

University Hospitals
Coventry and Warwickshire

NHS Trust



Digital pathology – disease processes by pixel analysis

Professor David Snead

University Hospitals of Coventry and Warwickshire
NHS Trust

University of Warwick



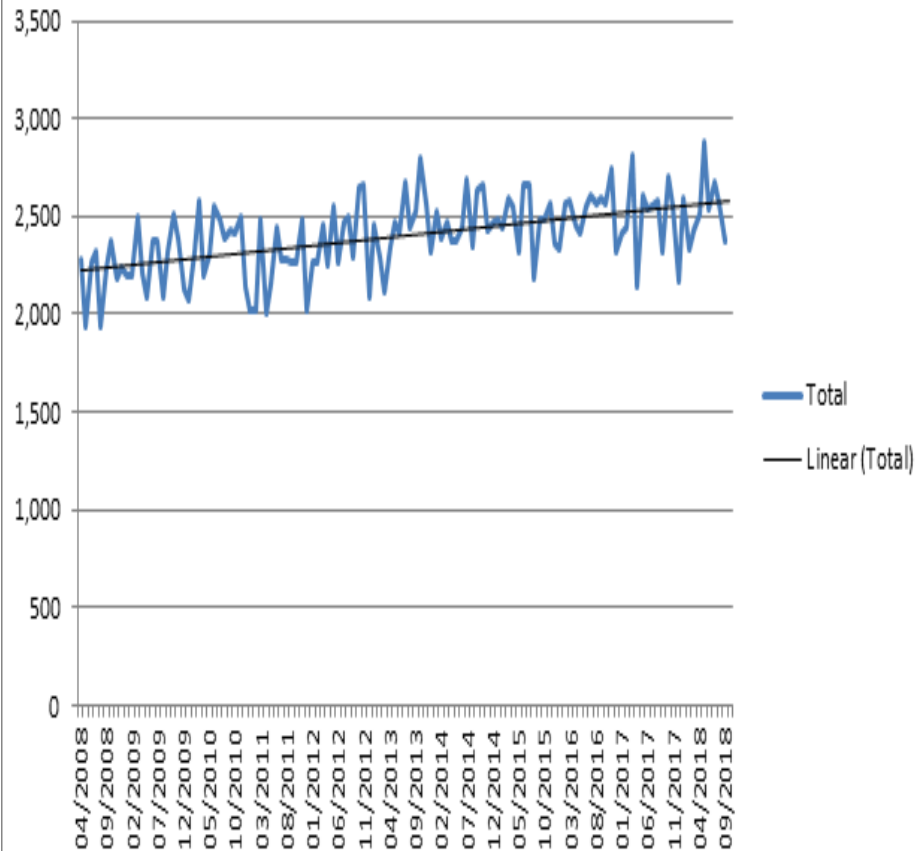
Disclaimer

- Philips Computational Pathology Board

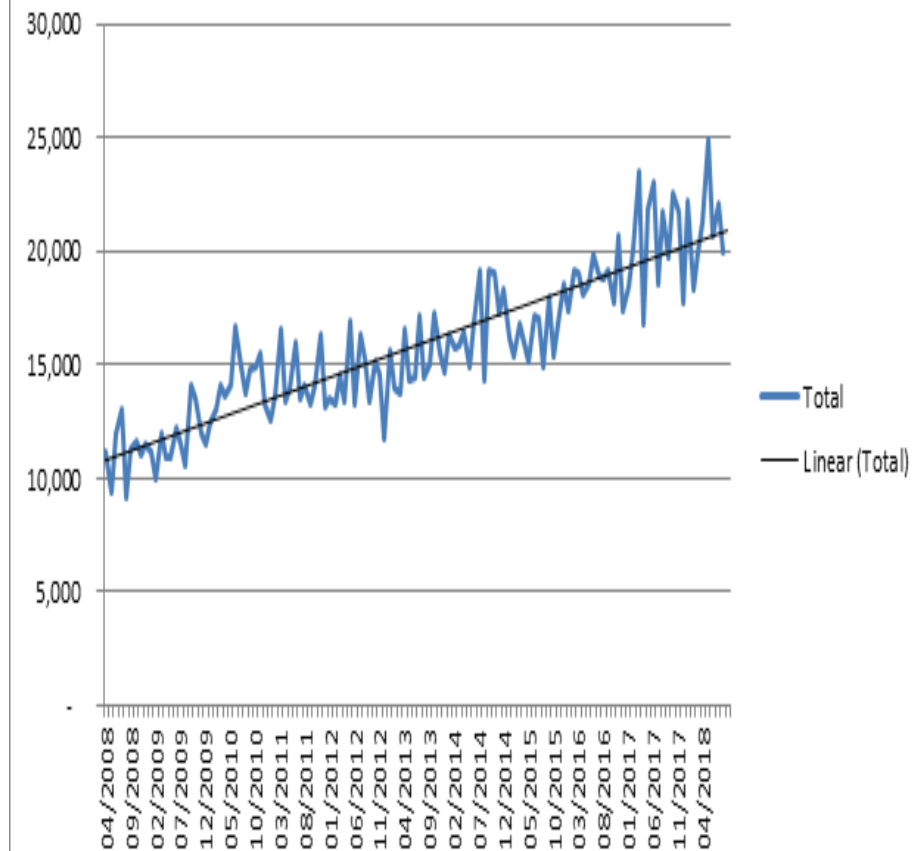


Pathology workload 2008-2018

Total Cases



Total Slides



File Home Insert Page Layout References Mailings Review View Add-Ins

Cut Copy Paste Format Painter Clipboard Font Paragraph Styles

Find Replace Select Change Styles Editing

Laboratory Number: **H18-27854**

CLINICAL DETAILS:
URGENT 3182
A) Exc BCC left post auricular area marker 12 o'clock
B) Wide exc melanoma in-situ left arm, marker 12 o'clock

SPECIMEN TYPE:
A) SKIN EXCISION left post auricular
B) SKIN EXCISION left arm

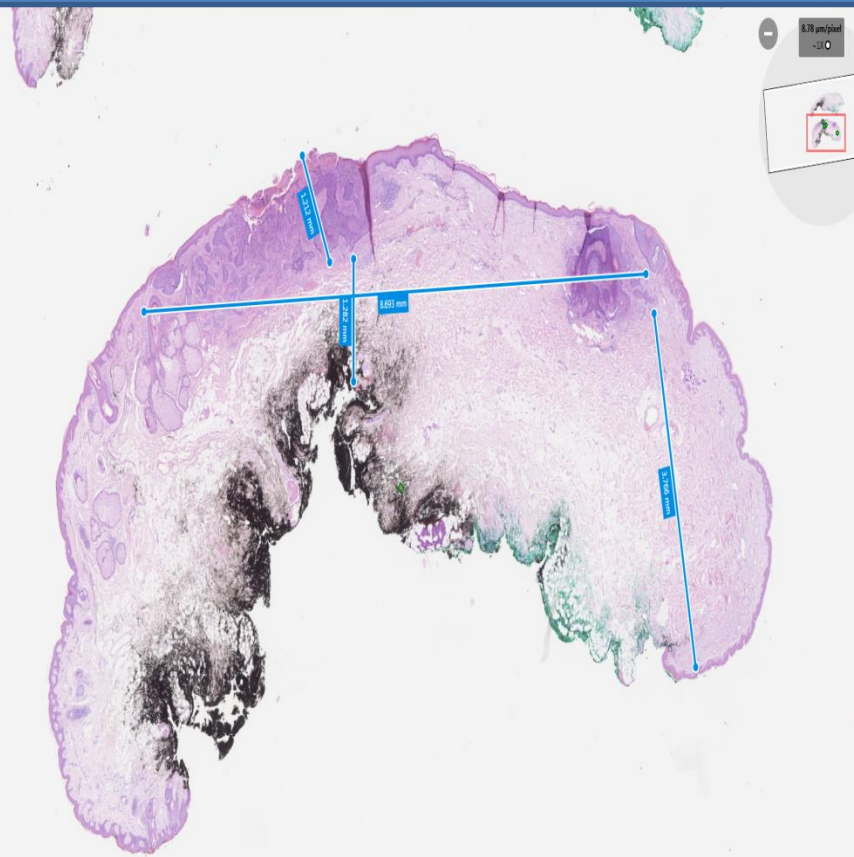
MACROSCOPY:
A) SKIN EXCISION left post auricular
- Disc of skin measuring 25 x 22 x 4mm. Surface bears a pale lesion measuring 17 x 17mm S = 12, 3 = 8, 9 = G, sectioned 12-6. All of lesion processed.
B) SKIN EXCISION left arm
- Ellipse of skin measuring 50 x 15 x 13mm. Surface bears a linear scar measuring 32mm in length. S = 12, 3 = 8, 9 = G, sectioned 12-6. Representative sections taken scar submitted. Cut surface shows a focus of haemorrhagic measuring 5mm across. No other lesion seen.

MICROSCOPY:
a) Basal cell carcinoma
Low risk component: nodular

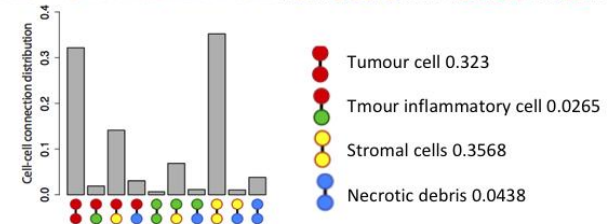
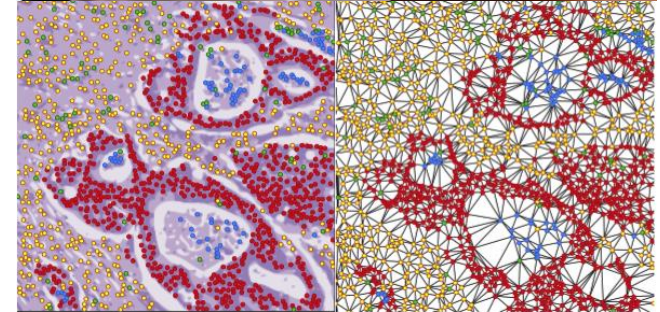
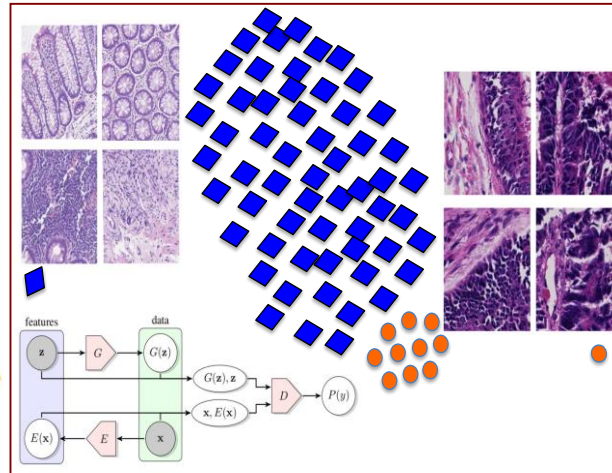
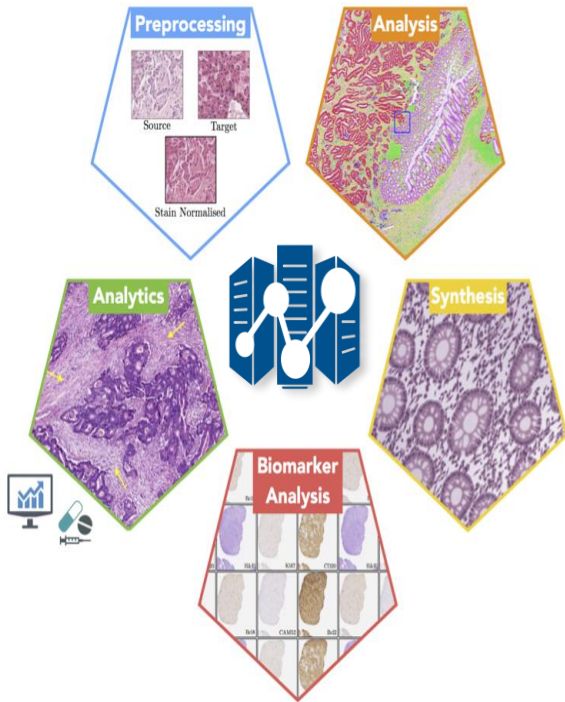
High risk component: none
Maximum diameter 8mm.
Thickness 1.2mm.
Pericardial invasion: no.
Pericardial invasion: no.
Lymphovascular invasion: no.
Radial margin 8mm.
Deep margin 1.2mm.
Stage T0N0 pT1
High risk case for MDT -no.
Is Skin containing a healing scar tissue. There is no residual melanoma. Excision appears complete.

DIAGNOSIS:
Basal cell carcinoma

Reporting Pathologist:
Authorising Pathologist:
Date of Report:



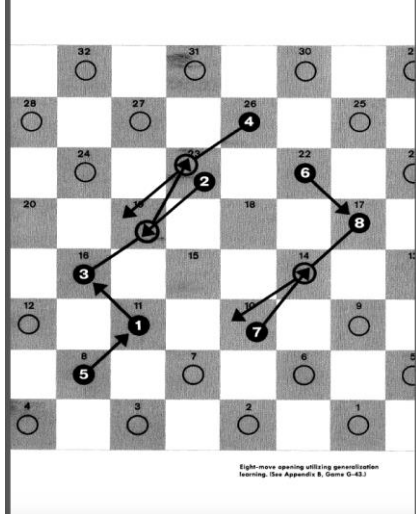
Pathology Image Analytics



Scope for AI in cellular pathology

- Automation
- Biomarker assessment
- Cancer detection
- Cancer grading
- Prognostic and predictive tools
- Research

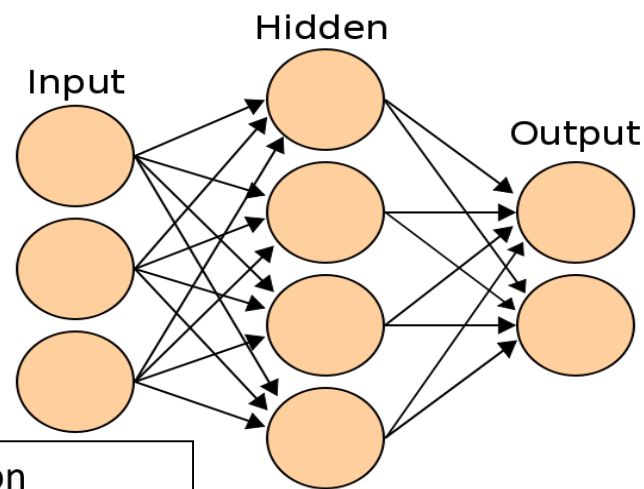




A. L. Samuel

Some Studies in Machine Learning Using the Game of Checkers

IBM JOURNAL • JULY 1959



Perceptron neural network 1958
F Rosenblatt

Cytopathology 1997, 8, 265-273

Image analysis of low magnification images of fine needle aspirates of the breast produces useful discrimination between benign and malignant cases

S. S. CROSS, J. P. BURY, T. J. STEPHENSON AND R. F. HARRISON*
Department of Pathology, University of Sheffield Medical School, and *Department of Automated Control and Systems Engineering, University of Sheffield, Sheffield, UK

Accepted for publication 4 February 1997

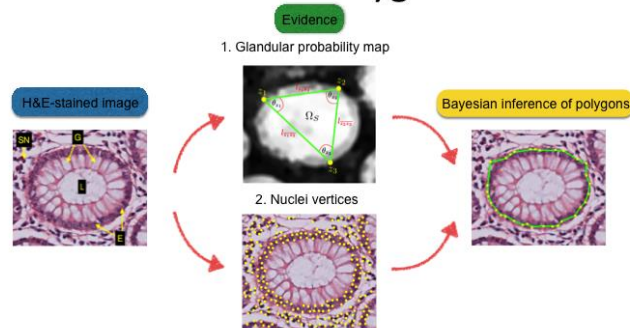
CURRENT ISSUES

PAPNET Computer-Aided Rescreening for Detection of Benign and Malignant Glandular Elements in Cervicovaginal Smears: A Review of 61 Cases

Charles D. Sturgis, M.D.,* Carol Isoe, S.C.T. (A.S.C.P.), C.M.I.A.C.,
Nodde E. McNeal, S.C.T. (A.S.C.P.), C.M.I.A.C., Gordon H. Yu, M.D.,
and Denise V.S. DeFries, M.D., F.I.A.C.

Diagn. Cytopathol. 1998;18:307-311.

Tubule formation The Random Polygons Model



Sirinukunwattana *et al.*, *IEEE Trans Med Imaging* (Nov 2015)

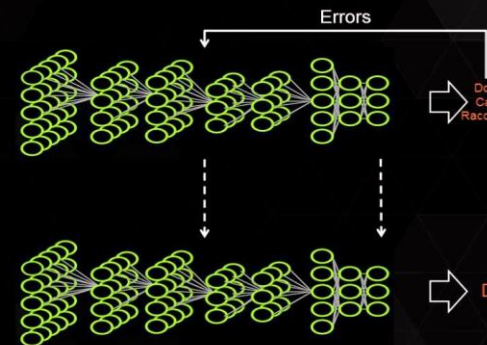
US patent application number 61452293

DEEP LEARNING APPROACH

Train:



Deploy:



Health Policy and Practice / Santé: politique et pratique médicale

Canadian Association of Radiologists White Paper on Artificial Intelligence in Radiology

An Tang, MD, MSc^{a,b,*}, Roger Tam, PhD^{c,d}, Alexandre Cadrin-Chênevert, MD, BIng^e,
Will Guest, MD, PhD^c, Jaron Chong, MD^f, Joseph Barfett, BESC, MSc, MD^g,
Leonid Chepelev, MD PhD^h, Robyn Cairns, MSc, MDⁱ, J. Ross Mitchell, PhD^j,
Mark D. Cicero, MD, BESC, FRCPC^g, Manuel Gaudreau Poudrette, MD^k,
Jacob L. Jaremko, MD, PhD^l, Caroline Reinhold, MD, MSc^f, Benoit Gallix, MD^f,
Bruce Gray, MD, FRCPC^g, Raym Geis, MD, FACR^m; for the Canadian Association of
Radiologists (CAR) Artificial Intelligence Working Group

^aDepartment of Radiology, Université de Montréal, Montréal, Québec, Canada

^bCentre de recherche du Centre hospitalier de l'Université de Montréal, Montréal, Québec, Canada

^cDepartment of Radiology, University of British Columbia, Vancouver, British Columbia, Canada

^dSchool of Biomedical Engineering, University of British Columbia, Vancouver, British Columbia, Canada

^eDepartment of Medical Imaging, CISSS Lanaudière, Université Laval, Joliette, Québec, Canada

^fDepartment of Radiology, McGill University Health Center, Montréal, Québec, Canada

^gDepartment of Medical Imaging, St. Michael's Hospital, University of Toronto, Toronto, Ontario, Canada

^hDepartment of Radiology, University of Ottawa, Ottawa, Ontario, Canada

ⁱDepartment of Radiology, British Columbia's Children's Hospital, University of British Columbia, Vancouver, British Columbia, Canada

^jDepartment of Research, Mayo Clinic, Phoenix, Arizona, USA

^kDepartment of Radiology, Université de Sherbrooke, Sherbrooke, Québec, Canada

^lDepartment of Radiology and Diagnostic Imaging, University of Alberta, Edmonton, Alberta, Canada

^mDepartment of Radiology, National Jewish Health, Denver, Colorado, USA

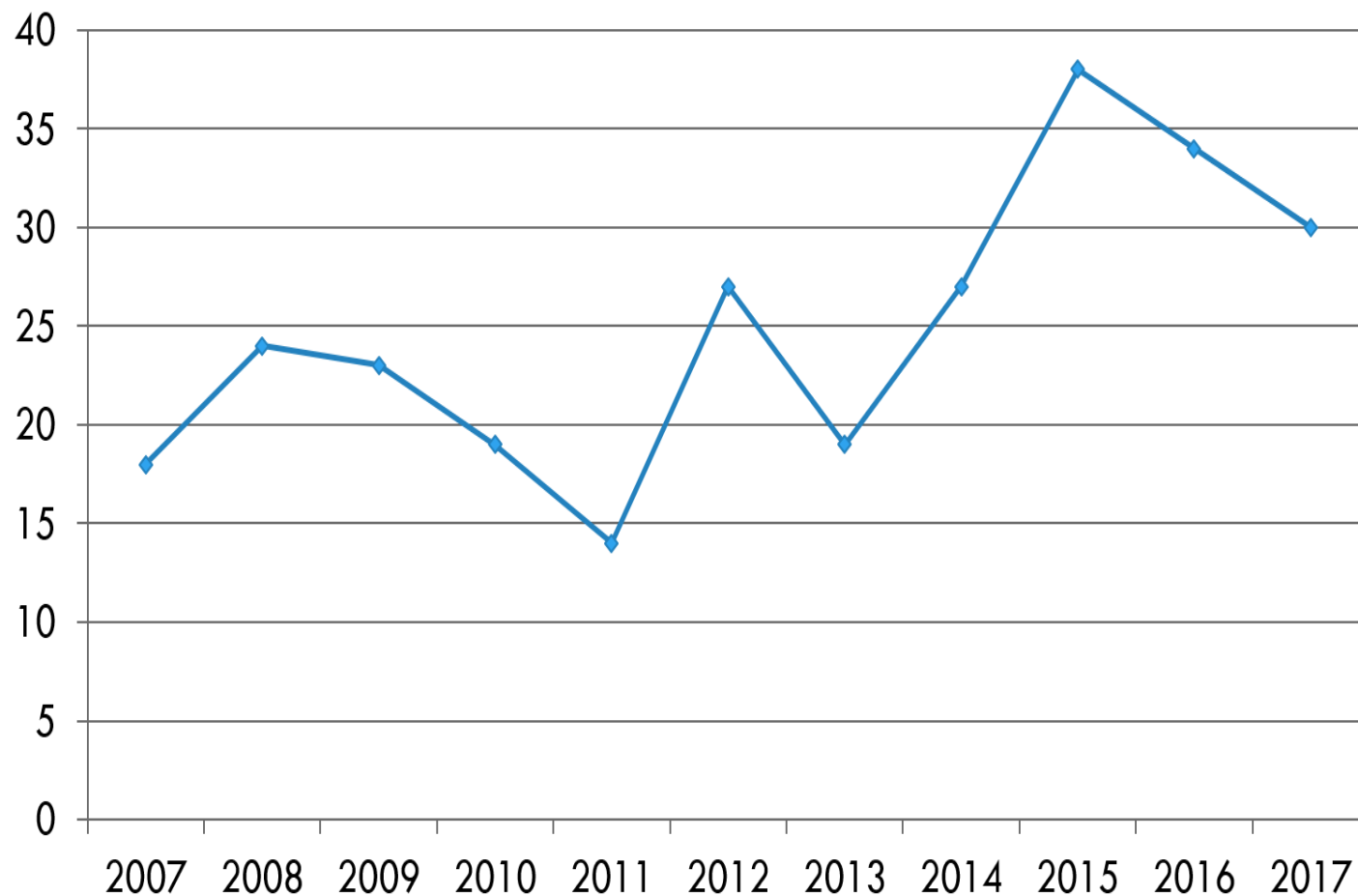
Abstract

Artificial intelligence (AI) is rapidly moving from an experimental phase to an implementation phase in many fields, including medicine. The combination of improved availability of large datasets, increasing computing power, and advances in learning algorithms has created major performance breakthroughs in the development of AI applications. In the last 5 years, AI techniques known as deep learning have delivered rapidly improving performance in image recognition, caption generation, and speech recognition. Radiology, in particular, is a prime candidate for early adoption of these techniques. It is anticipated that the implementation of AI in radiology over the next decade will significantly improve the quality, value, and depth of radiology's contribution to patient care and population health, and will revolutionize radiologists' workflows. The Canadian Association of Radiologists (CAR) is the national voice of radiology committed to promoting the highest standards in patient-centered imaging, lifelong learning, and research. The CAR has created an AI working group with the mandate to discuss and deliberate on practice, policy, and patient care issues related to the introduction and implementation of AI in imaging. This white paper provides recommendations for the CAR derived from deliberations between members of the AI working group. This white paper on AI in radiology will inform CAR members and policymakers on key terminology, educational needs of members, research and development, partnerships, potential clinical applications, implementation, structure and governance, role of radiologists, and potential impact of AI on radiology in Canada.

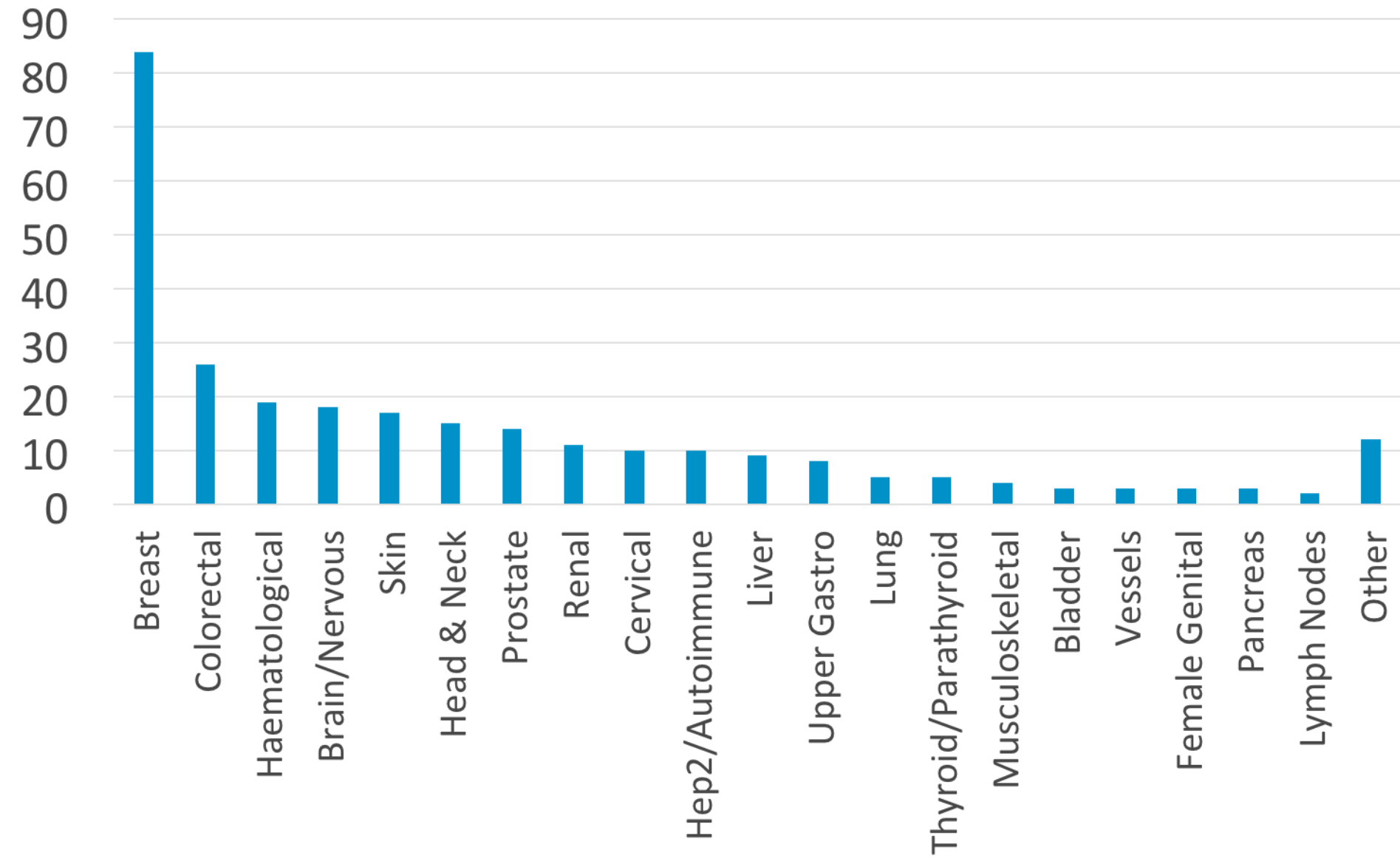
delivered rapidly improving performance in image recognition, caption generation, and speech recognition. Radiology, in particular, is a prime candidate for early adoption of these techniques. It is anticipated that the implementation of AI in radiology over the next decade will significantly improve the quality, value, and depth of radiology's contribution to patient care and population health, and will revolutionize

Digital pathology peer reviewed publications

Studies Published by Year



Tissue type



Automated ER & PR scoring

Simultaneous Automatic Scoring of Hormone Receptors in Tumour Areas in Whole Slide Images of Breast Cancer Tissue Slides

Nicholas Trahearn^a, Yee Wah Tsang^{b,c}, Ian Cree^c, David Snead^{b,c}, Nasir Rajpoot^a

^a Department of Computer Science, University of Warwick, United Kingdom

^b Department of Pathology & ^c Centre of Excellence for Digital Pathology, University Hospitals Coventry and Warwickshire, United Kingdom
Cytometry Part A 91A: 585-594, 2017.

Left Panel (ER Stain):

- File Name: H13-19850_A1ER_1.jp2
- Case ID: H13-19850
- Stain: ER
- Stain Type: Nuclear
- Resolution: 4.4 $\mu\text{m}/\text{pixel}$

Right Panel (H&E Stain):

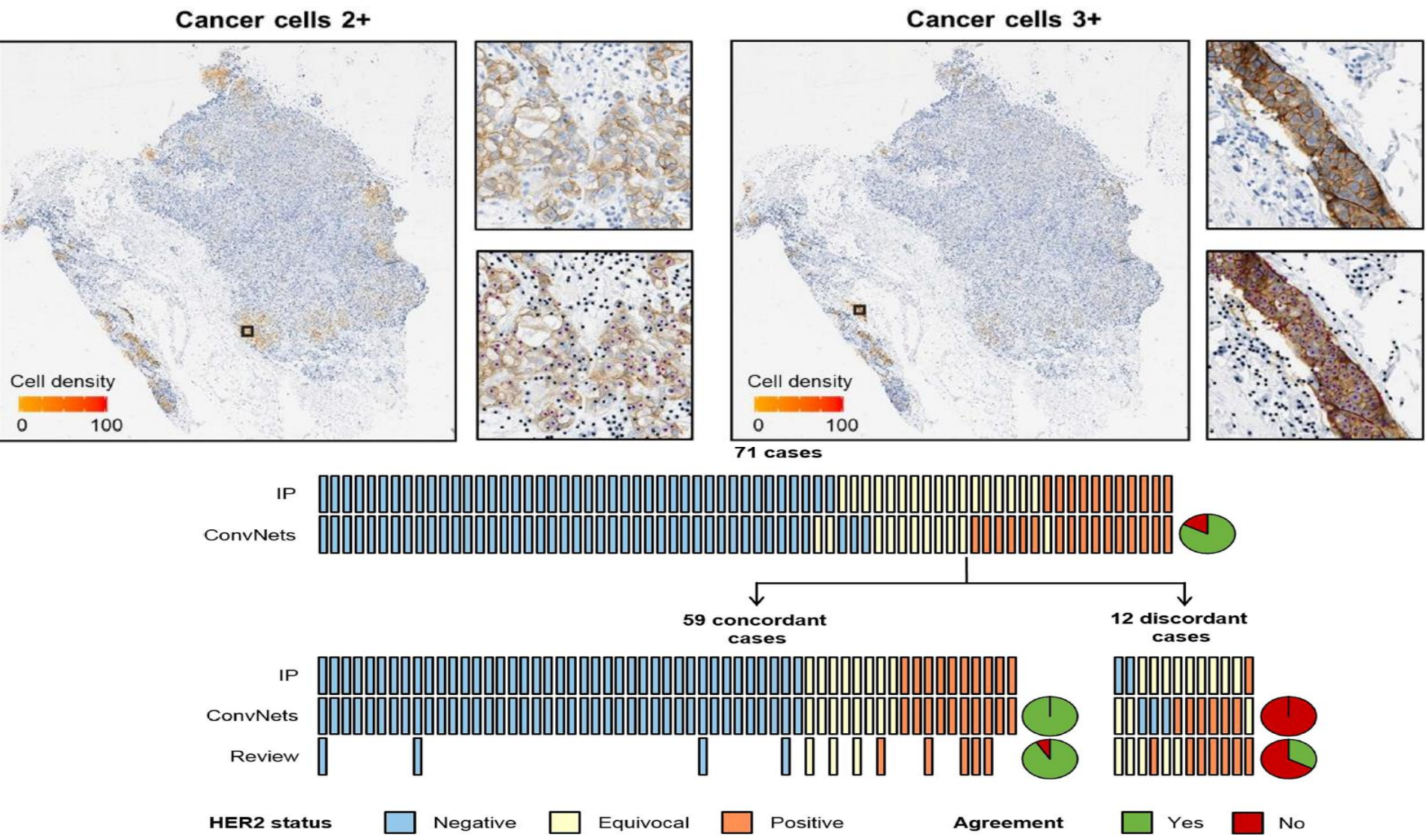
- File Name: H13-19850_A1LEV1_1.jp2
- Case ID: H13-19850
- Stain: H&E
- Stain Type: Nuclear/Cytoplasmic
- Resolution: 4.4 $\mu\text{m}/\text{pixel}$

Left Sidebar Controls:

- Buttons: Load Case, Select Slides, Register Slides, Reset, Refresh, Score Sections
- Slide List:
 - H13-19850_A1ER_1.jp2
 - H13-19850_A1LEV1_1.jp2
 - H13-19850_A1LEV2_1.jp2
 - H13-19850_A1LEV3_1.jp2
 - H13-19850_A1PR_1.jp2
 - H13-19850_A1PR_2.jp2
- Checkbox: ☒ Show Ruler

Relevance of deep learning to facilitate the diagnosis of HER2 status in breast cancer

Michel E. Vandenberghe¹, Marietta L. J. Scott¹, Paul W. Scorer¹, Magnus Söderberg², Denis Balcerzak¹ & Craig Barker¹

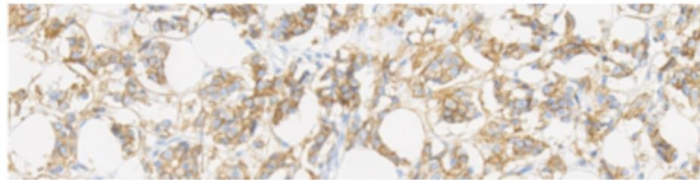


Automated Her2 Scoring



Her2 Scoring Contest

[Home](#) | [Background](#) | [Contest Registration](#) | [Contest Rules](#) | [Contact](#)



Welcome to the contest page of **HER2 scoring in histology images**. This challenge will be held in conjunction with [Nottingham Pathology 2016](#) (The Pathological Society of Great Britain & Ireland).



<http://www.warwick.ac.uk/TIAlab/Her2Contest>

Qaiser et al., Histopathology 72;227-238 2018

Her2 Scoring – Man vs Machine

Rank	Team Name	Score	Bonus	Score+Bonus
1	Team Indus	220	12.5	232.5
2	Pathologist 2	210	20.5	230.5
3	Visilab	212.5	15	227.5
4	MUCS (Ireland)	205	20.5	225.5
5	Pathologist 1	185	10	195
6	Pathologist 3	180	13	193

<http://www.warwick.ac.uk/TIAlab/Her2contest/>

Qaiser et al., Histopathology 72;227-238 2018

Digital image analysis outperforms manual biomarker assessment in breast cancer

Gustav Stålhammar^{1,2}, Nelson Fuentes Martinez^{1,3}, Michael Lippert⁴, Nicholas P Tobin⁵, Ida Mølholm^{4,6}, Lorand Kis⁷, Gustaf Rosin¹, Mattias Rantalainen⁸, Lars Pedersen⁴, Jonas Bergh^{1,5,9}, Michael Grunkin⁴ and Johan Hartman^{1,5,7}

¹Department of Oncology and Pathology, Karolinska Institutet, Stockholm, Sweden; ²St Erik Eye Hospital, Stockholm, Sweden; ³Södersjukhuset, Stockholm, Sweden; ⁴Visiopharm A/S, Hoersholm, Denmark; ⁵Cancer Center Karolinska, Stockholm, Sweden; ⁶Department of Applied Mathematics and Computer Science, Technical University of Denmark, Kongens Lyngby, Denmark; ⁷Department of Clinical Pathology, Karolinska University Hospital, Stockholm, Sweden; ⁸Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden and ⁹Department of Oncology, Karolinska University Hospital, Stockholm, Sweden

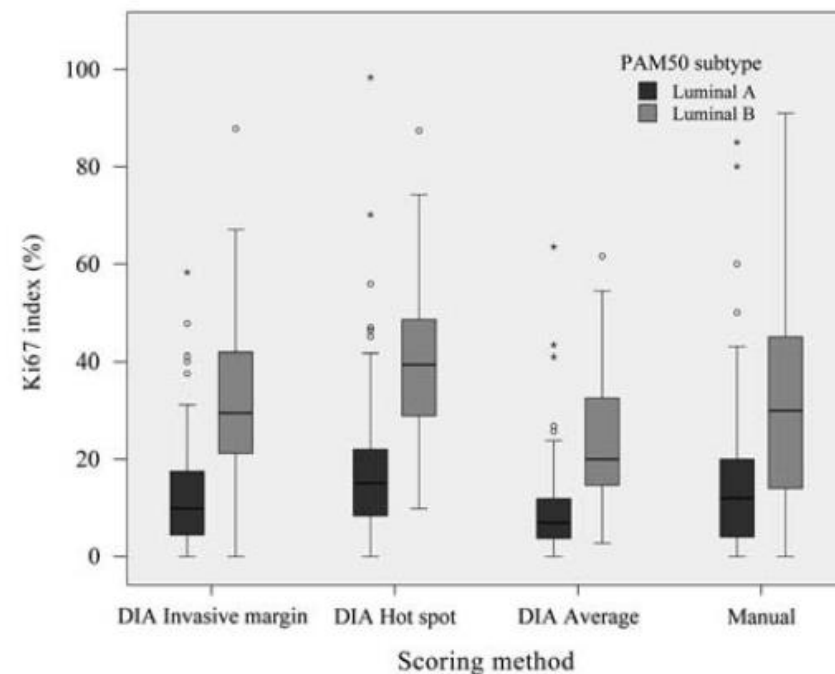
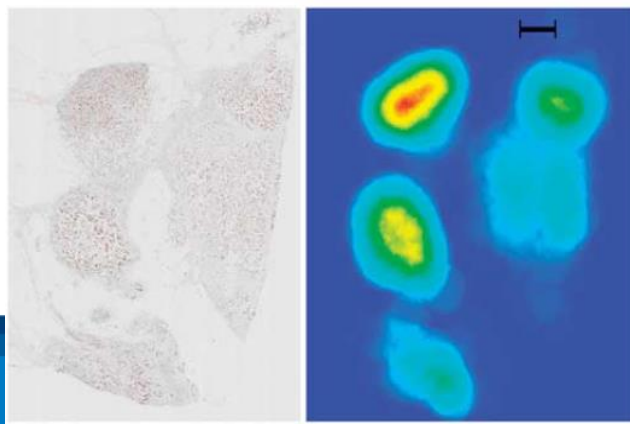
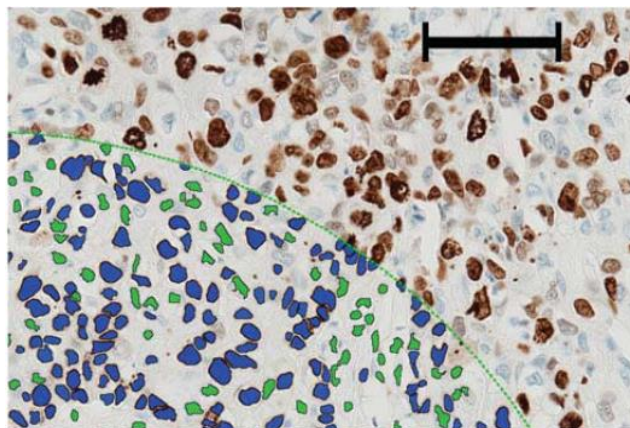


Figure 2 Clustered box plot for Ki67 index (%) by each scoring method in PAM50 Luminal A and B subtypes. Error bars represent 95% confidence interval. Circles represent outliers and asterisks represent extremes. DIA, digital image analysis ($n=214$).

Digital image analysis outperforms manual biomarker assessment in breast cancer

Gustav Stålhammar^{1,2}, Nelson Fuentes Martinez^{1,3}, Michael Lippert⁴, Nicholas P Tobin⁵, Ida Mølholm^{4,6}, Lorand Kis⁷, Gustaf Rosin¹, Mattias Rantalainen⁸, Lars Pedersen⁴, Jonas Bergh^{1,5,9}, Michael Grunkin⁴ and Johan Hartman^{1,5,7}

¹Department of Oncology and Pathology, Karolinska Institutet, Stockholm, Sweden; ²St Erik Eye Hospital, Stockholm, Sweden; ³Södersjukhuset, Stockholm, Sweden; ⁴Visiopharm A/S, Hoersholm, Denmark; ⁵Cancer Center Karolinska, Stockholm, Sweden; ⁶Department of Applied Mathematics and Computer Science, Technical University of Denmark, Kongens Lyngby, Denmark; ⁷Department of Clinical Pathology, Karolinska University Hospital, Stockholm, Sweden; ⁸Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden and ⁹Department of Oncology, Karolinska University Hospital, Stockholm, Sweden

Ki67 scoring method	Sensitivity for PAM50 Luminal B vs A	Specificity for PAM50 Luminal B vs A	Proportion misclassified
<i>DIA invasive margin</i>			
Cutoff ≥ 20%	84%	78%	20%
Cutoff ≥ 20.2% *	82%	79%	20%
<i>DIA hot spot</i>			
Cutoff ≥ 20%	90%	65%	24%
Cutoff ≥ 25.2% *	86%	77%	19%
<i>DIA average</i>			
Cutoff ≥ 20%	60%	90%	31%
Cutoff ≥ 15.5% *	80%	83%	19%
<i>Manual</i>			
Cutoff ≥ 20%	75%	70%	30%
Cutoff ≥ 22.5% *	74%	75%	29%

Manual scores retrieved from patient records.

* = Adjusted cutoffs.



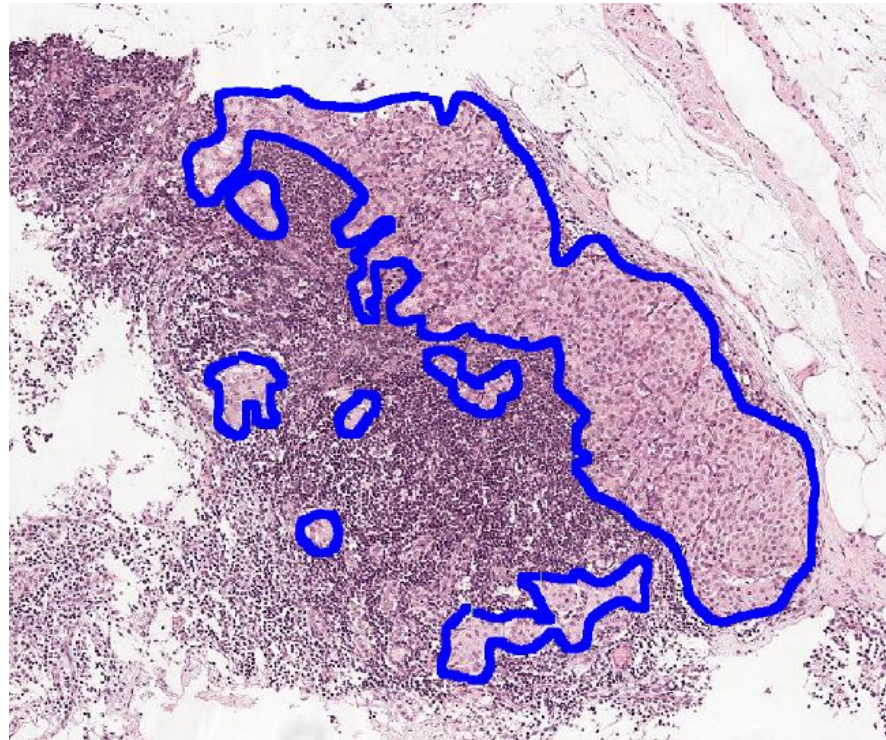
ISBI Challenge on cancer metastases detection in lymph node

Babak Ehteshami Bejnordi



Camelyon16 dataset

- Most of the tumor slides were exhaustively annotated
- The average time for annotating each slide was 1 hour

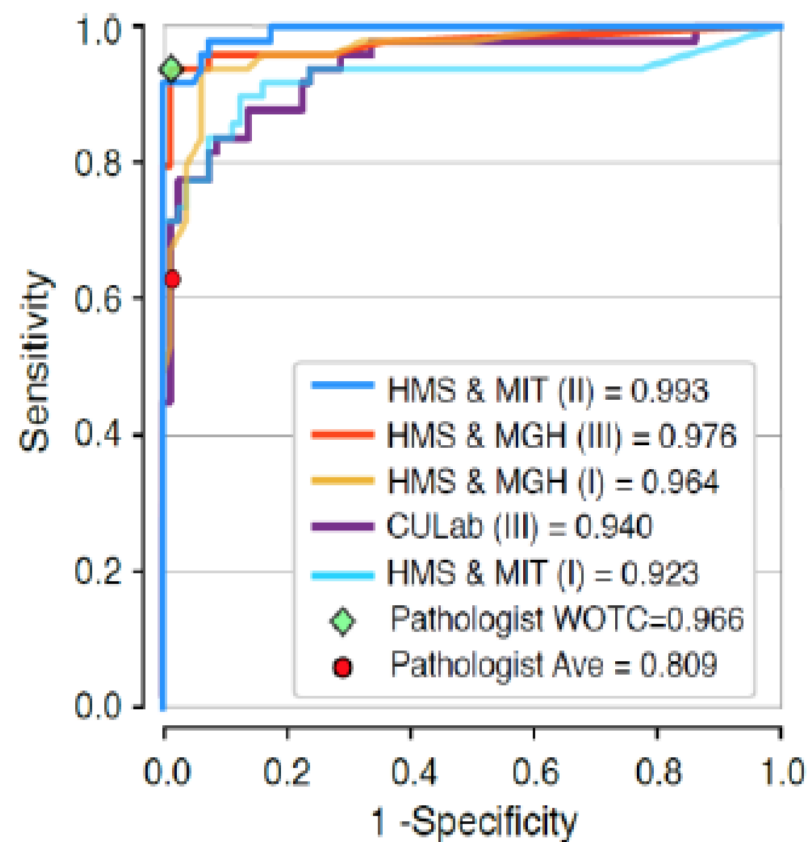
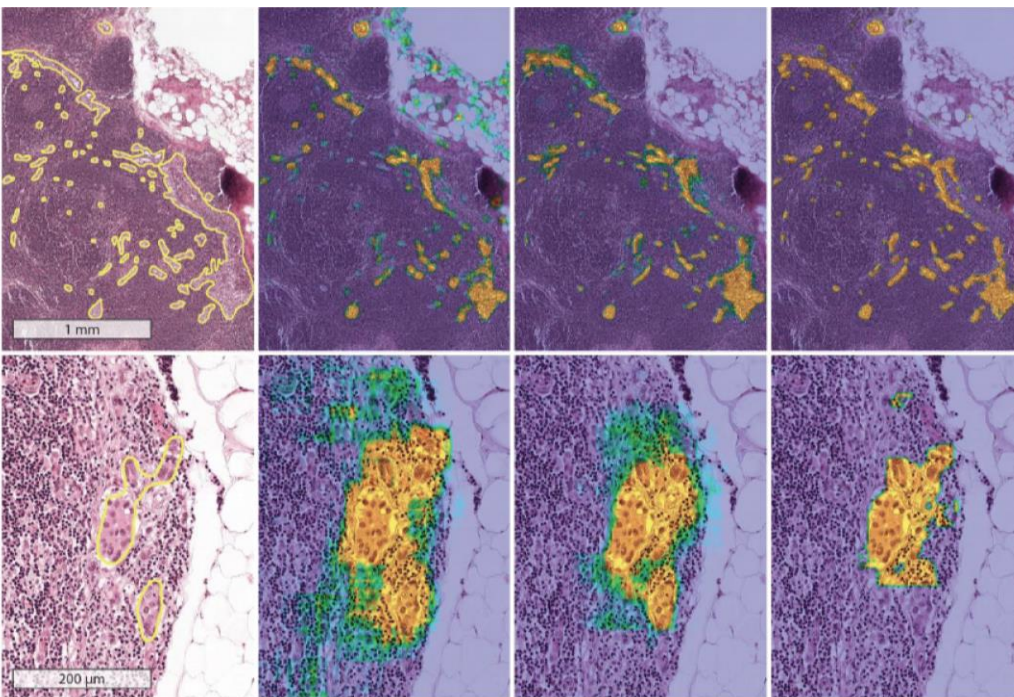


JAMA | Original Investigation

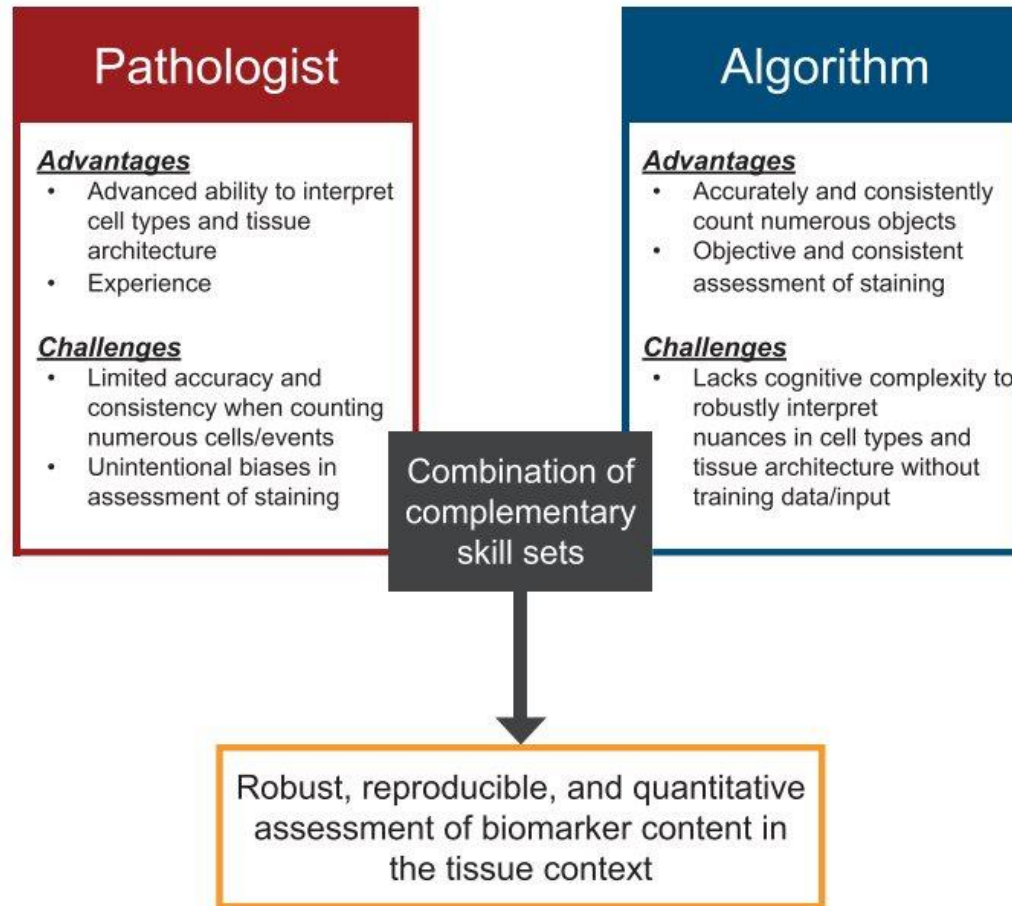
Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer

Babak Ehteshami Bejnordi, MS; Mitko Veta, PhD; Paul Johannes van Diest, MD, PhD; Bram van Ginneken, PhD; Nico Karssemeijer, PhD; Geert Litjens, PhD; Jeroen A. W. M. van der Laak, PhD; and the CAMELYON16 Consortium

JAMA. 2017;318(22):2199-2210.



Pathologist + Algorithm

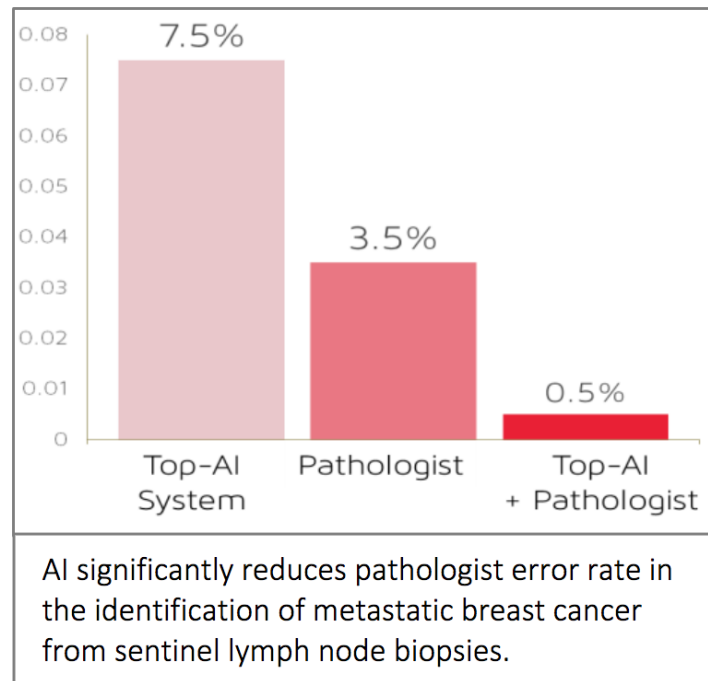


Aeffner *et al.*, Arch Path Lab Med (Sep 2017)

The White House Takes Note

ARTIFICIAL INTELLIGENCE FOR COMPUTATIONAL PATHOLOGY

Image interpretation plays a central role in the pathologic diagnosis of cancer. Since the late 19th century, the primary tool used by pathologists to make definitive cancer diagnoses is the microscope. Pathologists diagnose cancer by manually examining stained sections of cancer tissues to determine the cancer subtype. Pathologic diagnosis using conventional methods is labor-



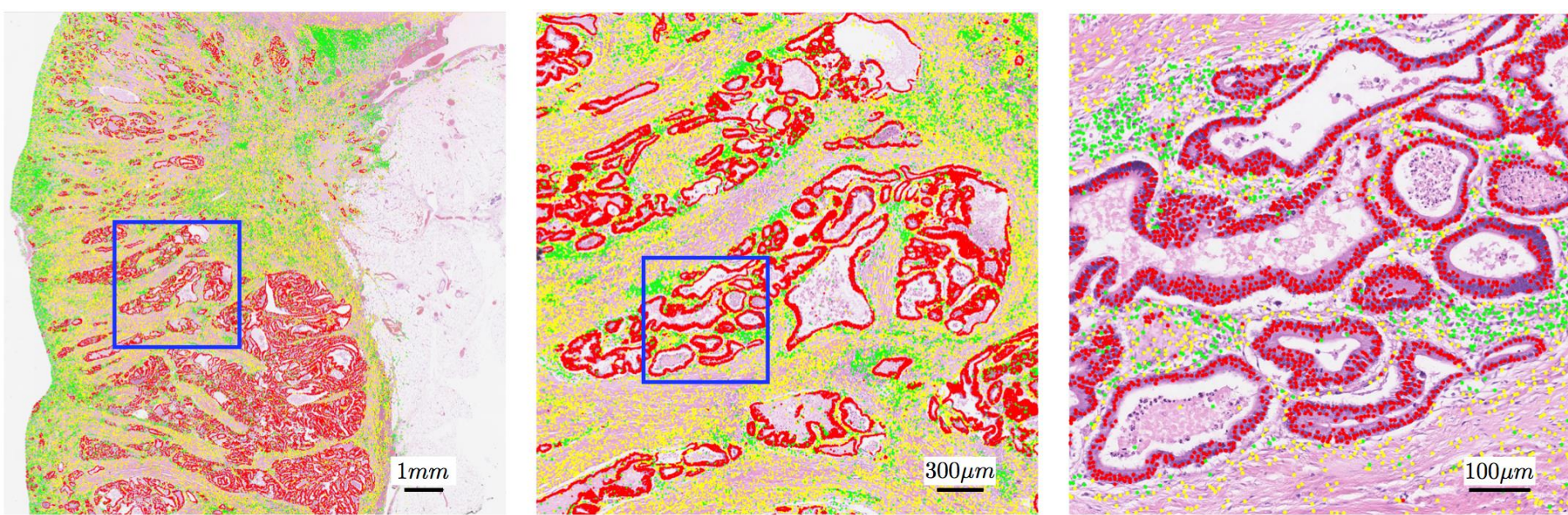
THE NATIONAL
ARTIFICIAL INTELLIGENCE
RESEARCH AND DEVELOPMENT
STRATEGIC PLAN

October 2016



Deep Learning - Profiling Tumour Microenvironment

- Cell recognition in large sets of whole-slide images
- Analytics for profiling the tumor micro-environment



Sirinukunwattana *et al.*, *IEEE Trans Medical Imaging* special issue on *Deep Learning in Medical Imaging* (May 2016)

OPEN

Novel digital signatures of tissue phenotypes for predicting distant metastasis in colorectal cancer

Received: 23 January 2018

Accepted: 7 August 2018

Korsuk Sirinukunwattana¹, David Snead², David Epstein³, Zia Aftab⁴, Imaad Mujeeb⁴, Yee Wah Tsang², Ian Cree⁵ & Nasir Rajpoot^{6,2,7}

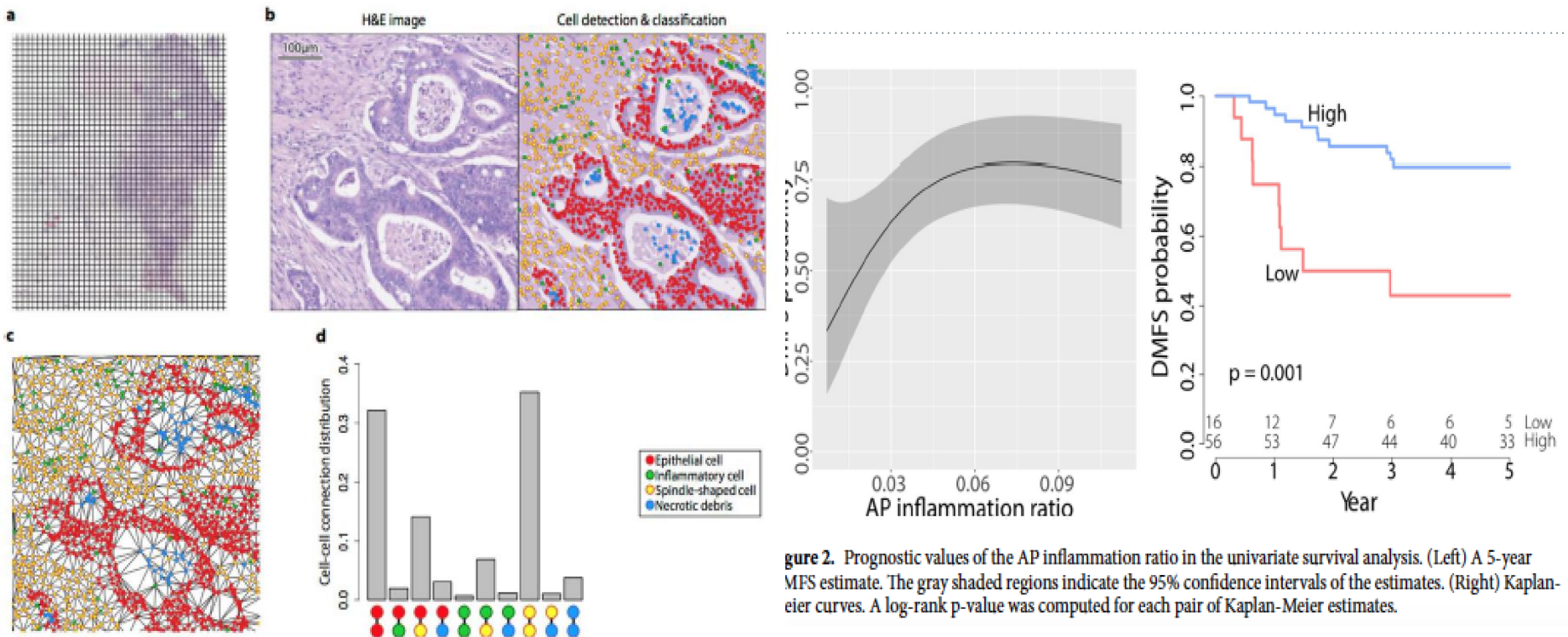


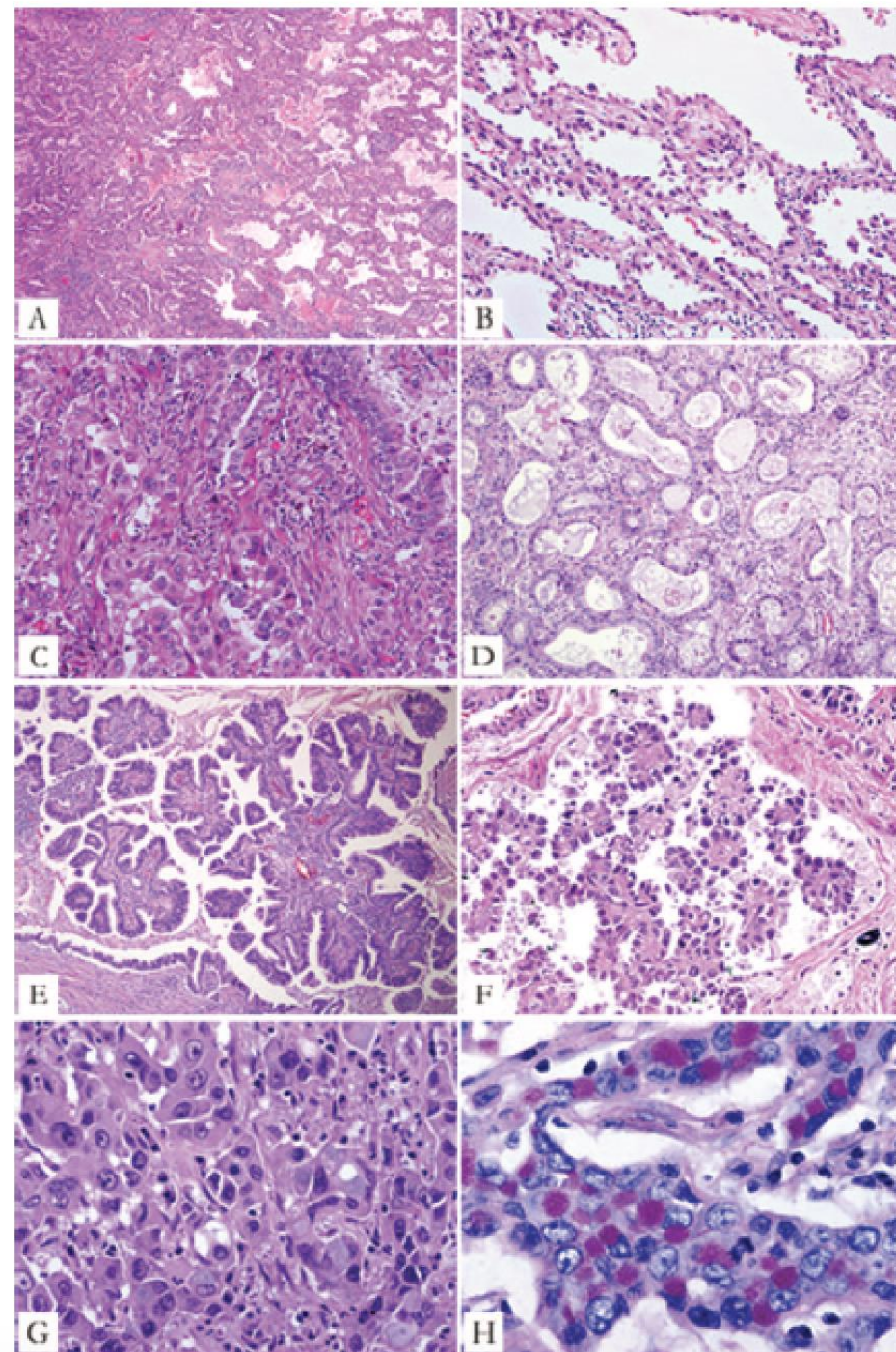
Figure 2. Prognostic values of the AP inflammation ratio in the univariate survival analysis. (Left) A 5-year MFS estimate. The gray shaded regions indicate the 95% confidence intervals of the estimates. (Right) Kaplan-Meier curves. A log-rank p-value was computed for each pair of Kaplan-Meier estimates.

Journal of Thoracic Oncology • Volume 6, Number 2, February 2011|

International Association for the Study of Lung Cancer/American Thoracic Society/European Respiratory Society International Multidisciplinary Classification of Lung Adenocarcinoma

William D. Travis, MD, Elisabeth Brambilla, MD, Masayuki Noguchi, MD, Andrew G. Nicholson, MD, Kim R. Geisinger, MD, Yasushi Yatabe, MD, David G. Beer, PhD, Charles A. Powell, MD, Gregory J. Riely, MD, Paul E. Van Schil, MD, Kavita Garg, MD, John H. M. Austin, MD, Hisao Asamura, MD, Valerie W. Rusch, MD, Fred R. Hirsch, MD, Giorgio Scagliotti, MD, Tetsuya Mitsudomi, MD, Rudolf M. Huber, MD, Yuichi Ishikawa, MD, James Jett, MD, Montserrat Sanchez-Cespedes, PhD, Jean-Paul Sculier, MD, Takashi Takahashi, MD, Masahiro Tsuboi, MD, Johan Vansteenkiste, MD, Ignacio Wistuba, MD, Pan-Chyr Yang, MD, Denise Aberle, MD, Christian Brambilla, MD, Douglas Flieder, MD, Wilbur Franklin, MD, Adi Gazdar, MD, Michael Gould, MD, MS, Philip Hasleton, MD, Douglas Henderson, MD, Bruce Johnson, MD, David Johnson, MD, Keith Kerr, MD, Keiko Kuriyama, MD, Jin Soo Lee, MD, Vincent A. Miller, MD, Iver Petersen, MD, PhD, Victor Roggli, MD, Rafael Rosell, MD, Nagahiro Saijo, MD, Erik Thunnissen, MD, Ming Tsao, MD, and David Yankelwitz, MD

- Adenocarcinoma in-situ
- Minimally invasive adenocarcinoma
- Lepidic adenocarcinoma
- Papillary adenocarcinoma
- Acinar adenocarcinoma
- Micropapillary adenocarcinoma
- Solid adenocarcinoma



Comprehensive Computational Pathological Image Analysis Predicts Lung Cancer Prognosis

Xin Luo, MD,^a Xiao Zang, BS,^b Lin Yang, MD,^{b,c} Junzhou Huang, PhD,^d
Faming Liang, PhD,^e Jaime Rodriguez-Canales, MD,^f Ignacio I. Wistuba, MD,^f
Adi Gazdar, MD,^{g,h} Yang Xie, MD, PhD,^{a,b} Guanghua Xiao, PhD^{a,b,*}

^aDepartment of Bioinformatics, University of Texas Southwestern Medical Center at Dallas, Texas

^bQuantitative Biomedical Research Center, Department of Clinical Sciences, University of Texas Southwestern Medical Center at Dallas, Texas

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^dDepartment of Computer Sciences and Engineering, University of Texas at Arlington, Arlington, Texas

^eDepartment of Biostatistics, University of Florida, Gainesville, Florida

^fDepartment of Translational Molecular Pathology, University of Texas M. D. Anderson Cancer Center, Houston, Texas

^gDepartment of Pathology, University of Texas Southwestern Medical Center at Dallas, Dallas, Texas

^hHamon Center for Therapeutic Oncology, University of Texas Southwestern Medical Center at Dallas, Dallas, Texas

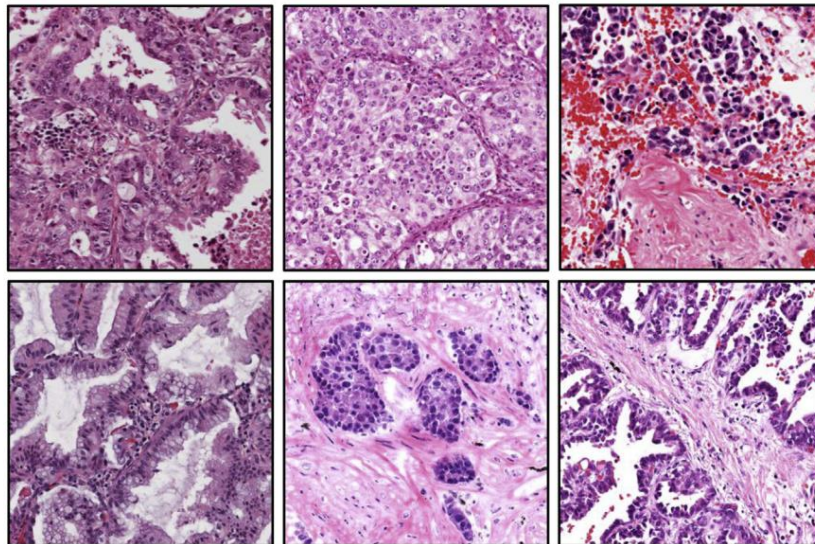
Received 9 June 2016; revised 28 September 2016; accepted 24 October 2016
Available online - 4 November 2016

A

ADC

High Risk

Low Risk



rch 2017

Computational Pathological Image 505

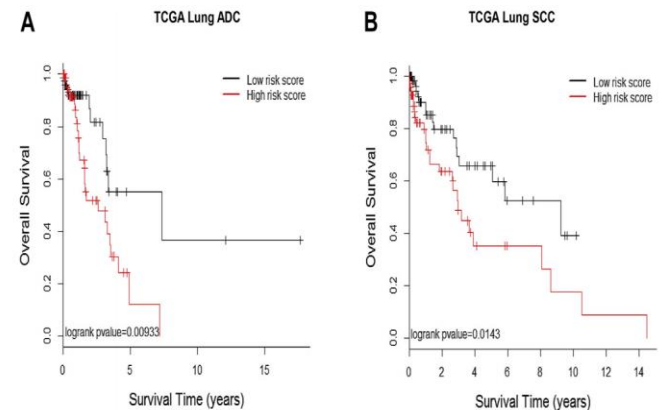


Figure 2. Associations between survival outcomes and morphological feature-defined risk groups in The Cancer Genome Atlas (TCGA) cohorts of patients with adenocarcinoma (ADC) and squamous cell carcinoma (SCC). Kaplan-Meier survival curves for patients in the high-risk group (red) and low-risk group classified by morphological feature-based prediction models for both ADC ($p = 0.009$) (A) and SCC ($p = 0.0143$) (B). The features and prediction model were derived from the training data, and survival analysis was performed in the testing data set.

Tumour Cell Morphometrics Predict Survival in Lung Adenocarcinoma

Najah Alsubaie^{1,2}, David Sneed³, Nasir Rajpoot^{1,4,5}
¹Department of Computer Science, University of Warwick, UK
²Department of Computer Science, Princess Nourah University, KSA
³Department of Pathology, University Hospitals Coventry and Warwickshire, UK
⁴The Alan Turing Institute, UK



Background

Tumour cell morphometrics are one of the most significant indicators of cancer aggressiveness. Pathologists assessment is limited to some morphological features due to their biological meaning and usefulness in most types of cancer. Besides the subjectivity of the assessment, it also requires time and effort. In this study, we characterise the heterogeneity of lung adenocarcinoma (LUAD) using morphometric features of tumour cells automatically extracted from the whole slide images (WSIs).

Dataset and Methods

We build the TCM (Tumour Cell Morphometric) system using a dataset of 78 LUAD patient collected from 2011 to 2014. The system aims to quantify standard nuclear morphometric features along with the topological, textural and global heat map statistics. We extracted malignant nuclei by combining nuclei detection and segmentation algorithms. Features are calculated for tumour cells on 40x magnification. We used 75% of the data to perform features selection and find the Cox model. The other 25% of the data is used to test the model.

Results

We find that nuclear graph and nuclear texture features are highly correlated with patient survival. Using the selected features, the Cox model is able to stratify patients into better and worse prognosis in both training and testing sets, see Figure 1. Figure 2 shows clustered heatmap for the average number of connected nuclei per nuclear cluster in low and high survival cases. The Maximum cluster is higher in the low survival case compared to the high survival case.

Conclusion

In this work we quantify heterogeneity of nuclear features in WSI of LUAD. We find that statistics extracted from the heatmap is highly correlated with patient overall survival.

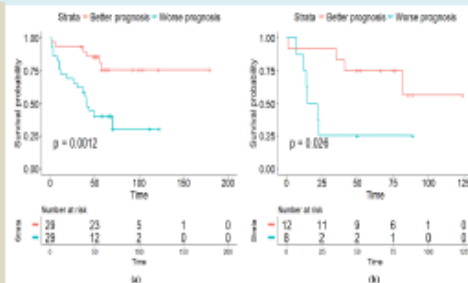


Figure 1: A Kaplan-Meier survival plots for the model prediction. Plots a and b show LUAD survival estimation on the training and testing sets, respectively.

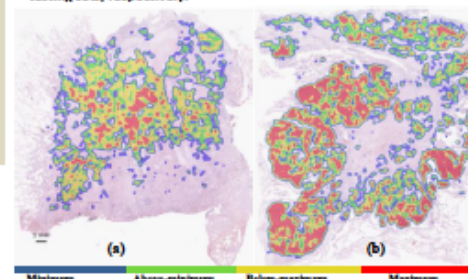


Figure 2: Heat map of average number of connected nuclei per nuclear cluster for higher survival case (left) compared to the lower survival case (right).

Automatic Quantification of Lung Adenocarcinoma Growth Patterns Predicts Five-Year Survival

Najah Alsubaie^{1,2}, David Sneed³, Syed Ali Khurram⁴, Nasir Rajpoot^{1,4,5}
¹Department of Computer Science, University of Warwick, UK
²Department of Computer Science, Princess Nourah University, KSA
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Background

Identifying lung adenocarcinoma (LUAD) growth patterns (GP) is critical for diagnosis and treatment of lung cancer patients. There are five main growth patterns: Acinar, lepidic, papillary, micropapillary and solid. The new LUAD classification system is based on the predominant growth pattern when measured semi-quantitatively in 5% increments. Clinical studies have shown show that some of these patterns might be correlated with prognosis and could predict patient response to therapy. LUAD GPs can have variable appearance, size and location with overlapping features, where it might be difficult to avoid inter-observer variability.

Dataset and Methods

We automatically locate and classify GPs of LUAD in whole slide images (WSI). The percentages of each pattern in relation to the tissue sample size is combined to build a features vector per case. Five-year survival is treated as a binary variable, i.e. patients with greater than five-year survival have an outcome of one and zero otherwise. We split our dataset of 78 LUAD patients into 60% for training and 40% for testing. We fit logistic regression model using training set and test the model on the testing set.

Results

The model has an accuracy of 0.826 on the training set and an area under curve of 0.65 on the testing set.

The logistic model shows that percentages of lepidic and micropapillary are significant predictors ($p < 0.05$). The model is able to stratify patients in our dataset into long and short term survival based on percentages of GPs ($p = 0.009$).

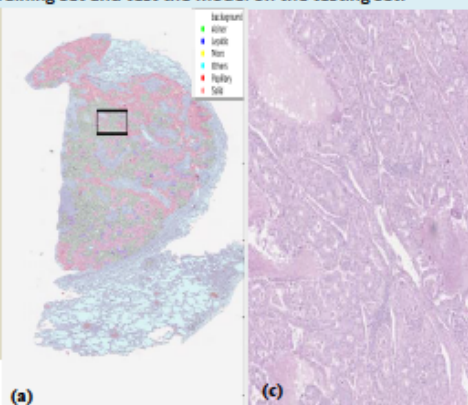


Figure 1: Whole slide image classification of GP for automatically identifying of pattern percentages.

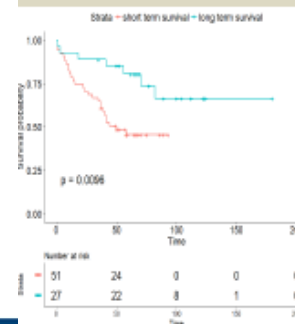


Figure 2: A Kaplan-Meier survival plot using the model prediction is able to stratify patients into short and long term survival using automatic quantification of GPs percentages.

Conclusion

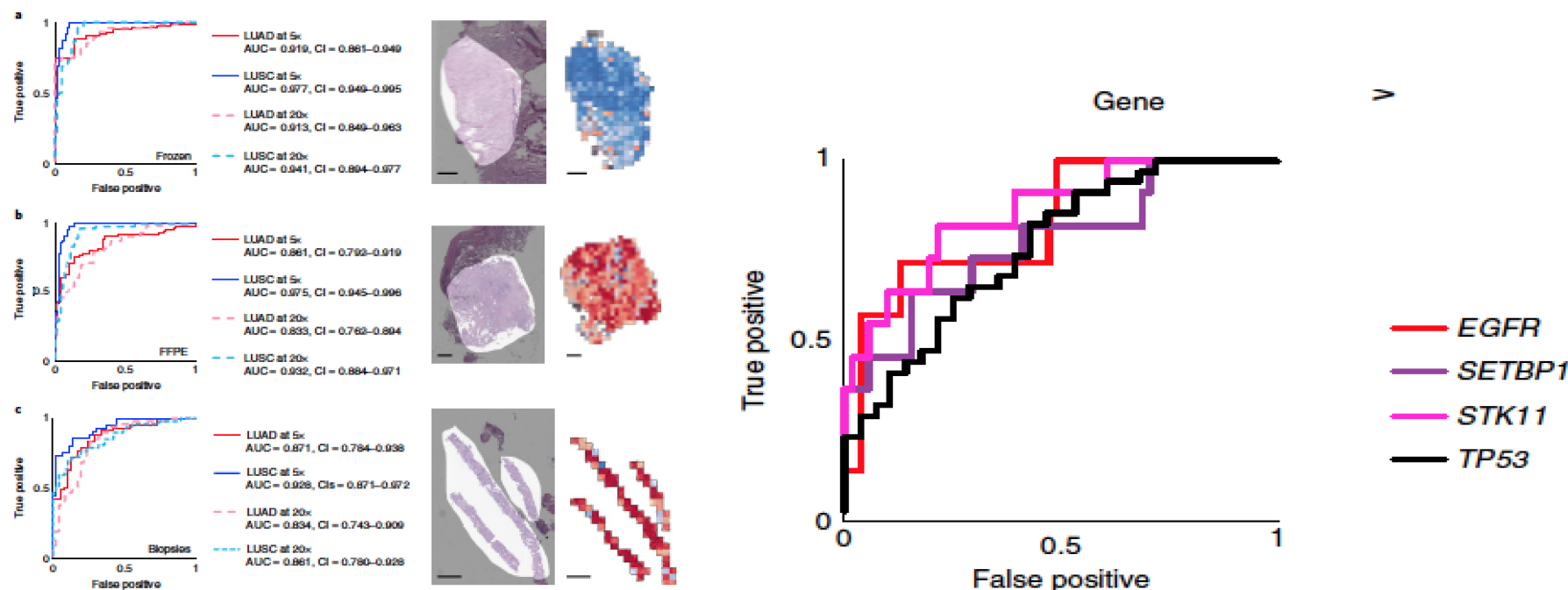
In this work, we automatically quantify LUAD GPs on WSIs. Percentages of GPs are combined to build a feature vector per case. We train on GPs percentages and find that model prediction is strongly correlated with patient survival.



Classification and mutation prediction from non-small cell lung cancer histopathology images using deep learning

Nicolas Coudray^{1,2,9}, Paolo Santiago Ocampo^{3,9}, Theodore Sakellaropoulos⁴, Navneet Narula³, Matija Snuderl³, David Fenyo^{5,6}, Andre L. Moreira^{3,7}, Narges Razavian^{1,8*} and Aristotelis Tsirigos^{1,3*}

Visual inspection of histopathology slides is one of the main methods used by pathologists to assess the stage, type and subtype of lung tumors. Adenocarcinoma (LUAD) and squamous cell carcinoma (LUSC) are the most prevalent subtypes of lung cancer, and their distinction requires visual inspection by an experienced pathologist. In this study, we trained a deep convolutional neural network (inception v3) on whole-slide images obtained from The Cancer Genome Atlas to accurately and automatically classify them into LUAD, LUSC or normal lung tissue. The performance of our method is comparable to that of pathologists, with an average area under the curve (AUC) of 0.97. Our model was validated on independent datasets of frozen tissues, formalin-fixed paraffin-embedded tissues and biopsies. Furthermore, we trained the network to predict the ten most commonly mutated genes in LUAD. We found that six of them—STK11, EGFR, FAT1, SETBP1, KRAS and TP53—can be predicted from pathology images, with AUCs from 0.733 to 0.856 as measured on a held-out population. These findings suggest that deep-learning models can assist pathologists in the detection of cancer subtype or gene mutations. Our approach can be applied to any cancer type, and the code is available at <https://github.com/ncoudray/DeepPATH>.



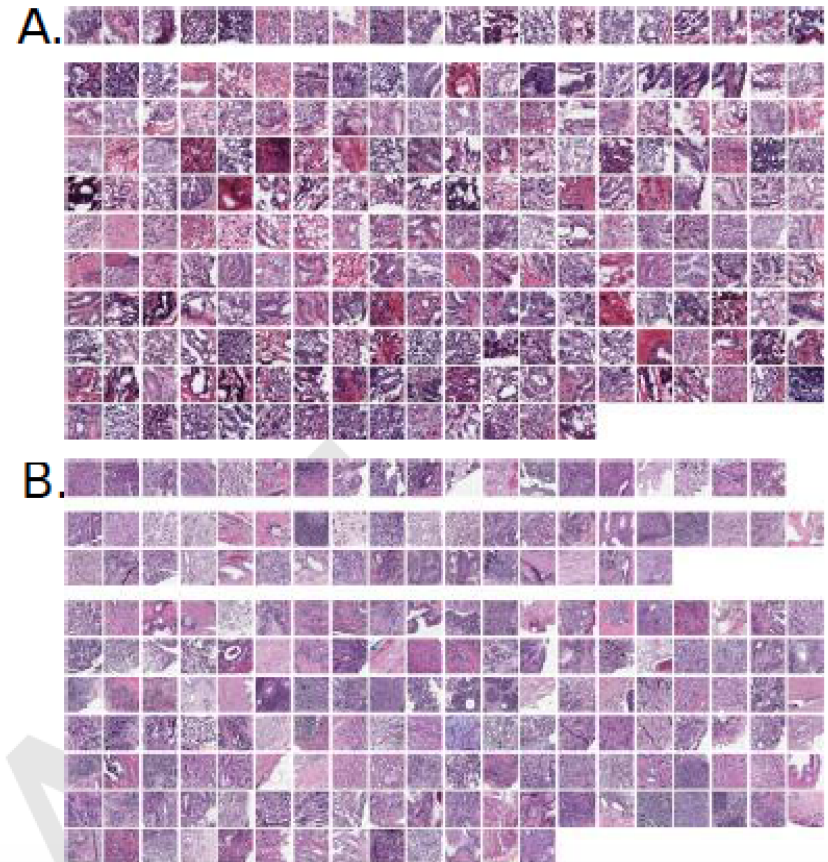
H&E-stained Whole Slide Image Deep Learning Predicts SPOP Mutation State in Prostate Cancer

Andrew J. Schaumberg^{a,b,*}, Mark A. Rubin^{c,d,e,*}, and Thomas J. Fuchs^{f,g,*}

^aMemorial Sloan Kettering Cancer Center and the Tri-Institutional Training Program in Computational Biology and Medicine; ^bWeill Cornell Graduate School of Medical Sciences; ^cCaryl and Israel Englander Institute for Precision Medicine, New York Presbyterian Hospital–Weill Cornell Medicine; ^dSandra and Edward Meyer Cancer Center at Weill Cornell Medicine; ^eDepartment of Pathology and Laboratory Medicine, Weill Cornell Medicine; ^fDepartment of Medical Physics, Memorial Sloan Kettering Cancer Center; ^gDepartment of Pathology, Memorial Sloan Kettering Cancer Center

This manuscript was compiled on October 1, 2018

A quantitative model to genetically interpret the histology in whole microscopy slide images is desirable to guide downstream immuno-histochemistry, genomics, and precision medicine. We constructed a statistical model that predicts whether or not SPOP is mutated in prostate cancer, given only the digital whole slide after standard hematoxylin and eosin [H&E] staining. Using a TCGA cohort of 177 prostate cancer patients where 20 had mutant SPOP, we trained multiple ensembles of residual networks, accurately distinguishing SPOP mutant from SPOP non-mutant patients (test AUROC=0.74, $p=0.0007$ Fisher's Exact Test). We further validated our full metaensemble classifier on an independent test cohort from MSK-IMPACT of 152 patients where 19 had mutant SPOP. Mutants and non-mutants were accurately distinguished despite TCGA slides being frozen sections and MSK-IMPACT slides being formalin-fixed paraffin-embedded sections (AUROC=0.86, $p=0.0038$). Moreover, we scanned an additional 36 MSK-IMPACT patients having mutant SPOP, trained on this expanded MSK-IMPACT cohort (test AUROC=0.75, $p=0.0002$), tested on the TCGA cohort (AUROC=0.64, $p=0.0306$), and again accurately distinguished mutants from non-mutants using the same pipeline. Importantly, our method demonstrates tractable deep learning in this “small data” setting of 20-55 positive examples and quantifies each prediction's uncertainty with confidence intervals. To our knowledge, this is the first statistical model to predict a genetic muta-



ARTICLE OPEN

Correlating nuclear morphometric patterns with estrogen receptor status in breast cancer pathologic specimens

Rishi R. Rawat¹, Daniel Ruderman¹, Paul Macklin², David L. Rimm³ and David B. Agus¹

In this pilot study, we introduce a machine learning framework to identify relationships between cancer tissue morphology and hormone receptor pathway activation in breast cancer pathology hematoxylin and eosin (H&E)-stained samples. As a proof-of-concept, we focus on predicting clinical estrogen receptor (ER) status—defined as greater than one percent of cells positive for estrogen receptor by immunohistochemistry staining—from spatial arrangement of nuclear features. Our learning pipeline segments nuclei from H&E images, extracts their position, shape and orientation descriptors, and then passes them to a deep neural network to predict ER status. After training on 57 tissue cores of invasive ductal carcinoma (IDC), our pipeline predicted ER status in an independent test set of patient samples (AUC ROC = 0.72, 95%CI = 0.55–0.89, $n = 56$). This proof of concept shows that machine-derived descriptors of morphologic histology patterns can be correlated to signaling pathway status. Unlike other deep learning approaches to pathology, our system uses deep neural networks to learn spatial relationships between pre-defined biological features, which improves the interpretability of the system and sheds light on the features the neural network uses to predict ER status. Future studies will correlate morphometry to quantitative measures of estrogen receptor status and, ultimately response to hormonal therapy.

npj Breast Cancer (2018)4:32 ; doi:10.1038/s41523-018-0084-4

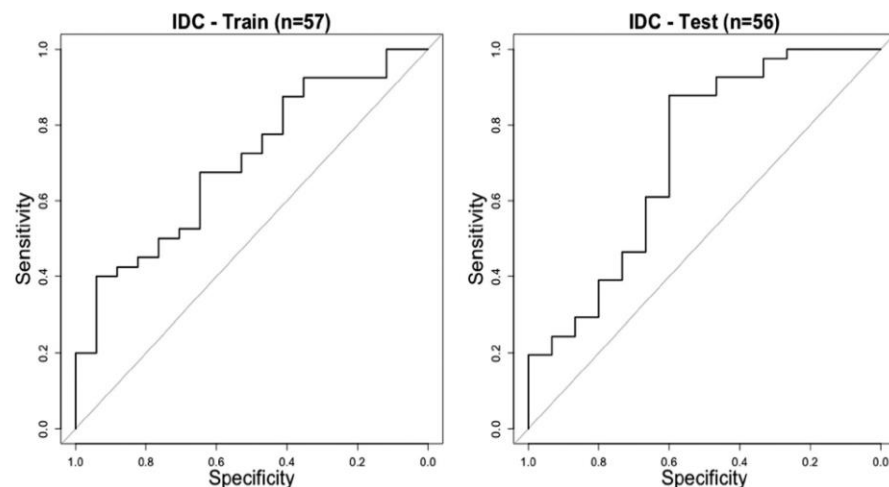
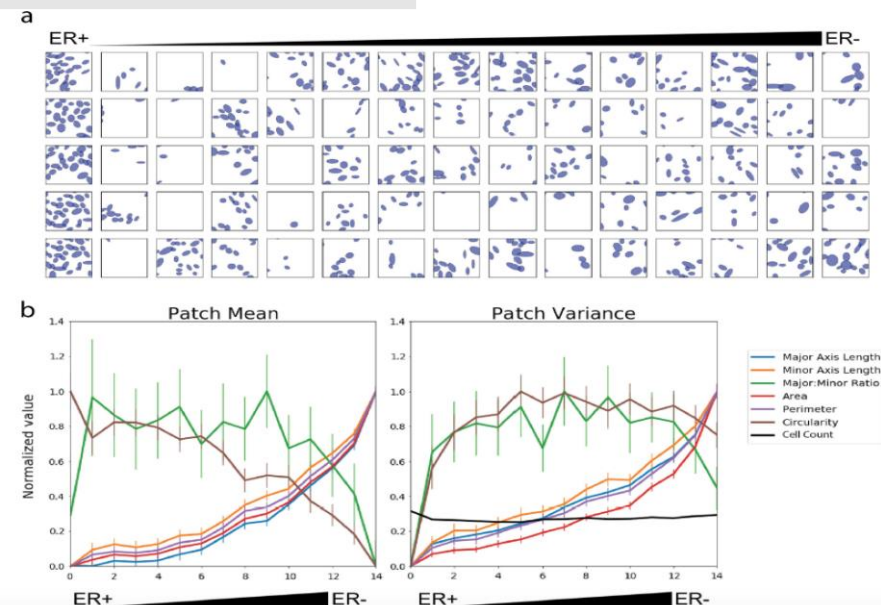


Fig. 1 Receiver operating characteristic (ROC) curves for the training dataset (AUC = 0.70, 95%CI = 0.56–0.85) (left), and test dataset (AUC = 0.72, 95%CI = 0.55–0.89) (right)





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£15m new Artificial Intelligence centre for Scotland to innovate and transform healthcare

Tuesday 6 November 2018

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WORKING WITH BUSINESS NEWS /// TUESDAY 6 NOVEMBER 2018

Leeds receives £10m investment for AI and digital pathology

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Press release

Artificial Intelligence to help save lives at five new technology centres

The UK's Artificial Intelligence revolution gets new backing, as the Business Secretary announces five new centres of excellence for digital pathology and imaging, including radiology, using AI medical advances.

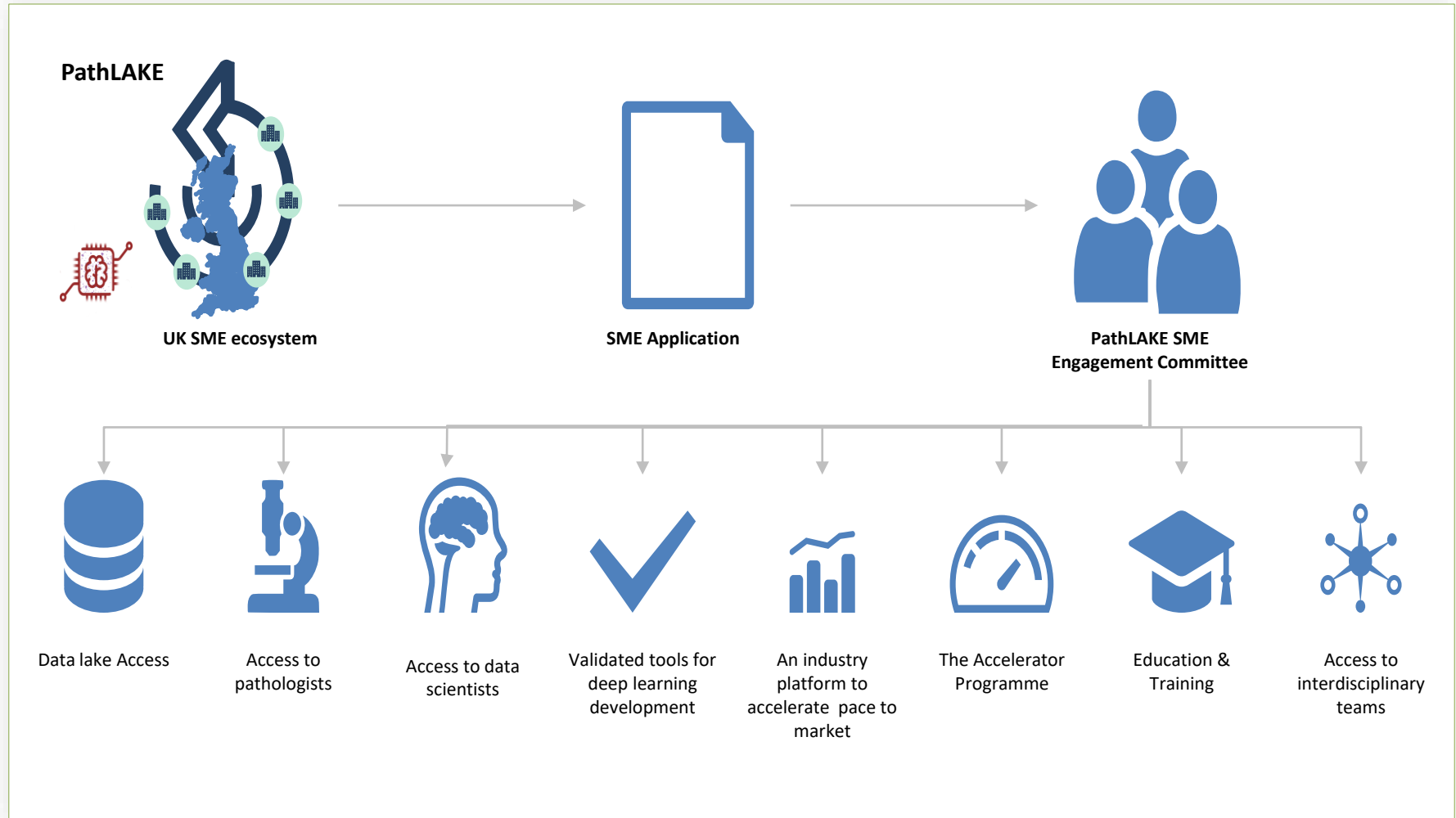
Published 6 November 2018

From: [Department for Business, Energy & Industrial Strategy](#), [UK Research and Innovation](#), [Innovate UK](#), [The Rt Hon Greg Clark MP](#), and [The Rt Hon Matt Hancock MP](#)



- Patients are set to benefit from radical advances in medical technology using artificial intelligence to diagnose diseases at an earlier stage
- The centres will use AI, an area the government is backing in its modern Industrial Strategy, to find new ways to speed up diagnosis of diseases to improve outcomes for patients
- Based in Leeds, Oxford, Coventry, Glasgow and London – but each with partners across many parts of the UK – the centres will develop more intelligent analysis of medical imaging, leading to better clinical decisions for patients, and freeing more staff time for direct patient care in the NHS

SME Engagement: Ensuring Access



CM-Path and BIVDA Artificial Intelligence/Image Analysis in Histopathology Workshop

This workshop will focus on the use and potential use of image analysis and artificial intelligence tools in clinical histopathology laboratories. The aim is to identify the steps in a roadmap from development to diagnostic use in a UKAS accredited laboratory with an emphasis on identifying challenges and potential solutions.

Britannia Room, The Tower Hotel, St Katharine's Way, London, E1W 1LD
Thursday 7th June 2018, 10.00am – 16.30pm

Agenda

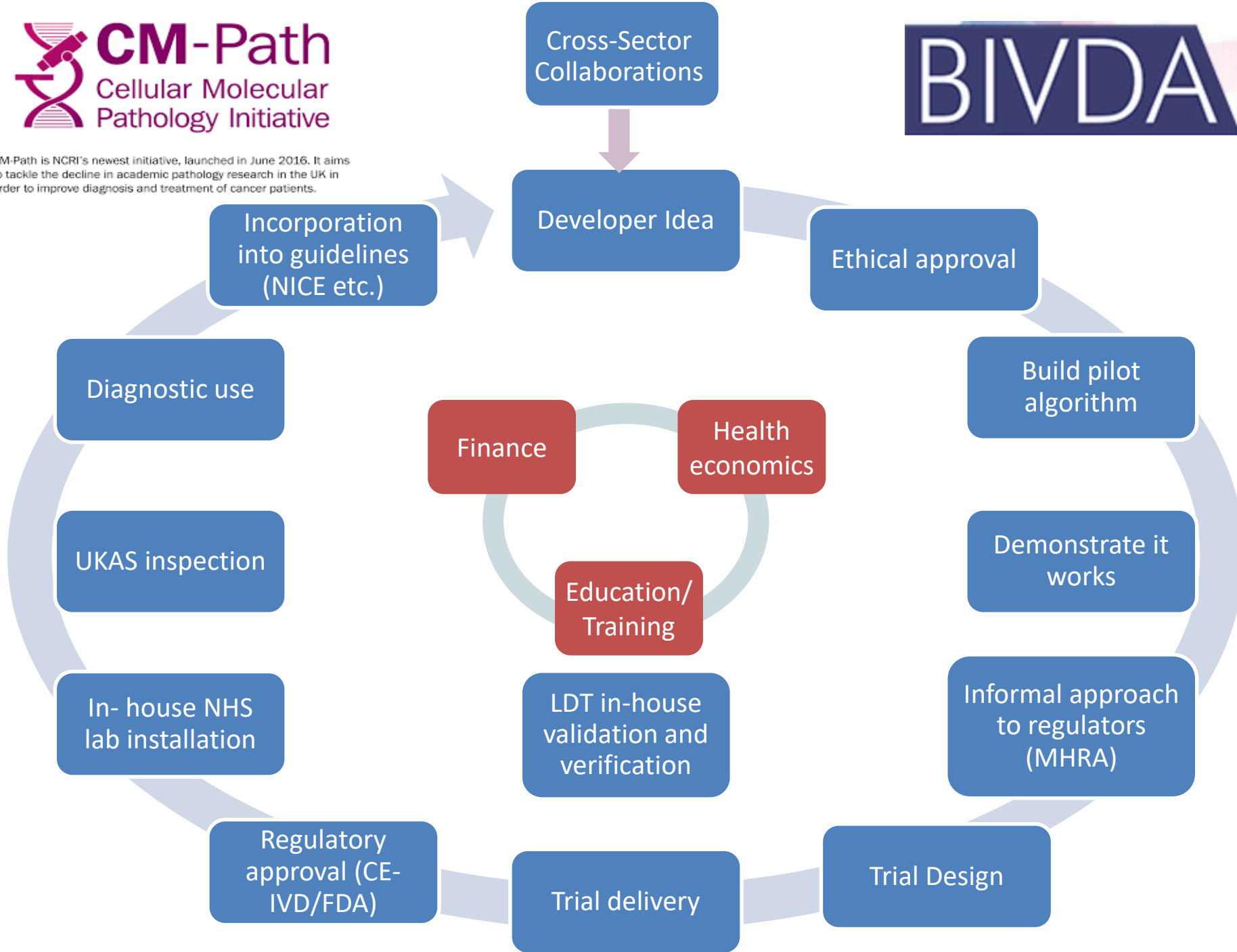


09.30	Arrival and registration	
10.00	Welcome and Introductions	Professor David Snead Professor Clare Verrill
10.10	"The bigger picture". The Industrial Life Sciences Strategy, AI and Pathology.	Professor David Snead
10.20	Overview of AI development from inception to clinical trial	Professor Nasir Rajpoot
10.40	Post-trial implementation of AI solutions, including regulatory approval	Professor Dirk Vossen
11.00	Regulatory processes for AI in clinical practice	Dr Stephen Lee
11.20	Coffee break	
11.35	Concept to regulatory approval	Breakout Sessions
	<ul style="list-style-type: none"> Purpose: Groups work together to highlight the stages in the development of algorithms Groups: Attendees will be mixed into set groups including a variety of disciplines Outputs: An outline of the journey and associated challenges with possible solutions 	
12.20	Feedback from breakout groups and discussion	All
12.40	Lunch	
13.25	Using digital pathology in an NHS histopathology laboratory – what do UKAS expect?	Dr Jonathan Bury
13.45	The role of UKAS in monitoring Digital Pathology and use	Mrs Alyson Bryant

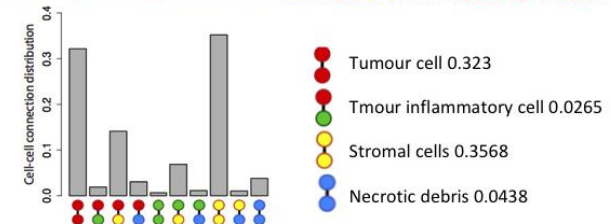
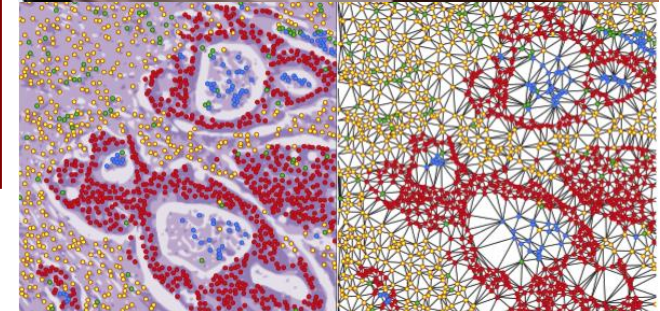
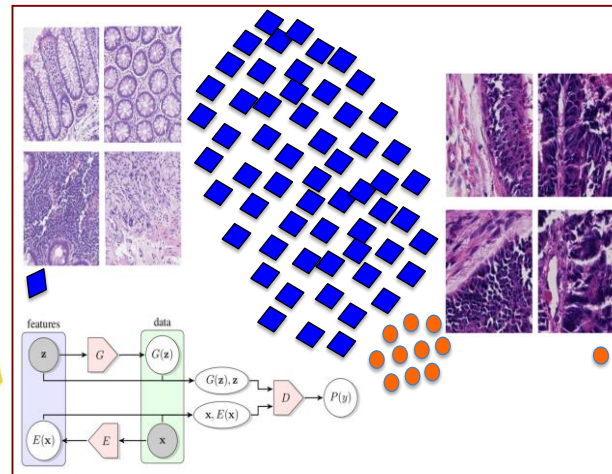
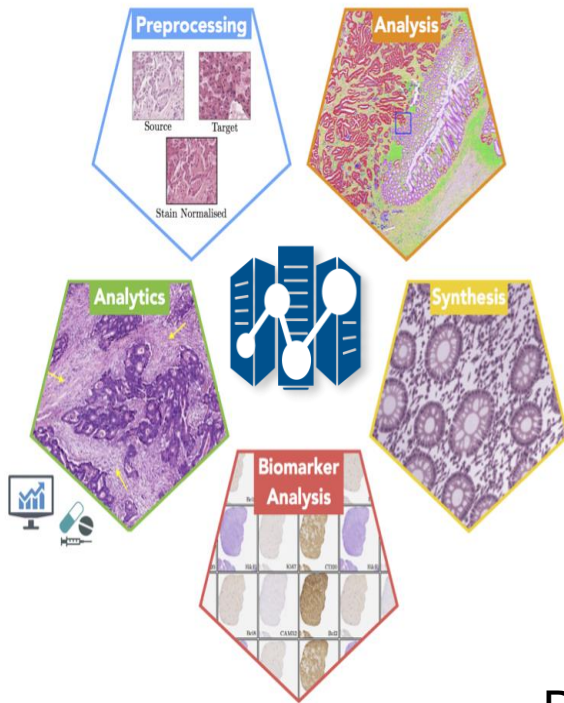
Artificial Intelligence product development

- Product purpose
- Engage with regulators early
- Entire pathway scrutinised
- Control of software used
- Pathologist certification
- Quality assurance of annotations
- Trial design





Pathology Image Analytics



Deployment in practice
 Interoperability across platforms
 Variability of sections
 Variability of staining
 Quality assurance of performance
 Implementation controls
 Accreditation

Acknowledgements

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