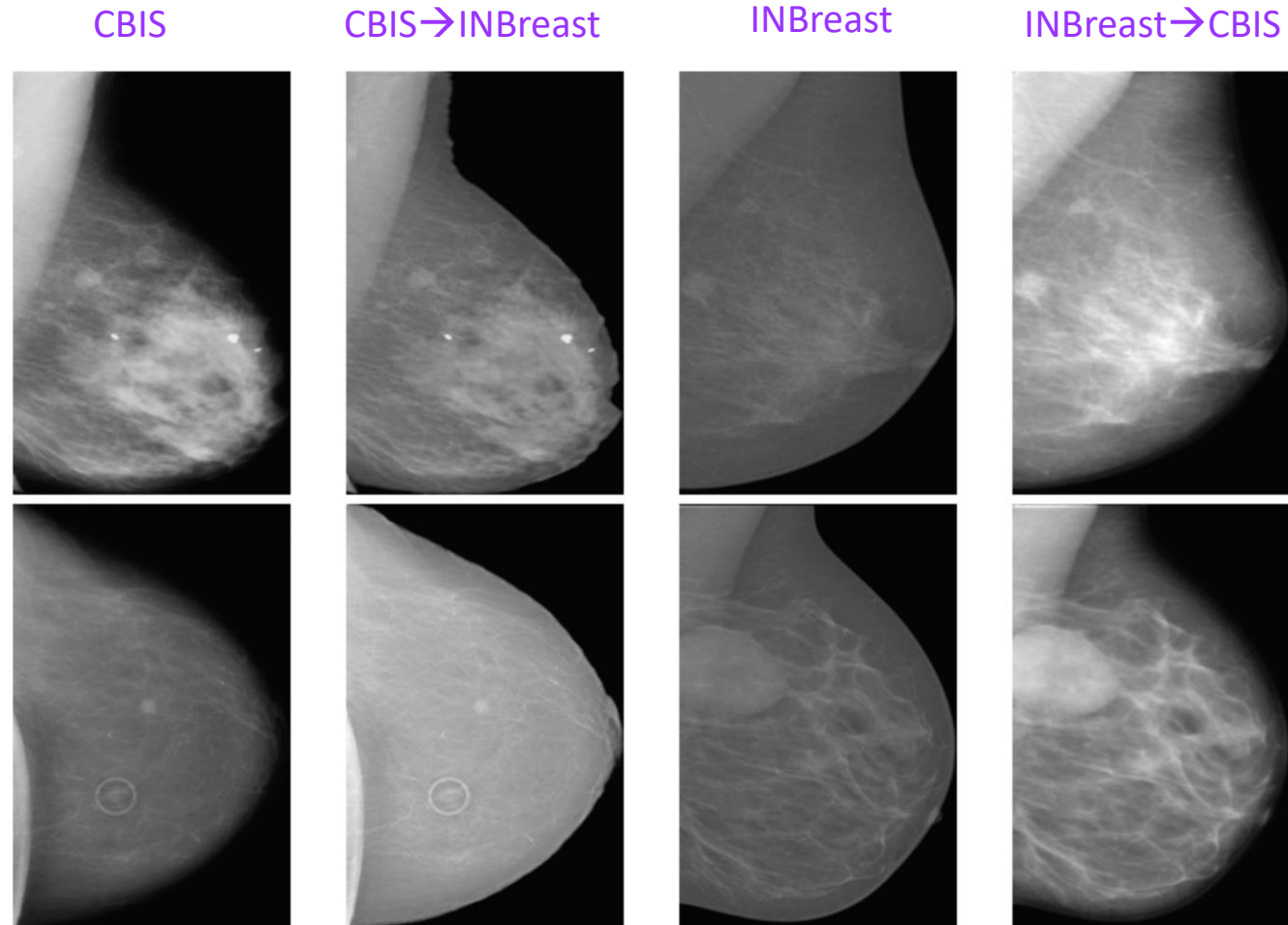
Domain Adaptation



[Tao Wang, Adapting multiple datasets for better mammography tumor detection, KTH 2018]

[Ronneberger et al. "U-Net: Convolutional Networks for Biomedical Image Segmentation" MICCAI 2015]

Domain Adaptation



[Tao Wang, Adapting multiple datasets for better mammography tumor detection, KTH 2018]

Domain Adaptation

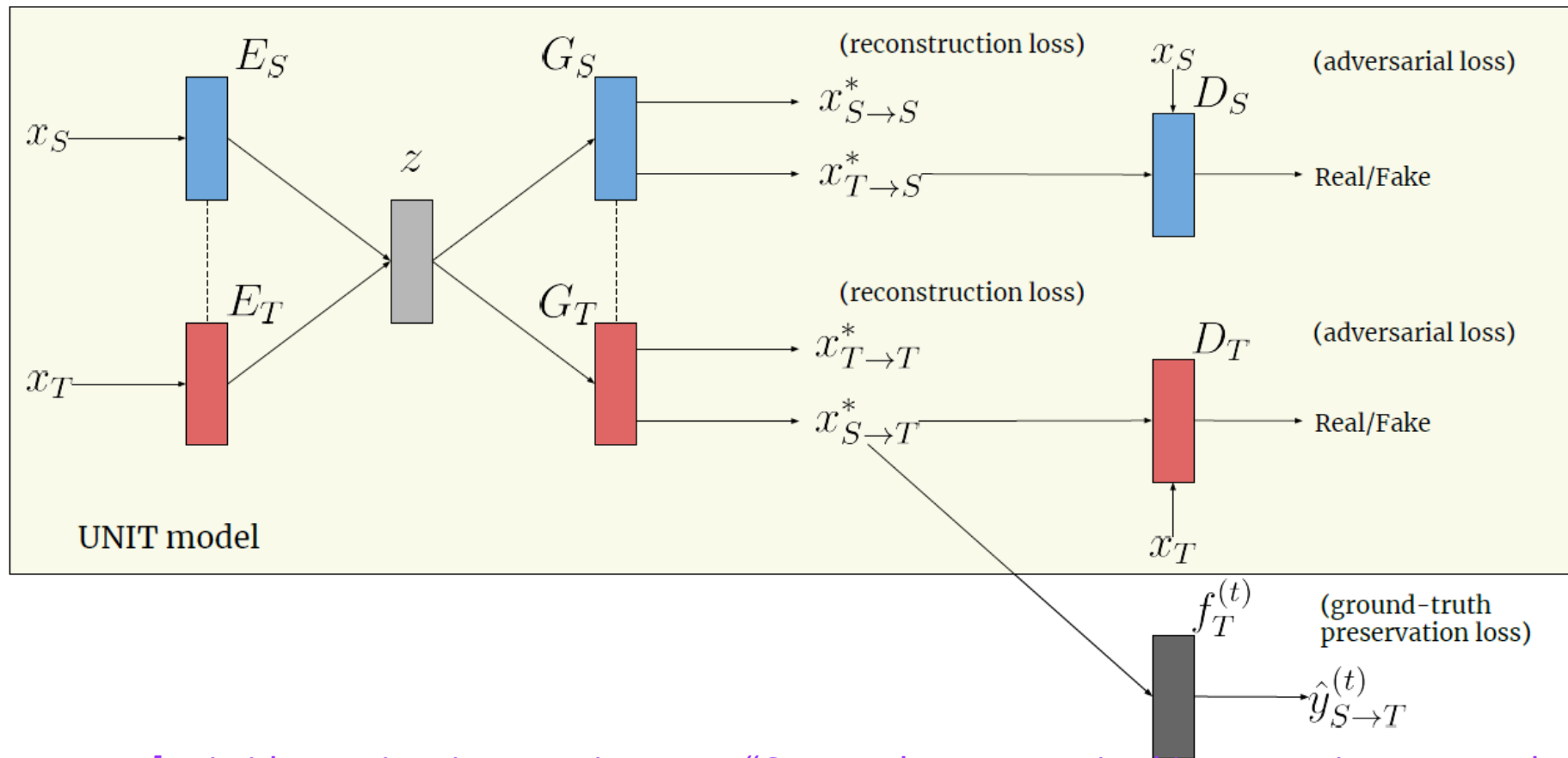


		Pixel Level Metrics					Instance Level Metrics					
Training dataset	Testing dataset	Dice	Precision	Recall	MCC	IoU	$P_{0.25}$	$R_{0.25}$	$P_{0.5}$	$R_{0.5}$	AP	AR
CBIS	INBreast	0.1170	0.1965	0.1648	0.2029	0.1188	0.16	0.32	0.12	0.24	0.1072	0.2145
CBIS	Transferred INBreast	0.1412	0.1544	0.2934	0.2334	0.2108	0.1467	0.44	0.133	0.4	0.1151	0.3455
Transferred CBIS	INBreast	0.1934	0.2521	0.3076	0.3377	0.2992	0.25	0.56	0.2321	0.52	0.1996	0.4472

[Tao Wang, Adapting multiple datasets for better mammography tumor detection, KTH 2018]

Domain Adaptation

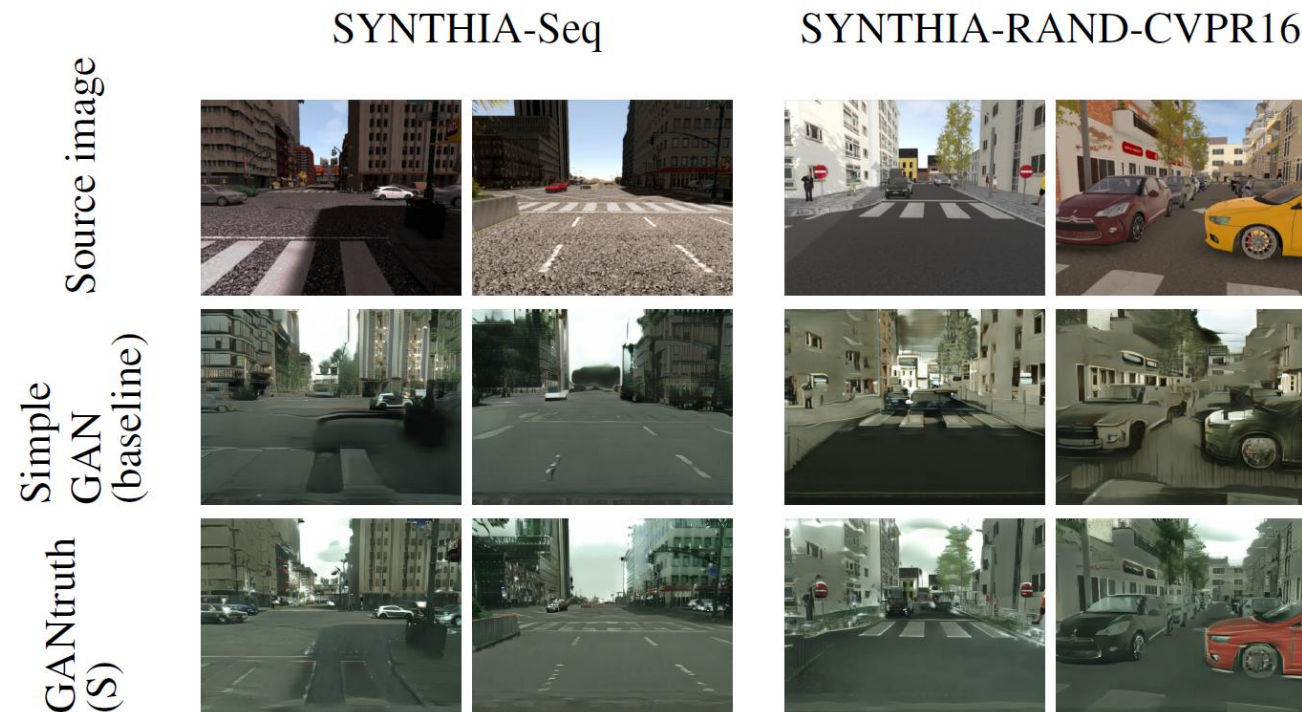
Synthetic-to-Real Adaptation



[Bujwid, Marti, Azizpour, Pieropan, "GANtruth – an unpaired image-to-image translation method for driving scenarios", NeurIPS MLIT workshop 2018]

Domain Adaptation

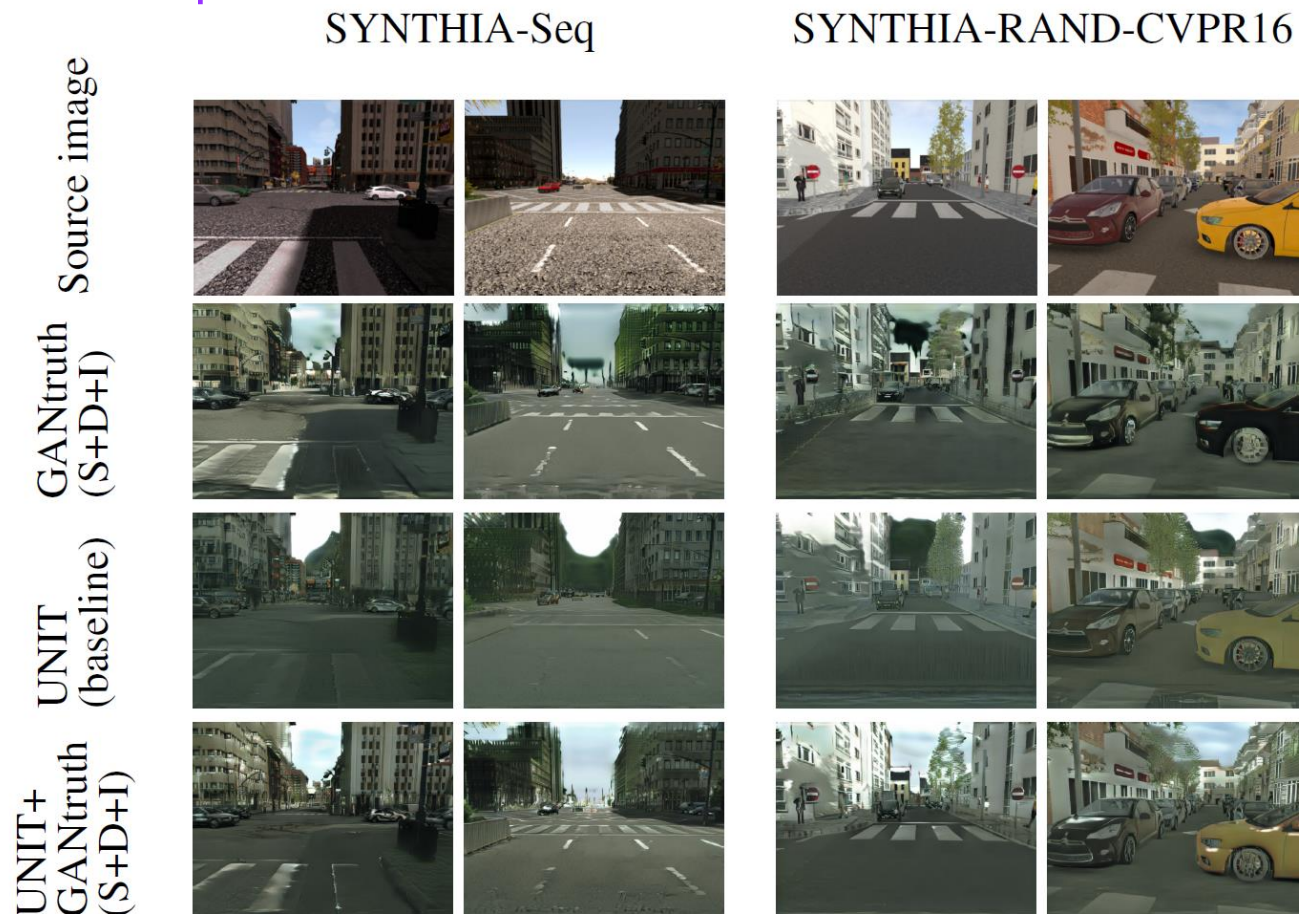
Synthetic-to-Real Adaptation



[Bujwid, Marti, Azizpour, Pieropan, “GANtruth – an unpaired image-to-image translation method for driving scenarios”, NeurIPS MLIT workshop 2018]

Domain Adaptation

Synthetic-to-Real Adaptation



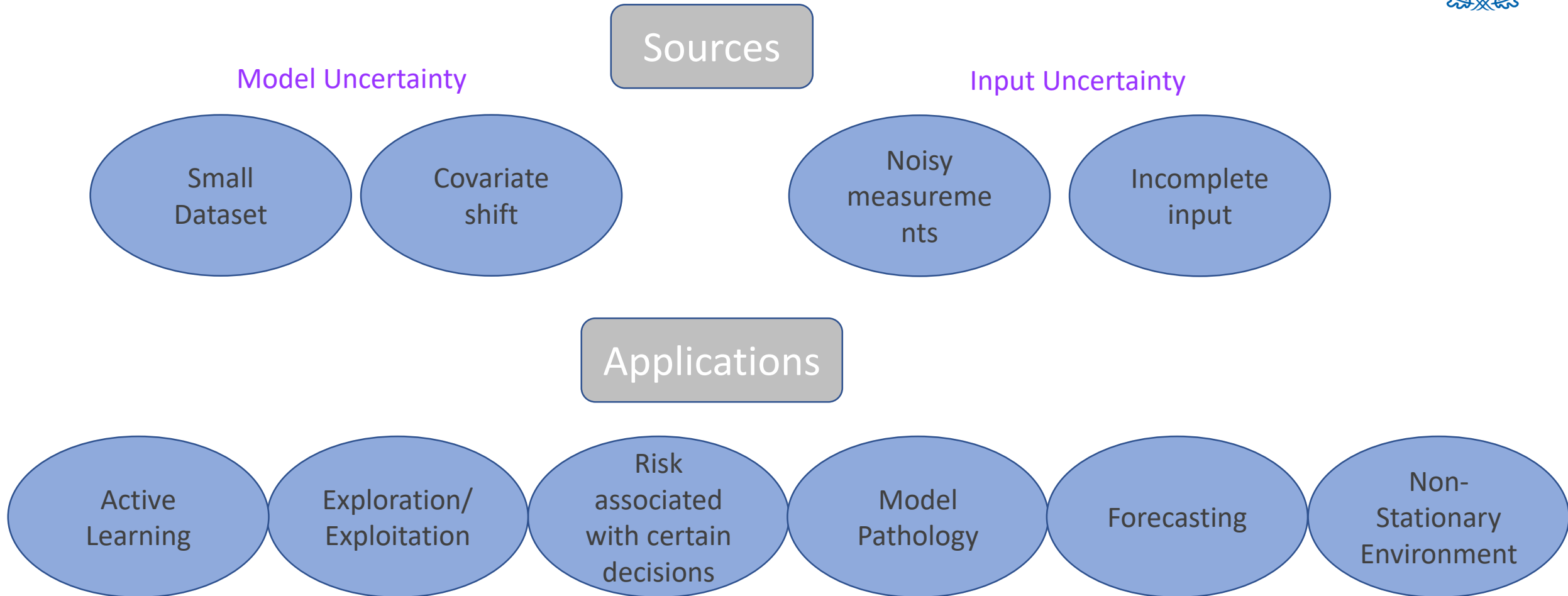
[Bujwid, Marti, Azizpour, Pieropan, “GANtruth – an unpaired image-to-image translation method for driving scenarios”, NeurIPS MLIT workshop 2018]

Contents



- Problem Definition
- Opportunities and challenges
- An example pipeline
- Domain Adaptation
- **Uncertainty Estimation**
- Future Directions

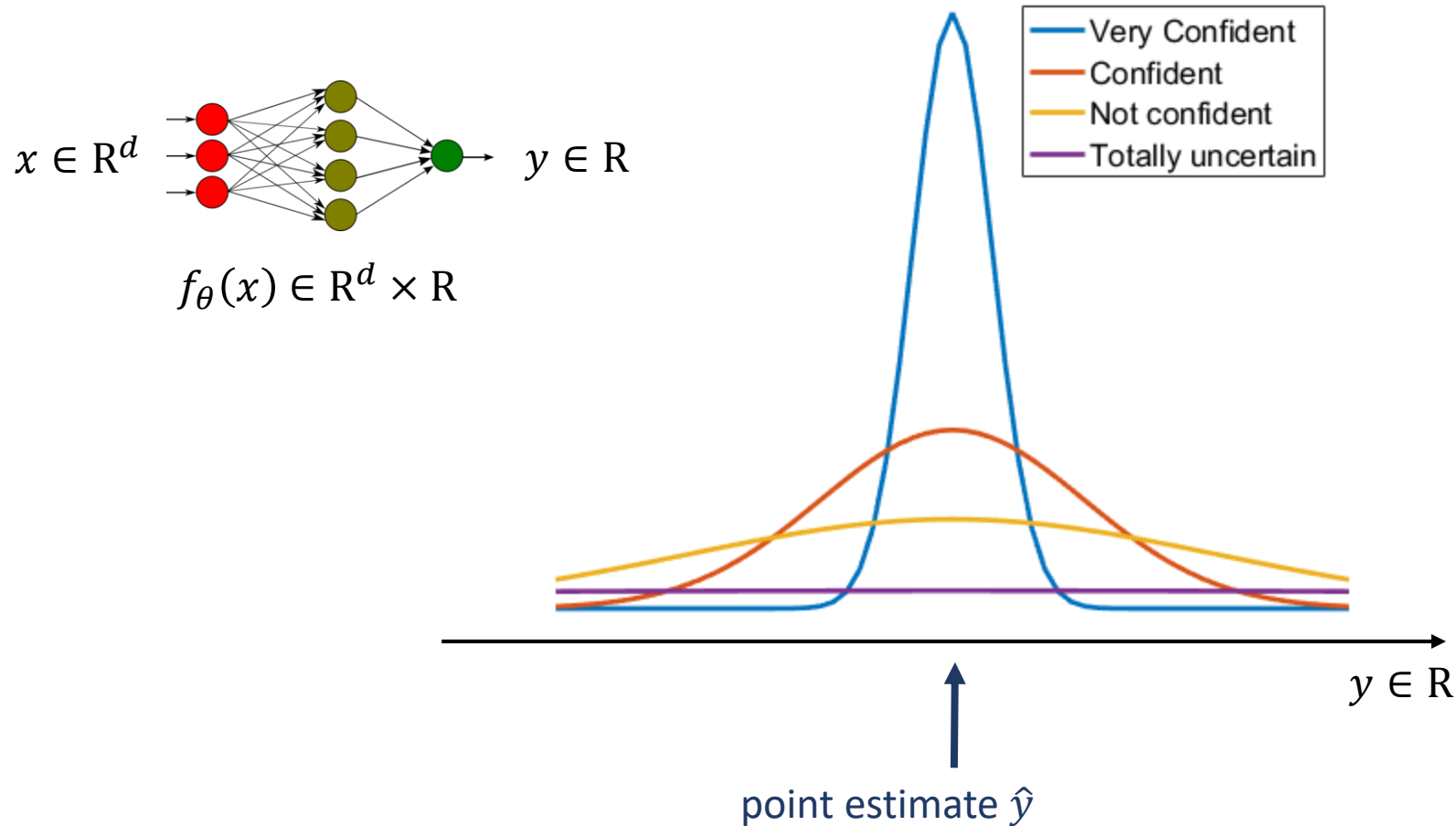
Why do we care about uncertainty?



And many more...

What do we mean by modelling uncertainty

A regression example



Multi-modal distributions!

Bayesian Modeling

for epistemic uncertainty



$$P(y|x, D) = \int P(y|x, D, \theta) P(\theta|D) d\theta$$

$$P(\theta|D) = \frac{P(D|\theta)P(\theta)}{P(D)}$$

Uncertainty with Deep Networks

These approaches require redesigning the architecture and training procedure and are usually computationally expensive to train

- Directly output probability distributions [Le et al. 2005, Huang et al. 2016, Kendall&Gal 2017]
- Place distribution over model parameters [Denker&LeCun 1991, Neal 1995]
- Variational Approximation [Hinton&Camp 1993, Graves 2011, Blundell et al. 2015]
- Expectation Propagation [Jylanki et al. 2014, Soudry et al. 2014]
- Probabilistic Backpropagation [Rezenede et al. 2014, Lobato&Adams 2015]
-

Uncertainty with Deep Networks

No change in the training procedure



- Monte Carlo Dropout [[Gal&Ghahramani 2016](#)]
- Batch Normalization Dropout [[Azizpour, Teye, Smith 2018](#)]
- Frequentist Uncertainty [[Lakshminarayanan 2017](#)]
- Other approaches (e.g. entropy of the softmax distribution)



Stochastic Regularization as VI

Stochastic Regularization Techniques (SRT)

as approximate
Bayesian inference

DropOut



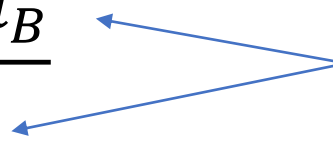
$$\theta_i = \begin{cases} w_i & \text{with prob } p \\ 0 & \text{with prob } 1 - p \end{cases}$$

Batch Normalization

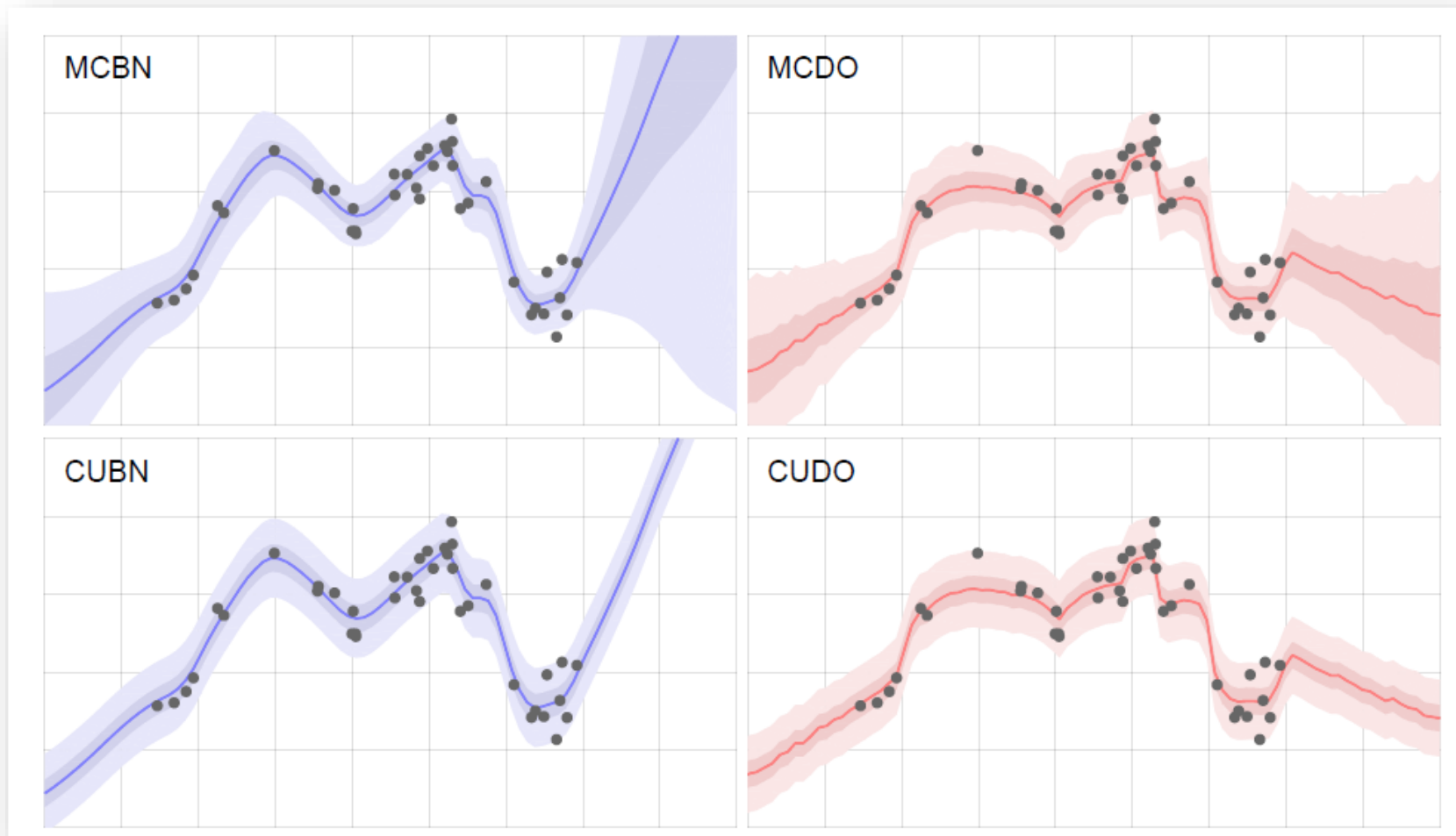


$$\overline{w}_i = \frac{w_i - \mu_B}{\sigma_B}$$

mini-batch statistics



Toy Dataset



[Teye, Azizpour, Smith, “Bayesian Uncertainty Estimation For Batch Normalized Deep Networks” arXiv 2018]

Quantitative Results

Regression - Normalized Measure



$$\sum_{i=1}^N \log P(\hat{y}_i = y_i)$$

Lower bound variance: τ^{-1}

Upper bound variance: σ^*

Dataset	$\overline{\text{PLL}}$	
	MCBN	MCDO
Boston Housing	10.49 ****	5.51 ****
Concrete	-36.36 **	10.92 ****
Energy Efficiency	10.89 ****	-14.28 *
Kinematics 8nm	1.68 ***	-0.26 ns
Power Plant	0.33 **	3.52 ****
Protein Tertiary Structure	2.56 ****	6.23 ****
Wine Quality (Red)	0.19 *	2.91 ****
Yacht Hydrodynamics	45.58 ****	-41.54 ns

[Teye, Azizpour, Smith, “Bayesian Uncertainty Estimation For Batch Normalized Deep Networks” arXiv 2018]

Quantitative Results

Classification - CIFAR



$$\sum_{i=1}^N \log P(\hat{y}_i = y_i)$$

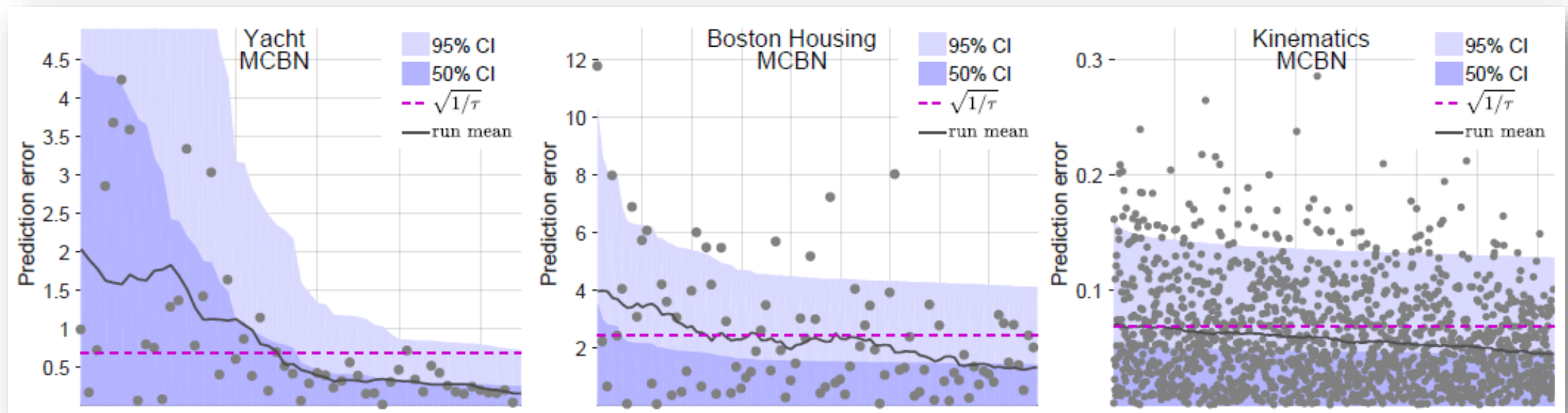
Baseline (standard network with dataset-average BN): **-0.32**

	Number of stochastic forward passes							
	1	2	4	8	16	32	64	128
PLL	-0.36	-0.32	-0.30	-0.29	-0.29	-0.28	-0.28	-0.28

[Teye, Azizpour, Smith, “Bayesian Uncertainty Estimation For Batch Normalized Deep Networks” arXiv 2018]

Qualitative Results

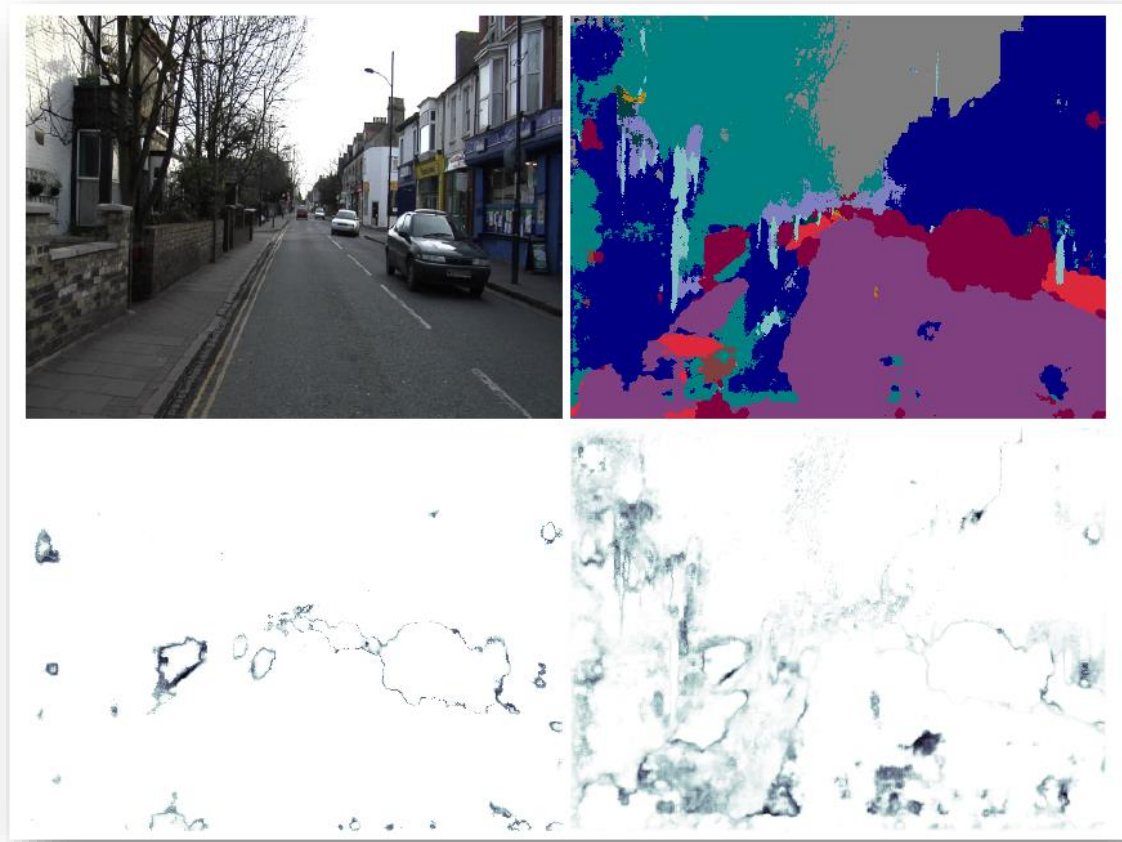
Error plot



[Teye, Azizpour, Smith, "Bayesian Uncertainty Estimation For Batch Normalized Deep Networks" arXiv 2018]

Qualitative Results

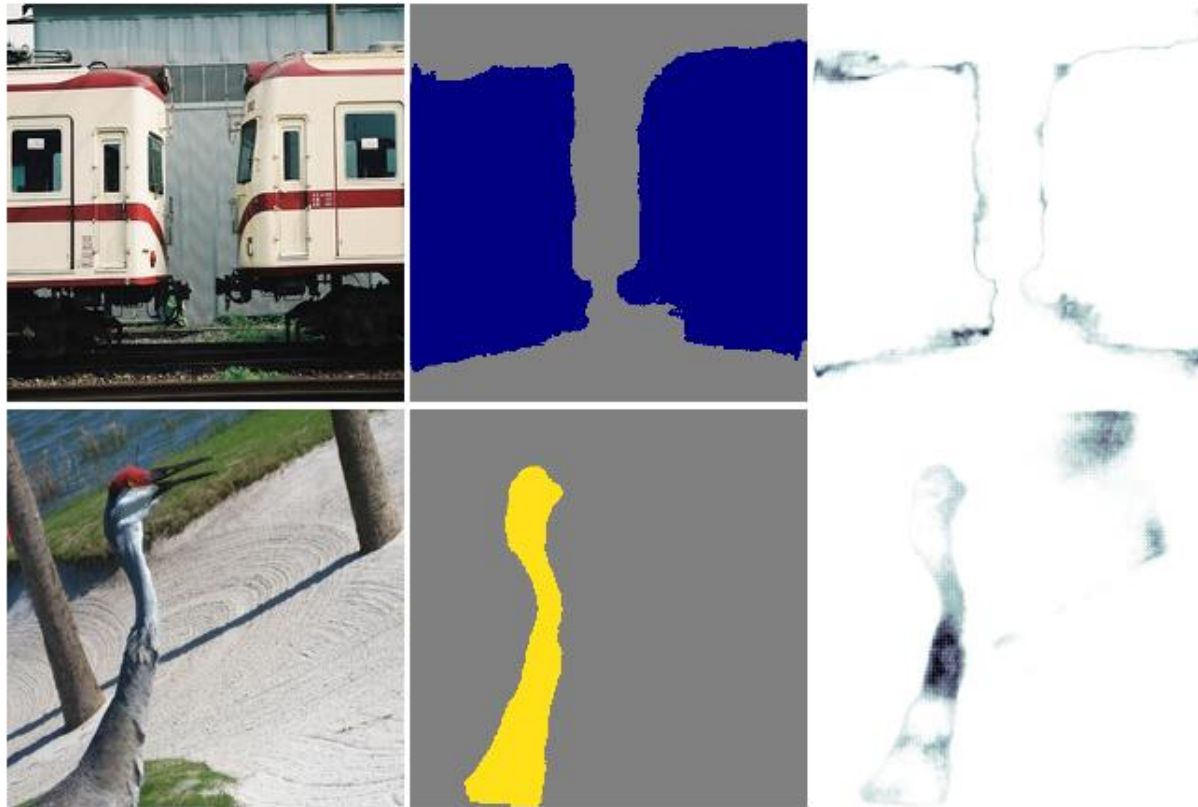
Semantic Segmentation - CamVid



[Teye, Azizpour, Smith, "Bayesian Uncertainty Estimation For Batch Normalized Deep Networks" arXiv 2018]

Qualitative Results

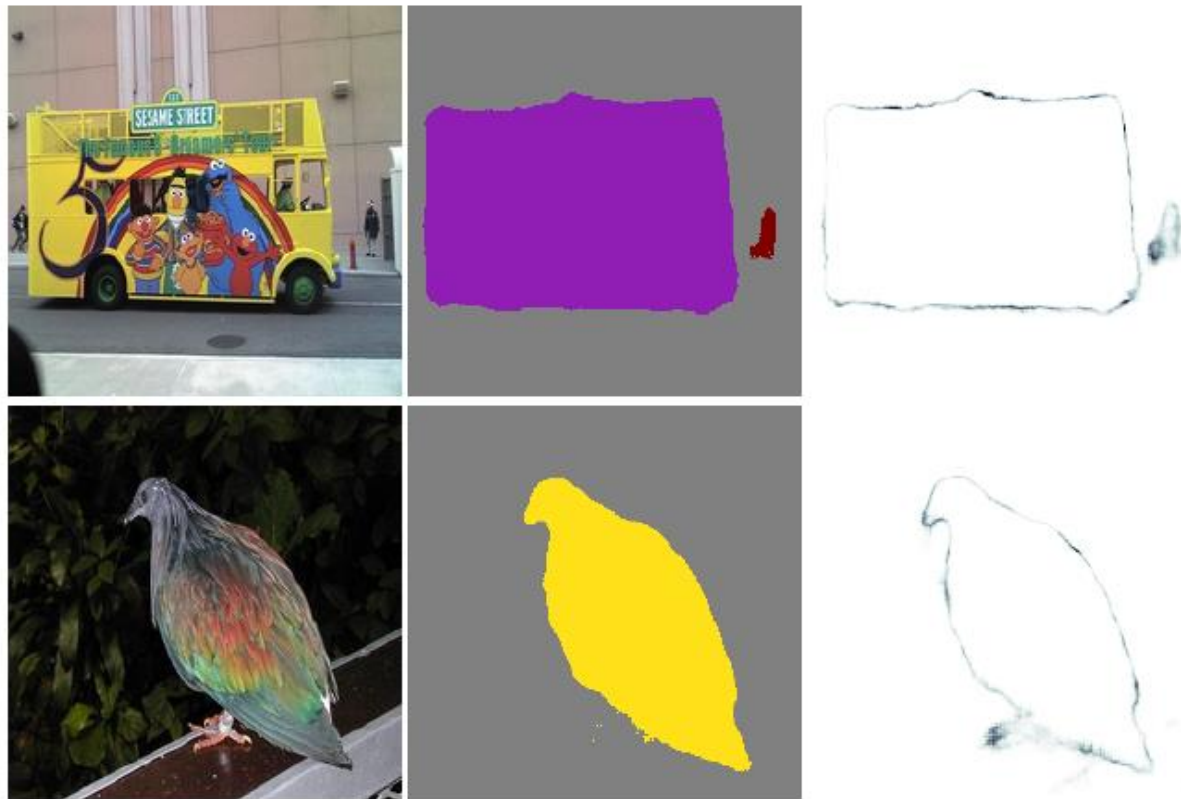
Semantic Segmentation – Pascal VOC



[Teye, Azizpour, Smith, “Bayesian Uncertainty Estimation For Batch Normalized Deep Networks” arXiv 2018]

Qualitative Results

Semantic Segmentation – Pascal VOC



[Teye, Azizpour, Smith, “Bayesian Uncertainty Estimation For Batch Normalized Deep Networks” arXiv 2018]

Simple Recipe



- Take any pretrained network with batch normalization and/or dropout layers
- Calculate constant observation noise on training/validation set, call it τ^{-1}
- At test time, sample different batches and/or dropout masks, get the predictions set
- Calculate the mean and standard deviation of the predictions, μ, σ
- The new point estimate of our prediction is: μ
- The associated uncertainty to it is: $\tau^{-1} + \sigma^2$

Conclusion

- Positive points
 - Standard training
 - Simple algorithm
 - Vast applicability
- Negative points
 - Lots of assumptions
 - Under/over estimating the uncertainty
 - Considerable computation at test time

Contents



- Problem Definition
- Opportunities and challenges
- An example pipeline
- Domain Adaptation
- Uncertainty Estimation
- **Future Directions**

Future Directions



- Geometric Deep Learning
- Side information (clinical information) as well as privileged information
- In a general scale: Multi-modal learning (unformatted textual description, images, clinical information, sequencing data)
- Probabilistic Uncertainty
- Weakly supervised learning (finding patterns that specialists are not aware of) new biomarkers, would make big leaps in life science
- Causality
- With missing data
- Encrypted networks
- Learning with noisy labels

Questions

