Artificial Intelligence in Prostate Cancer Diagnostics

Dr. ir. Geert Litjens Computational Pathology Group Department of Pathology

Help, the robots are coming!



HealthTech Market Insights Powered by Data

Reason 1 - Shortage of radiologists in many countries



In most countries there is an insufficient number of radiologists to meet the everincreasing demand for imaging and diagnostic services

The situation will get worse, as imaging volumes are increasing at a faster rate than new radiologists are entering the field.

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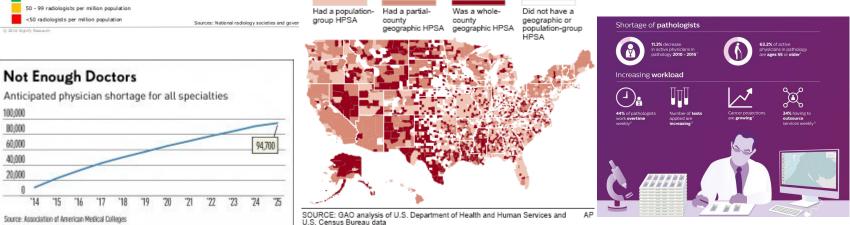
predictive improvin

Most areas lack doctors

The current shortage of U.S. physicians is about 16,000, which affects about 35 million people. As of September 2005, there were 5,594 Health Professional Shortage Areas (HPSA).

departments have enough staff to meet demand. The Royal College of Pathologists Pathology: the science behind the cure

of histopathology





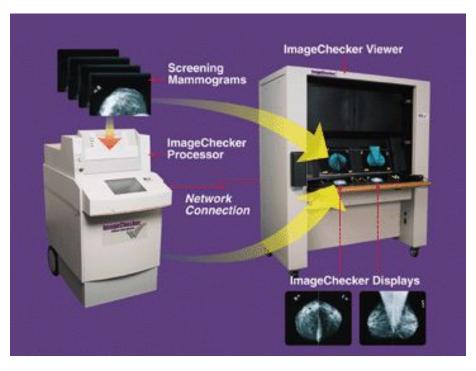
HOME AMSTERDAM OPINIE STADSGIDS

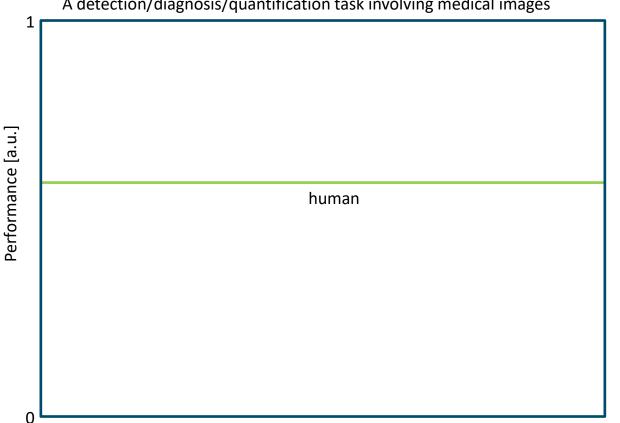
Hurray, the robots are coming!

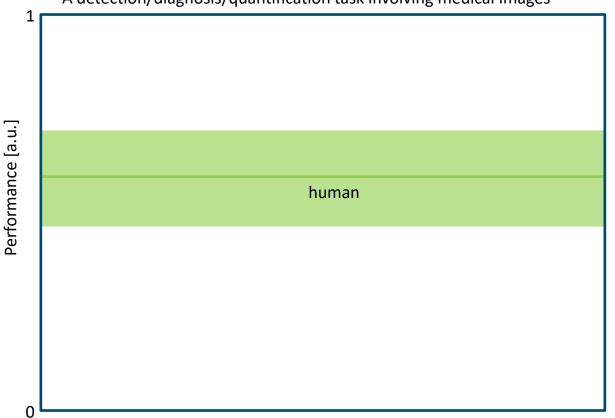


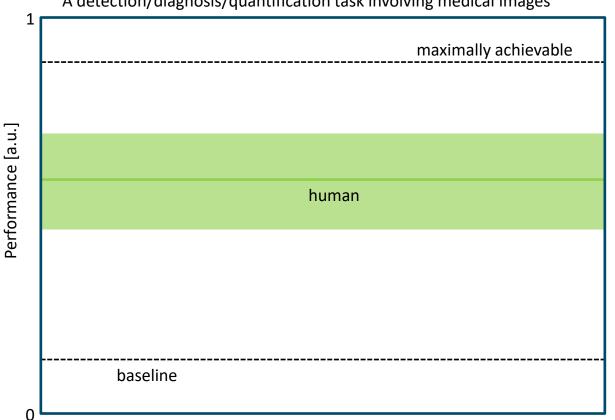
De menselijke robot Asimo is al behoorlijk slim en handig - en hij kan ook nog eens negen kilometer per uur rennen. © REUTERS

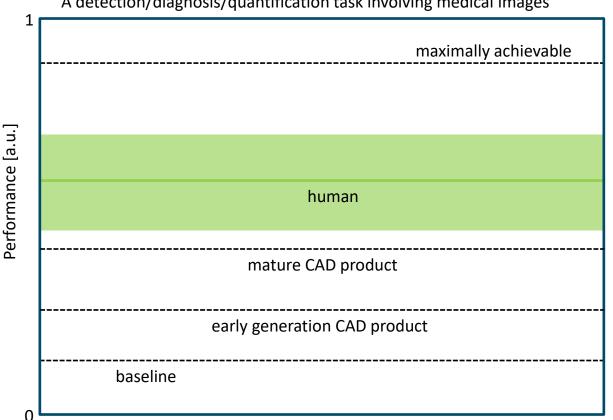
Computer-aided diagnosis

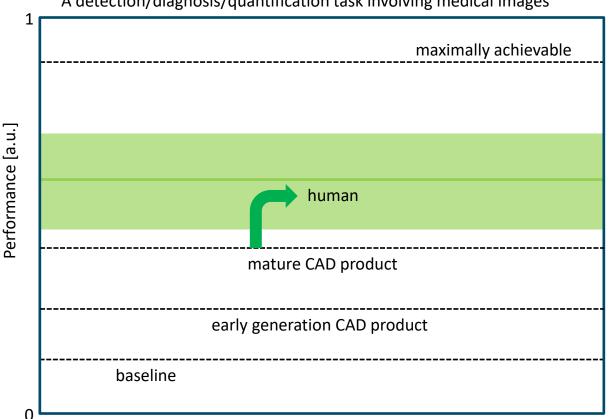




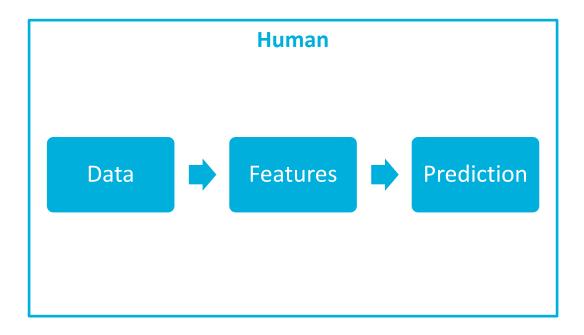








Timeline of computer-aided diagnosis

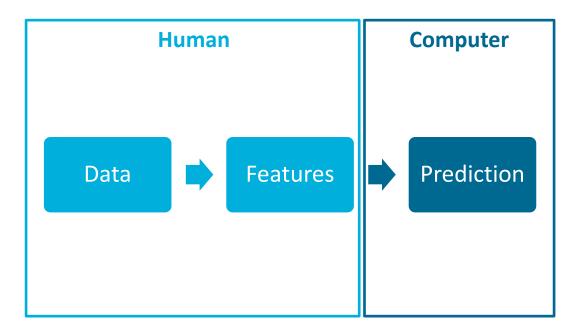




Prostate cancer risk models

Risk	Stage	Prostate-specific antigen (PSA)	Gleason score
Low	T1c – T2a	< 10 ng/mL	< 7
Medium	T2b-c	10 – 20 ng/mL	7
High	Т3	>20 ng/mL	>7

Timeline of computer-aided diagnosis



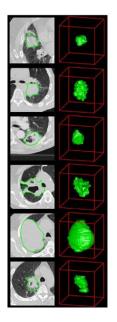
Lung cancer risk models

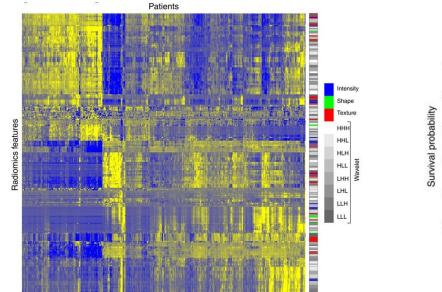
Calculator: Solitary pulmonary nodule malignancy risk in adults (Brock University cancer prediction equation)

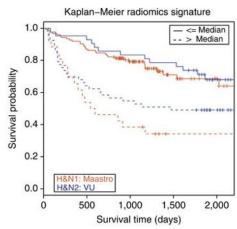
Logodds = (0.0287 * (Age - 62)) + Sex + FamilyHistoryLungCa + Emphysema - (5.3854 * ((Nodulesize/10)^{-0.5} - 1.58113883)) + Noduletype + NoduleUpperLung - (0.0824 * (Nodulecount - 4)) + Spiculation -6.7892 Cancerprobability = 100 * (e^(Logodds) / (1 + e^(Logodds)))



Radiomics



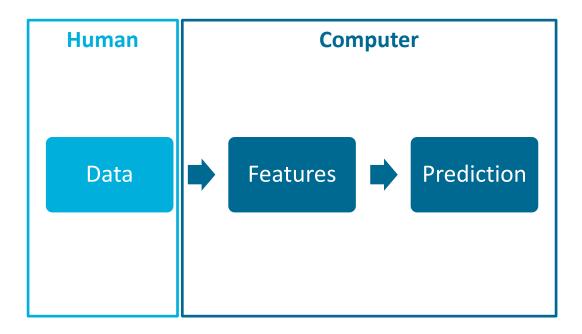




Radboudumc

Aerts et al. Nature Communications, 2014

Timeline of computer-aided diagnosis



JASON TANZ IDEAS 05.17.16 06:50 AM

SOON WE WON'T PROGRAM COMPUTERS. WE'LL TRAIN THEM LIKE DOGS



🕒 EDWARD C. MONAGHAN





BEFORE THE INVENTION of the computer, most experimental psychologists thought the brain was an unknowable black box. You could analyze a subject's behavior—*ring bell, dog salivates*—but thoughts, memories, emotions? That stuff was obscure and inscrutable, beyond the reach of science. So these behaviorists, as they called themselves, confined their work to the study of stimulus and response, feedback and response to be support to be support.

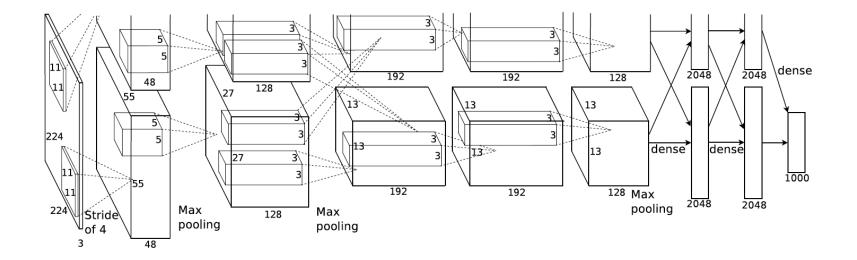
MOST POPULAR



TRANSPORTATION

JASON TANZ IDEAS 05.17.16 06:50 AM SOON WE WON'T PROGRAM COMPUTERS. WE'LL TRAIN THEM LIKE DOGS

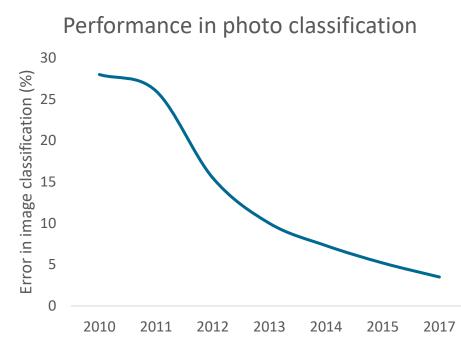
The breakthrough



Krizhevsky et al. NeurIPS, 2012

The breakthrough





The breakthrough



Alex Krizhevsky Unknown affiliation Verified email at cs.toronto.edu

Machine Learning

🖂 FOLLOW

	TITLE	CITED BY	YEAR		
Imagenet classification with deep convolutional neural networks A Krizhevsky, I Sutskever, GE Hinton Advances in neural information processing systems, 1097-1105				28245	2012
	The Journal of Machine Learning Research 15 (1), 1929-1958 Improving neural networks by preventing co-adaptation of feature detectors GE Hinton, N Srivastava, A Krizhevsky, I Sutskever, RR Salakhutdinov arXiv preprint arXiv:1207.0580	3020	2012		
	Learning multiple layers of features from tiny images A Krizhevsky, G Hinton Technical report, University of Toronto 1 (4), 7	2611	2009		
	Learning hand-eye coordination for robotic grasping with deep learning and large-scale data collection S Levine, P Pastor, A Krizhevsky, J Ibarz, D Quillen The International Journal of Robotics Research 37 (4-5), 421-436	352	2018		



nature THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE At last — a computer program that can beat a champion Go player PAGE 484 **ALL SYSTEMS GO** CONSERVATION ➔ NATUREASIA.COM **RESEARCH ETHICS POPULAR SCIENCE** SONGBIRDS SAFEGUARD WHEN GENES À LA CARTE TRANSPARENCY GOT 'SELFISH Illegal harvest of millions Don't let openness backfire Dawkins's calling of Mediterranean birds on individuals card 40 years on

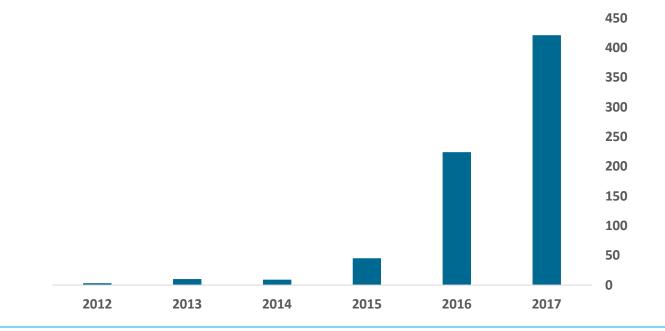
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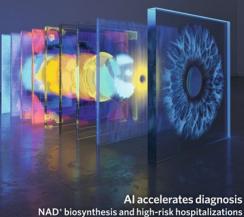
Queue the hype...

Journal papers on deep learning in medical imaging





nature September 2018 VOL WWW.nature.com/hatures medicine SEPTEMBER 2018 VOL 24 NO 9 www.nature.com/naturemedicine



Targeted microbiome therapy for thrombosis

Paravel

JAMA | Original Investigation

Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer

Rabak Ehteshami Beinordi, MS: Mitko Veta, PhD: Paul Johannes van Diest, MD, PhD: Bram van Ginneken, PhD: Nico Karssemeijer, PhD: Geert Littlers, PhD: Jeroen A. W. M. van der Laak, PhD: and the CAMELYONI6 Consortium

Editorial page 2184

IMPORTANCE Application of deep learning algorithms to whole-slide pathology images can potentially improve diagnostic accuracy and efficiency.

OBJECTIVE Assess the performance of automated deep learning algorithms at detecting metastases in hematoxylin and eosin-stained tissue sections of lymph nodes of women with breast cancer and compare it with pathologists' diagnoses in a diagnostic setting.

Related articles page 2211 and page 2250

E Supplemental conten CME Quiz at nanetwork.com/learning and CME Questions page 2252

DESIGN, SETTING, AND PARTICIPANTS Researcher challenge competition (CAMELYON16) to develop automated solutions for detecting lymph node metastases (November 2015-November 2016). A training data set of whole-slide images from 2 centers in the Netherlands with (n = 110) and without (n = 160) nodal metastases verified by immunohistochemical staining were provided to challenge participants to build algorithms. Algorithm performance was evaluated in an independent test set of 129 whole-slide images (49 with and 80 without metastases). The same test set of corresponding glass slides was also evaluated by a panel of 11 pathologists with time constraint (WTC) from the Netherlands to ascertain likelihood of nodal metastases for each slide in a flexible 2-hour session. simulating routine pathology workflow, and by 1 pathologist without time constraint (WOTC).

EXPOSURES Deep learning algorithms submitted as part of a challenge competition or pathologist interpretation.

MAIN OUTCOMES AND MEASURES The presence of specific metastatic foci and the absence vs presence of lymph node metastasis in a slide or image using receiver operating characteristic curve analysis. The 11 pathologists participating in the simulation exercise rated their diagnostic confidence as definitely normal, probably normal, equivocal, probably tumor, or definitely tumor.

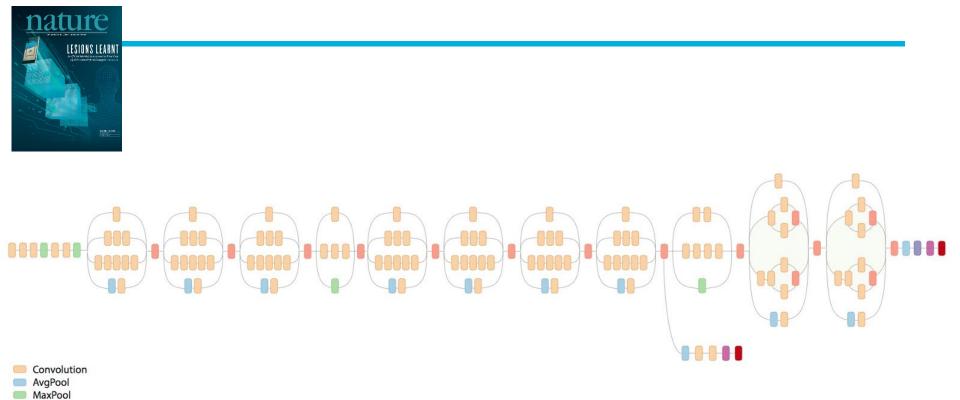
RESULTS The area under the receiver operating characteristic curve (AUC) for the algorithms ranged from 0.556 to 0.994. The top-performing algorithm achieved a lesion-level, true-positive fraction comparable with that of the pathologist WOTC (72.4% [95% CI. 64.3%-80.4%]) at a mean of 0.0125 false-positives per normal whole-slide image. For the whole-slide image classification task, the best algorithm (AUC, 0.994 [95% CI, 0.983-0.999]) performed significantly better than the pathologists WTC in a diagnostic simulation (mean AUC, 0.810 [range, 0.738-0.884]; P < .001). The top 5 algorithms had a mean AUC that was comparable with the pathologist interpreting the slides in the absence of time constraints (mean AUC, 0.960 [range, 0.923-0.994] for the top 5 algorithms vs 0.966 [95% CI, 0.927-0.998] for the pathologist WOTC).

CONCLUSIONS AND RELEVANCE In the setting of a challenge competition, some deep learning algorithms achieved better diagnostic performance than a panel of 11 pathologists participating in a simulation exercise designed to mimic routine pathology workflow algorithm performance was comparable with an expert pathologist interpreting whole-slide images without time constraints. Whether this approach has clinical utility will require evaluation in a clinical setting

IAMA 2017/219(22)-2109-2210 doi-10.1001/j.sma.201714595

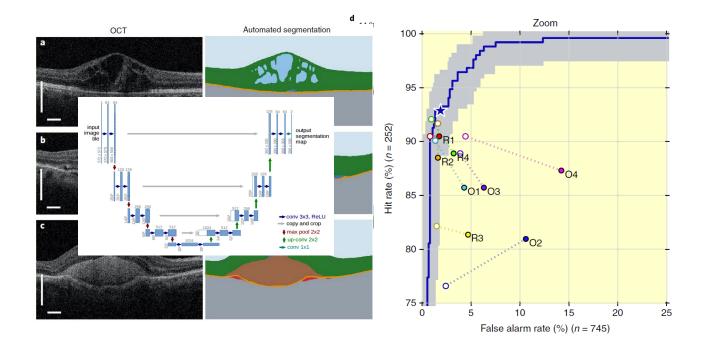
Author Affiliations: Diagnostic Image Analysis Group, Department of Radiology and Nuclear Medicine. Radboud University Medical Center, Nijmegen, the Netherlands (Ehteshami Beinordi, van Ginneker Karssemeijer); Medical Image Analysis Group, Eindhoven University of Technology, Eindhoven, the Netherlands (Veta): Department of Pathology, University Medical Center Utrecht, Utrecht, the Netherlands Johannes van Diest): Department of Pathology, Radboud University Medical Center, Nijmegen, the Netherlands (Litjens, van der Laak) Group Information: The CAMELYONIE Consortium authors and collaborators ar listed at the end of this article. Corresponding Author: Babak Ehteshami Bejnordi, MS, Postbus 9101, 6500 HB Nijmegen

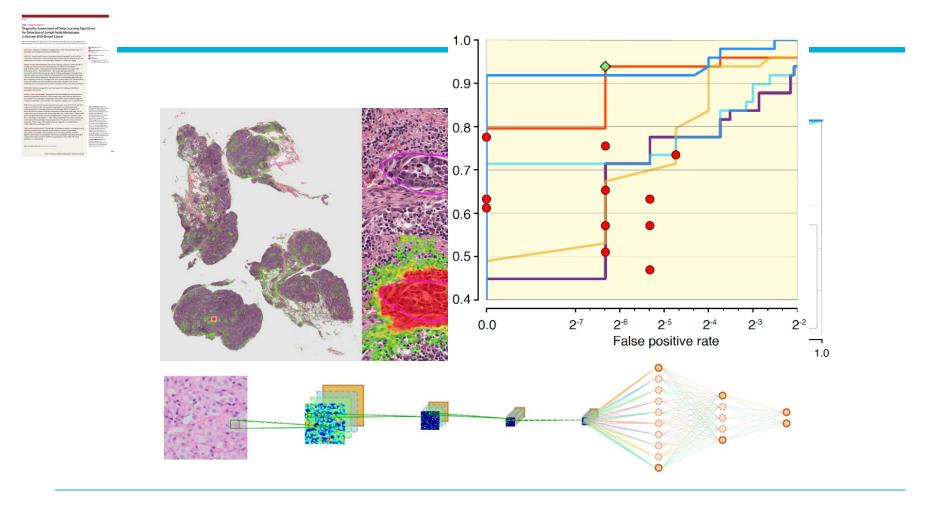
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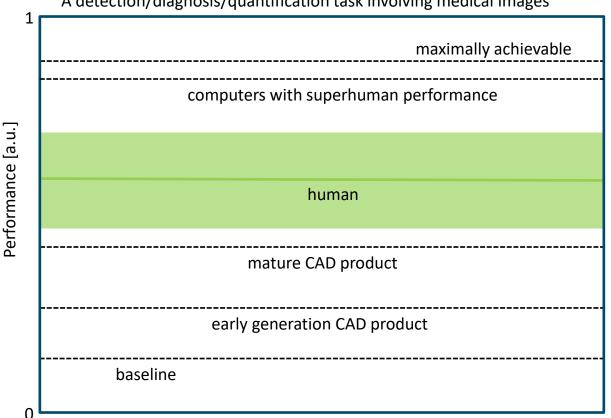


- Concat
- Dropout
- Fully connected
- Softmax

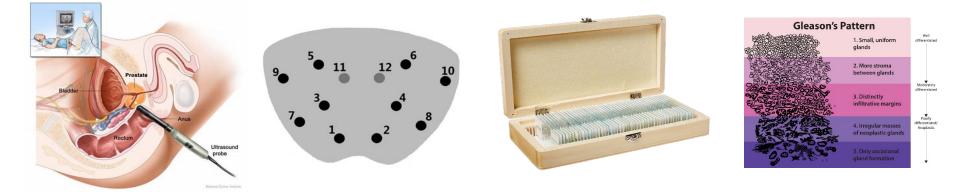




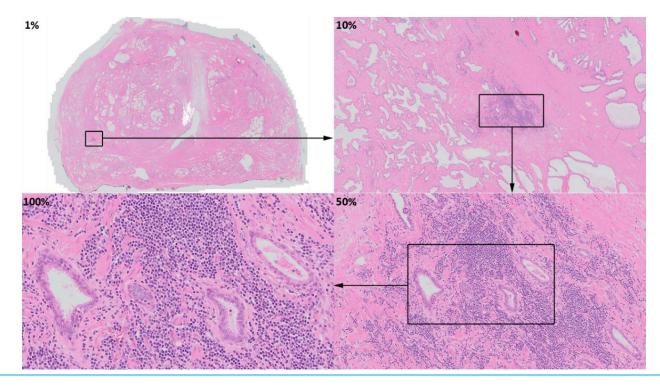




Prostate Cancer Diagnosis



Histopathology data not digital



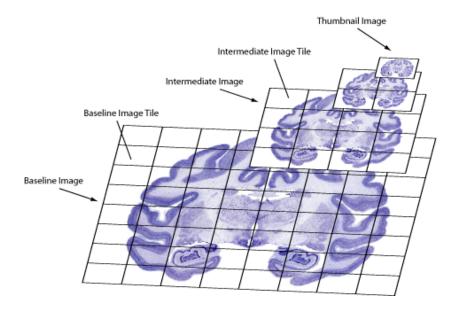
Whole-slide imaging

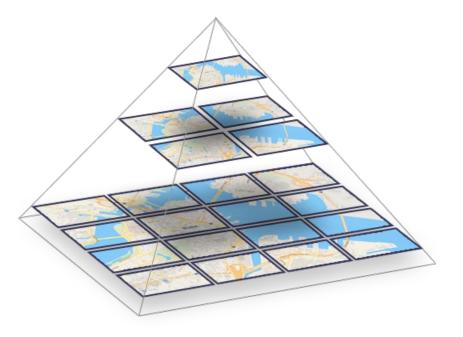
Digital acquisition of an entire histopathology slide

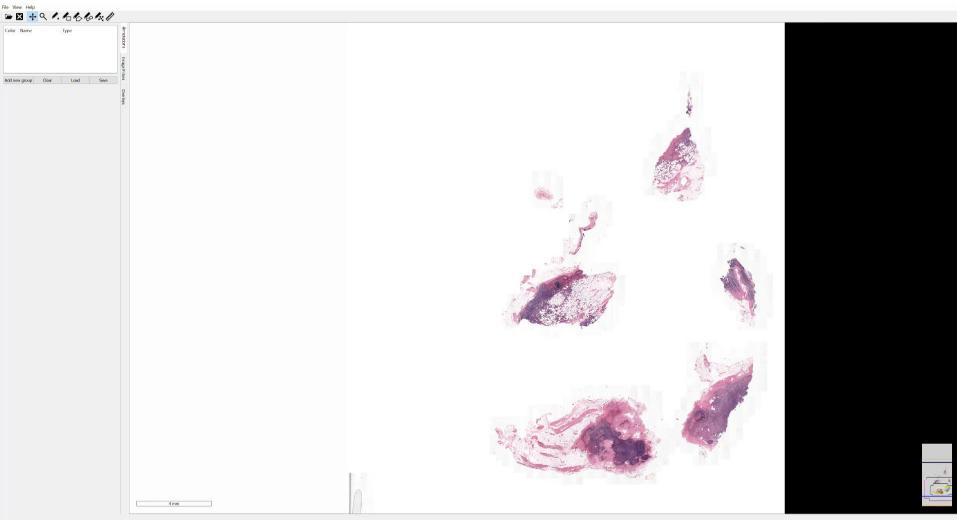




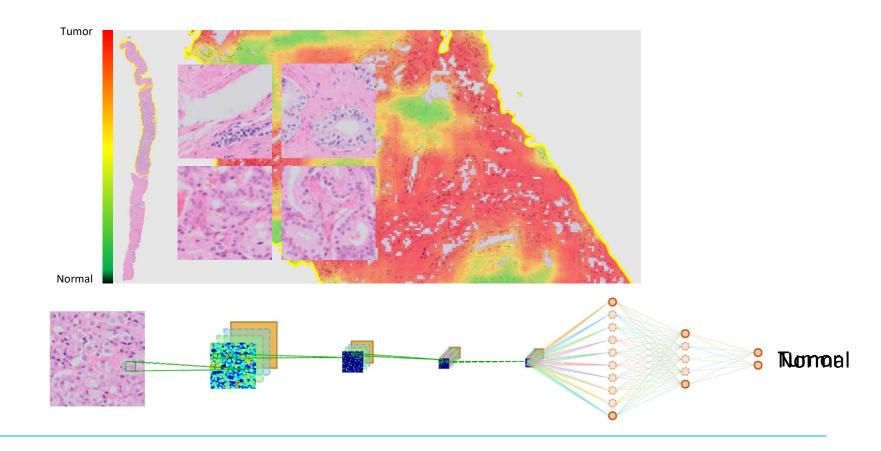
Whole-slide imaging





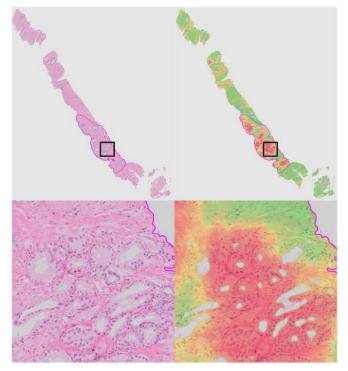


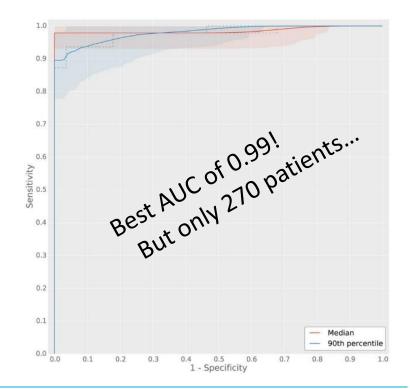
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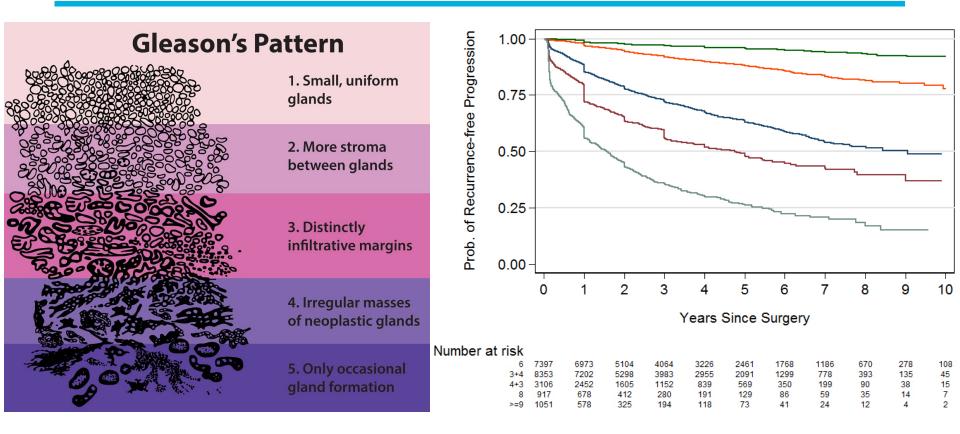
Bulten et al. Sci Rep. (2016)

Cancer detection

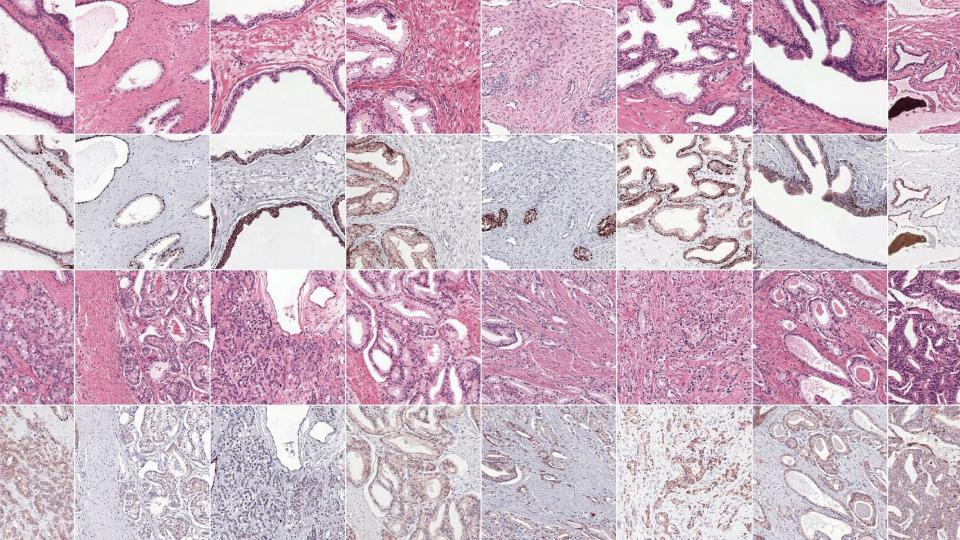












1) Training of IHC network



Input data: 25 IHC WSIs (20 training, 5 validation)

Specimens are stained with CK8/18 and P63 to mark epithelial tissue and basal cell layer.



Color deconvolution is applied to each slide. Only the channel representing the epithelial tissue is used, the rest is discarded.

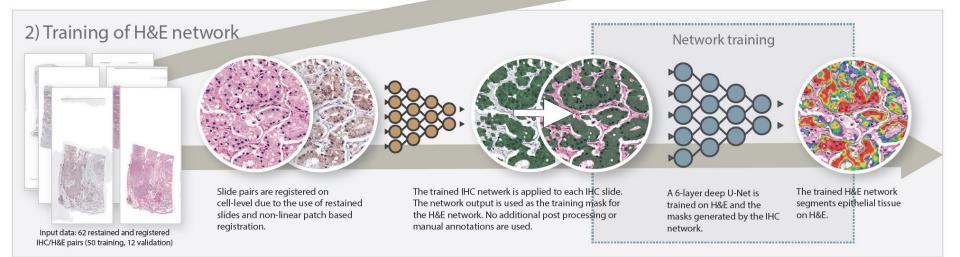
Artifacts are introduced due to imperfections in the staining and color deconvolution method (Example: top left corner).

Artifacts are removed manually in selected regions. Training data is sampled from these regions.

A 5-layer deep U-Net is trained on the corrected IHC regions. Areas with artifacts are sampled more.

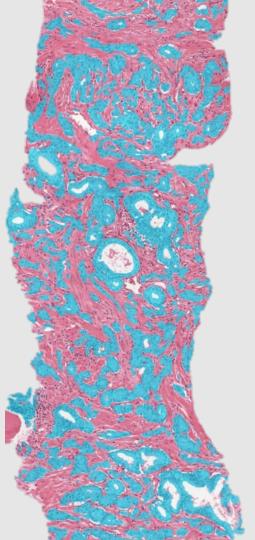
Network training

The IHC network produces precise segmentation masks given an IHC slide, independent of the color deconvolution.



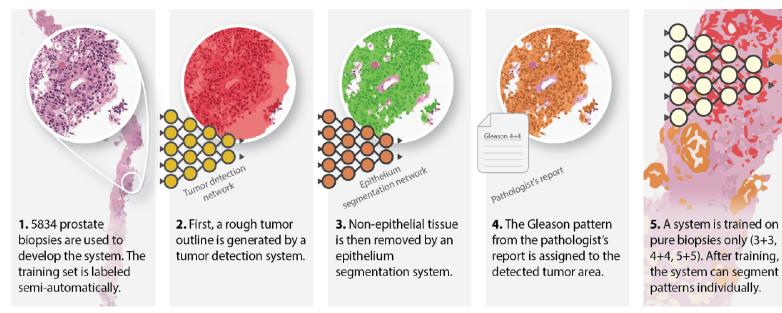
Kadboudumc

Bulten et al. Sci Rep. (2019)



Gleason grading

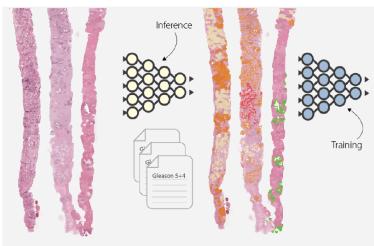
1. Semi-automatic data labeling



Bulten et al. Automated Gleason Grading of Prostate Biopsies using Deep Learning. Lancet Oncology. Accepted

Gleason grading

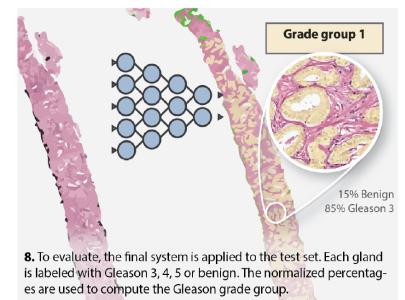
2. Refinement & training

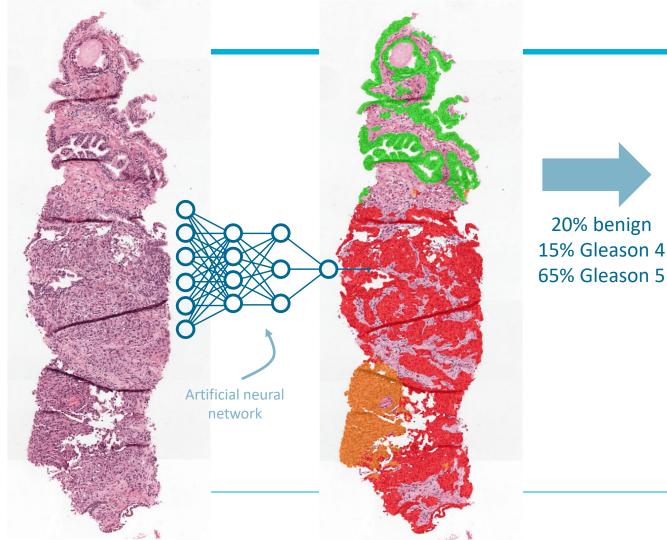


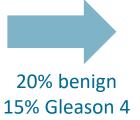
6. The full training set is labeled using the network trained on pure biopsies. Reports are used to further refine the labels.

7. Using the new labels the final system is trained.

3. Grade group prediction

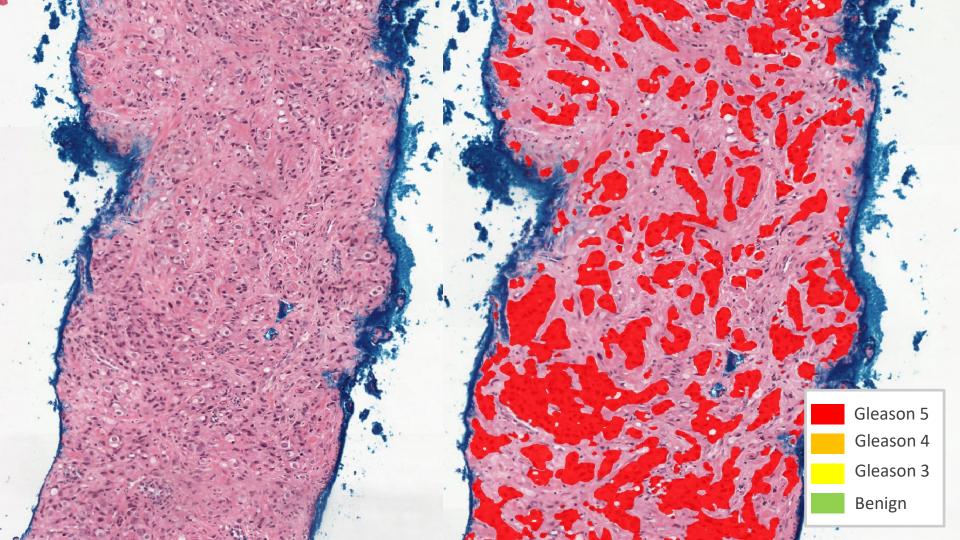


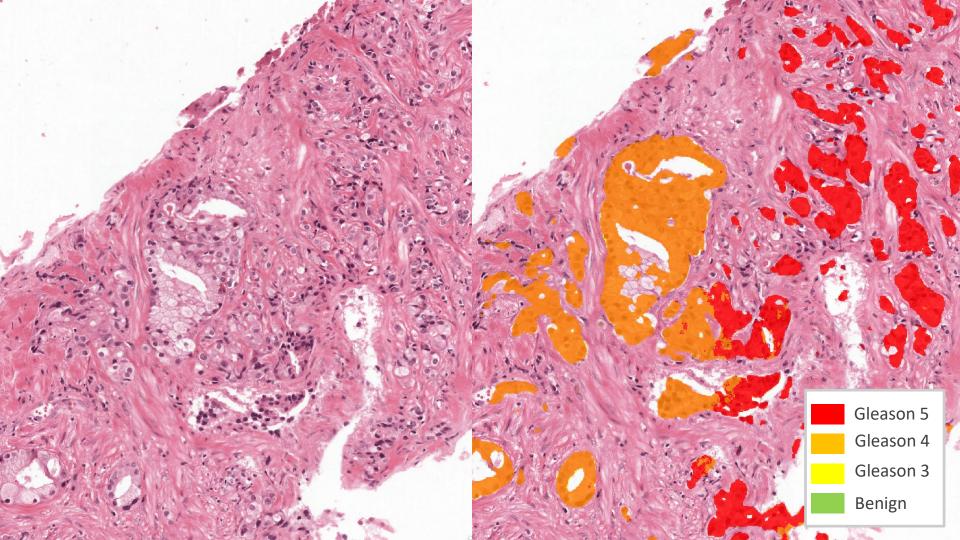


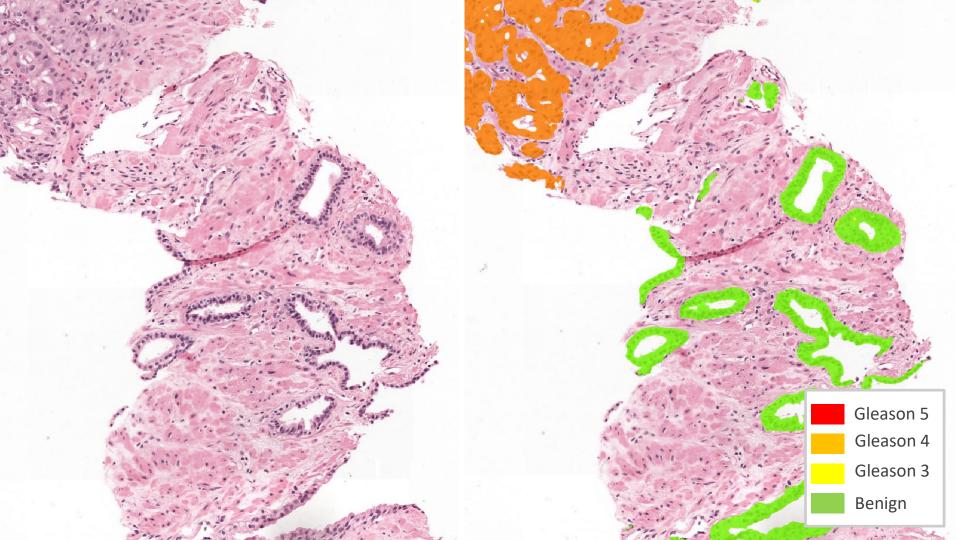






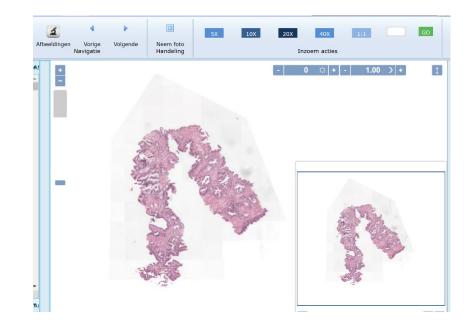




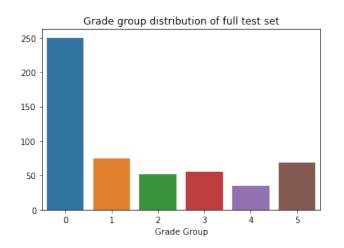


Reference standard

- 3 expert uropathologists
- 550 prostate biopsies
- Gleason growth patterns, tumor volumes & grade groups

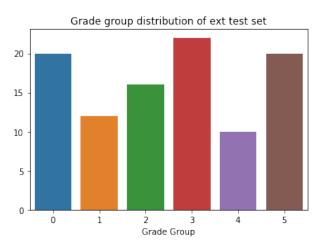


Case distribution



Full test set:

- 550 biopsies
- 3 experts



Subset

- 100 biopsies (selected from the 550)
- 15 external pathologists

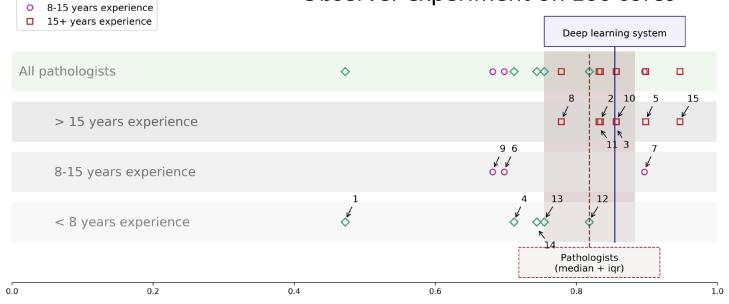


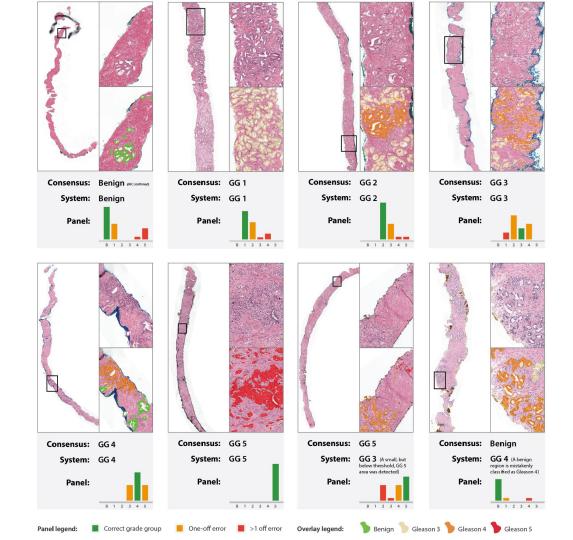
Gleason grading

< 8 years experience

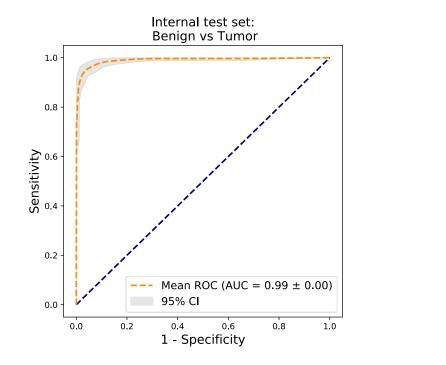
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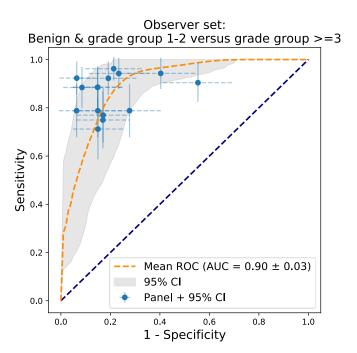
Observer experiment on 100 cores



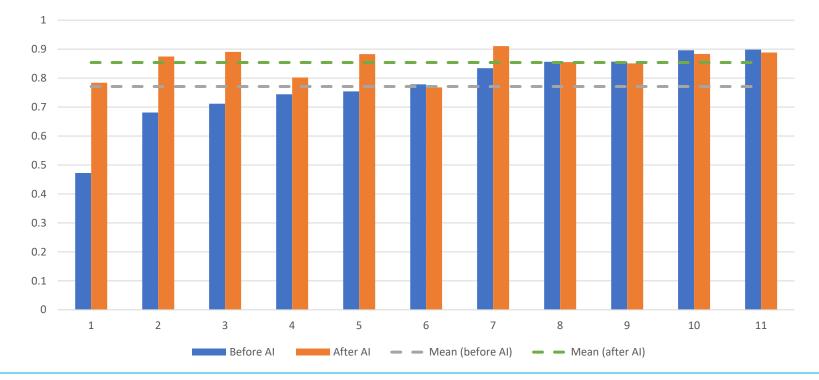


Classification – ROC





Usefulness of AI in practice



Future directions

- Algorithm available via grand-challenge.org
- Decision thresholds for grade groups
- Correlation with survival / recurrence
- Direct prediction of survival / recurrence from morphological patterns





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Maschenka Balkenhol Pathology resident and PhD student





Meyke Hermsen PhD student

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Elke Loskamp-

Huntink

Study manager



Yiping Jiao

PhD student

Peter Bandi PhD student



Wouter Bulten

PhD student





Swiderska-Chadai Postdoc



Jeffrey Hoven Research technician



Rijthoven Scientific researcher





Maud Wekking Research technician









Patrick Sonsma Master student

Scientific programmer

Mooij



Emiel Stoelinga Master student



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