The YUKAKO YAGI

Pathology Digital Imaging Laboratory

2019

Memorial Sloan Kettering Cancer Center™

Welcome Message

Yukako Yagi, PhD

2019 has been an incredible year for the Pathology Digital Imaging Laboratory. Since its inception in 2017, the Laboratory has served as an incubator to explore, develop and evaluate new technology to advance medical imaging in a clinical setting and actively engage vendors to improve the technology and develop clinical applicability. Through collaborations with research and clinical departments (e.g., Surgery, Radiology, Medical Physics, and Information Systems (IS) groups), our lab enhances the assessment and creates opportunities for multidisciplinary applications.

The central aim of our research is to further enrich our knowledge of disease by integrating computational pathology data and yield a comprehensive, multidimensional analysis to discover novel morphological features and disease patterns that can lead to faster diagnoses and positively impact patient care.

This year has led to substantial progress in each of our projects, and our success would not have been possible without the incredible work and support from our partners and collaborators. We are proud to present an overview of our 2019 projects and look forward to working with you in the New Year!

Meet the Team

Patricia Ashby
Administrative Assistant

Ziv Frankenstein, PhD
Machine Learning Engineer

Marc-Henri Jean
Digital Imaging Associate

Kareem Ibrahim
Senior Application Analyst

Takashi Inoue, MD
Visiting Investigator

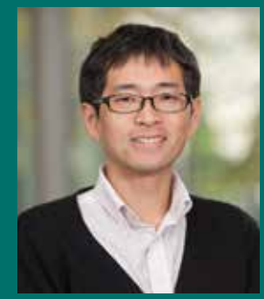
Noboru Kawata, MD
Visiting Investigator

Takashi Ohnishi, PhD
Visiting Investigator

Hossain Md. Shakhawat
Graduate Research Assistant

Benjamin Stueben, MD
Research Fellow

Alexei Teplov
Image Analyst



Naohiro Uraoka, MD, PhD
Research Fellow

Christina M. Virgo, Esq.
Project Portfolio Manager

2019 Projects

Building a Digital Pathology Image Database and Library for Clinical Review and Research

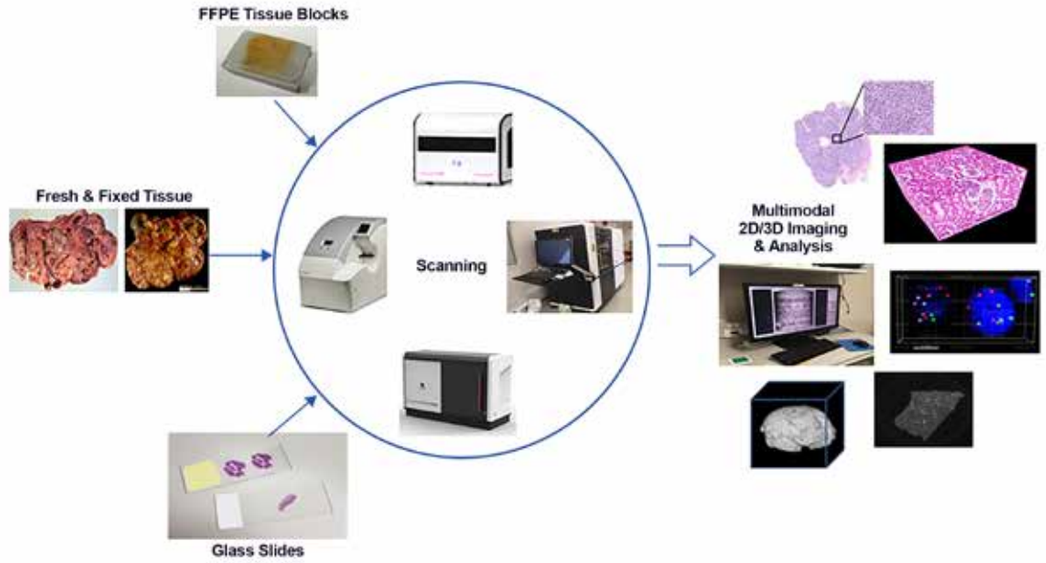
Project Participants

Marc-Henri Jean, Shirley Vargas, Allyne Manzo, Lorraine Corsale

In 2019, we scanned approximately 800,000 pathology glass slides with a cumulative digital archive of approximately 1.2 million digital images in total by end of year, more than doubling our numbers from 2018.

The MSK digital scanning team works tirelessly to keep up with the fast pace of our research needs and oversees the entire process, from intake to quality control. This workflow is continuously optimized and includes the assessment of scanners, scanning platforms, and scanning techniques that allow for the scanning and analysis of traditional slide images and whole mount blocks.

In research, this allows for the integration of computational pathology data with other specimen-related data (genomics, proteomics, radiographic imaging, etc.), to bring an unprecedented breadth and depth of information to each individual case, yielding a comprehensive, multidimensional analysis that would otherwise be impossible. These AI and decision support tools will assist pathologists in both research and clinical diagnostics.



2019 Projects

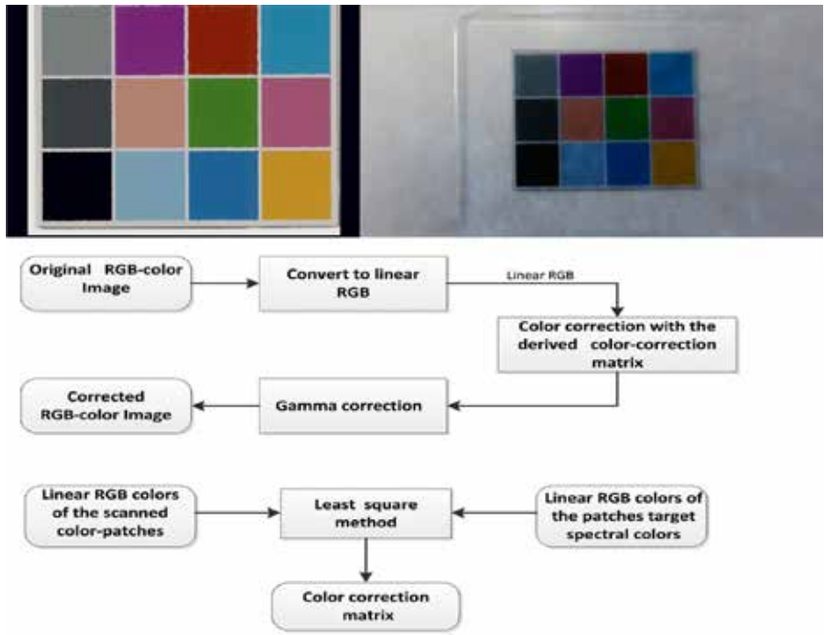
Clinical Standardization for Digital Pathology

Project Participants

Takashi Inoue, MD, Marc-Henri Jean, Yukako Yagi, PhD

The uses of whole slide imaging (WSI) are varied, not only for developing decision support systems, image analysis, education, conferences and remote diagnostics, but also in the development of artificial intelligence using machine learning methods. There are still many issues to solve before WSI can be implemented successfully within the clinical setting. One of the most important issues lies in the lack of color standardization methods for WSI. There are five major reasons for color variation, which include specimen thickness, staining, scanner type, viewer system and display source. Recognizing that the color is not homogenous in WSI is the first step towards standardization. It is difficult to ascertain where the image discrepancy occurs during the process (i.e., tissue preparation, staining, scanning, screen quality, etc.), which is difficult to standardize in and of itself.

2019 Updates:
We are currently working to develop a standardization slide that enables users to adjust/ correct color variation. We are also writing a review paper about color standardization for submission.

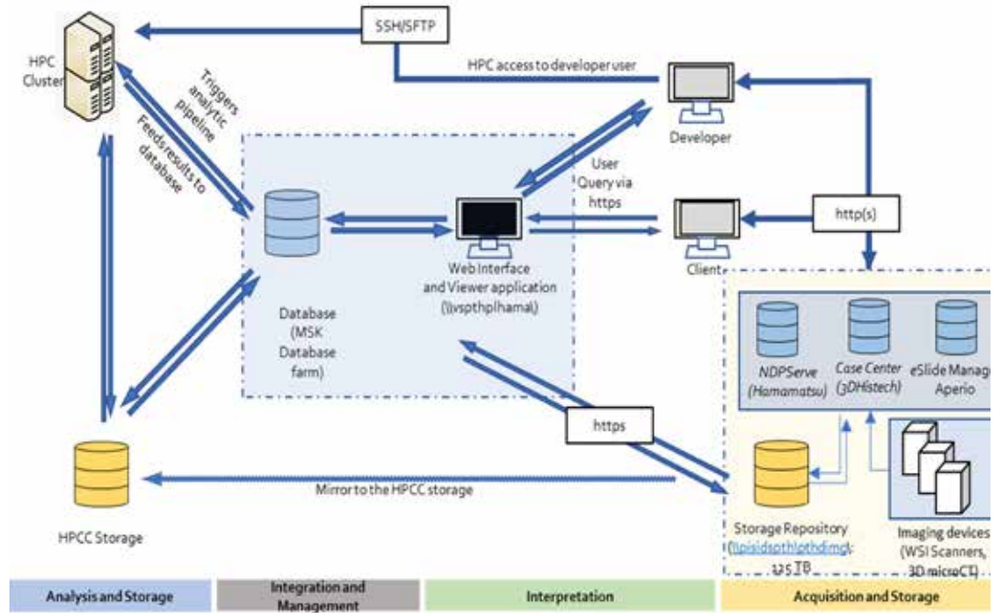


OneDB: A Multimodality Data Management System

Project Participants

James Relyea, Kareem Ibrahim, Himanshu Joshi, MD, PhD, Ziv Frankenstein, PhD, Naohiro Uraoka, MD, PhD, Hossain MD. Shakhawat, Marc-Henri Jean, Alexie Teplov, Meera R. Hameed, MD, Yukako Yagi, PhD

The Pathology Digital Imaging Laboratory, led by Dr. Yukako Yagi, is experienced in managing diverse datasets and file formats. The objective of this project is to create a novel database system that allows for the compilation and analysis of various sources of medical information (i.e., pathology, radiology, molecular, whole slide and whole block images, etc.) regardless of its format, source or size. Once completed, this singular database (a.k.a. "OneDB") will improve not only the efficiency of 2D and 3D image analysis but also ensure diagnostic accuracy. For example, the team has been developing methods for the reliable automated analysis of FISH, CISH, Micro-CT and histology 3D imaging on a cellular level. Deep-learning technologies such as these, will also be deployed utilizing the data housed within OneDB and can be a valuable tool for efficient data/image review, correlation, analysis, and AI application development. This type of tool will not only help to facilitate new diagnostic discovery and research but can also help pathologists in performing time-prohibitive tasks in an efficient manner via data/image correlation and visualization.



2019 Projects

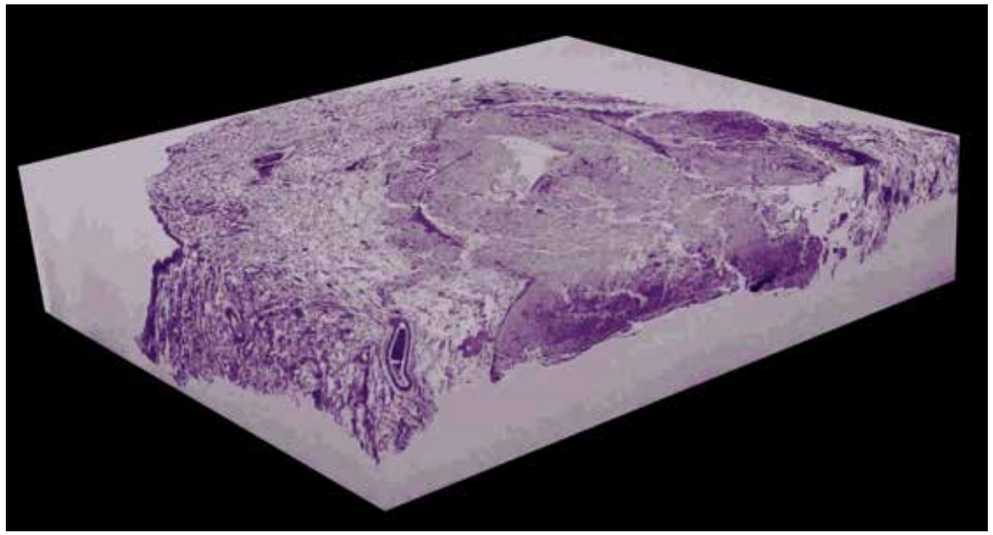
Thoracic | Whole Block Imaging (WBI) of Lung Carcinoid Tumors by Micro-CT: 3-Dimensional Morphometric Analysis of Spread Through Air Spaces (STAS)

Project Participants

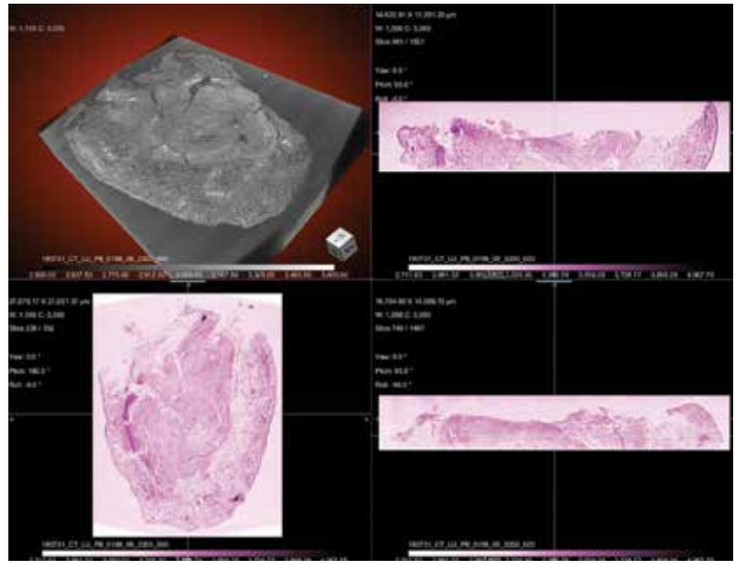
Rania G. Aly, MD, Alexei Teplov, Naohiro Uraoka, MD, PhD, Kareem Ibrahim, Natasha Rekhtman, MD, PhD, Meera R. Hameed, MD, William D. Travis, MD, Yukako Yagi, PhD

In previous work we found that STAS was an independent poor prognostic factor in atypical carcinoid (AC), large cell neuroendocrine carcinoma, (LCNEC) and small cell carcinoma (SCLC). Using 3D histology, we have also shown that STAS is a mechanism of invasion in lung adenocarcinoma. Micro-computed tomography (micro- CT), is a non-invasive method which allows for 3-dimensional (3D) morphometric analysis of tissues in formalin fixed paraffin-embedded (FFPE) blocks. The aim of the current study is to analyze the presence of STAS and its relation to the surrounding lung parenchyma in lung neuroendocrine tumors (NETs).

A cohort of FFPE tissue blocks containing samples of lung NETs and all histological subtypes were scanned using the custom-built micro-CT scanner. Tumors were then selected by Pathologists that showed STAS with exclusion of artifacts in accordance with established criteria. They consisted of one typical carcinoid and AC. The data was reconstructed into 3D volumetric images then digitally stained with H&E for visualization as needed. A hematoxylin and eosin (H&E) slide was scanned using a Whole Slide Image (WSI) scanner and matched to the WBI by micro-CT.



STAS was identified in both typical carcinoid (TC) and AC. STAS was seen as solid nests extending from the edge of the main tumor invading the lung parenchyma. Near the tumor many of the STAS nests appeared detached in 2-dimensional glass slides, but with micro-CT, 3D images revealed that these STAS clusters were connected to each other and frequently to the main tumor with a pattern of tumor islands.



WBI by micro-CT allowed for the identification of STAS in FFPE blocks in a non-invasive and non-destructive manner. The attachment of STAS to the (1) adjacent STAS clusters, (2) main tumor and/or (3) adjacent lung parenchyma, supports the concept that STAS is a biological process reflecting invasive growth in carcinoid tumor. This helps to explain its poor prognostic impact in lung AC.

The Roles of Micro-Computed Tomography (CT) in Lung Adenocarcinoma

Project Participants

Takashi Inoue, MD, Alexei Teplov, William D. Travis, MD, Yukako Yagi, PhD

Micro-computed tomography (Micro-CT), is a non-invasive method which allows 3-dimensional morphometric analysis of tissues in formalin fixed paraffin-embedded (FFPE) tissue blocks without any sectioning or loss of sample. Lung adenocarcinoma has five major tissue patterns according to the 2015 World Health Organization (WHO) classification (lepidic, acinar, papillary, solid and micropapillary). Each tissue pattern has different prognostic indicators and outcomes. In practice, pathologists have to diagnose a predominant tissue pattern and measure each percentage of tissue pattern. Micro-CT of FFPE blocks highlighted the structure of lung adenocarcinoma. Whole block imaging by Micro-CT allows for the identification of lung adenocarcinoma tissue patterns in FFPE blocks in a non-invasive and non-destructive manner.

2019 Projects

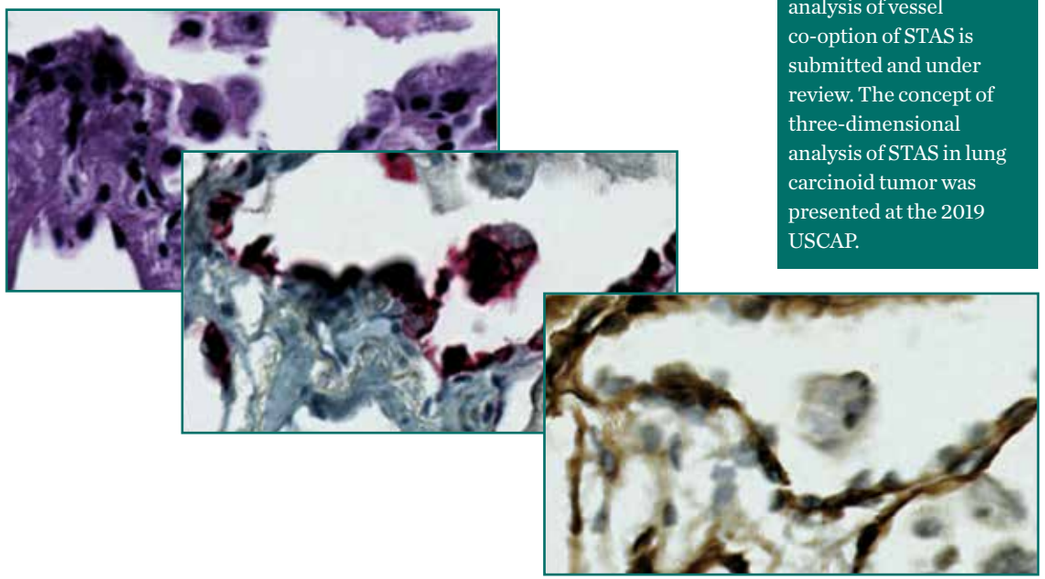
Three-Dimensional Assessment of Spread Through Air Spaces in Lung Carcinoma: Insights and Implications

Project Participants

Kazuhiro Tabata, MD, PhD, Natasha Rekhtman, MD, PhD, Prasad S. Adsumilli, MD, FACS, Rania G. Aly, MD, William D. Travis, MD, Yukako Yagi, PhD

Tumor spread through air space (STAS) is a newly recognized form of invasion in lung adenocarcinoma and squamous cell carcinoma that growing evidence shows is associated with recurrence and survival. The observation that tumor STAS clusters/nests, or single cells, within air spaces on two-dimensional hematoxylin and eosin slides raised the question: "How could these cells survive within air spaces without a vascular supply?" This, in turn, has led some to speculate that STAS is an artifact. Herein, we perform the high-resolution high-quality three-dimensional reconstruction and visualization of normal lung and tumor in lung adenocarcinoma to investigate the invasive pattern of STAS.

2019 Updates:
The concept of three-dimensional immunochemistry analysis of dynamic vessel co-option of single cell type spread through air spaces (STAS) in lung adenocarcinoma was determined. A manuscript featuring the concept of three-dimensional immunofluorescence analysis of vessel co-option of STAS is submitted and under review. The concept of three-dimensional analysis of STAS in lung carcinoid tumor was presented at the 2019 USCAP.



Head and Neck | Micro-CT and Histology 3D Analysis in Thyroid Cancer

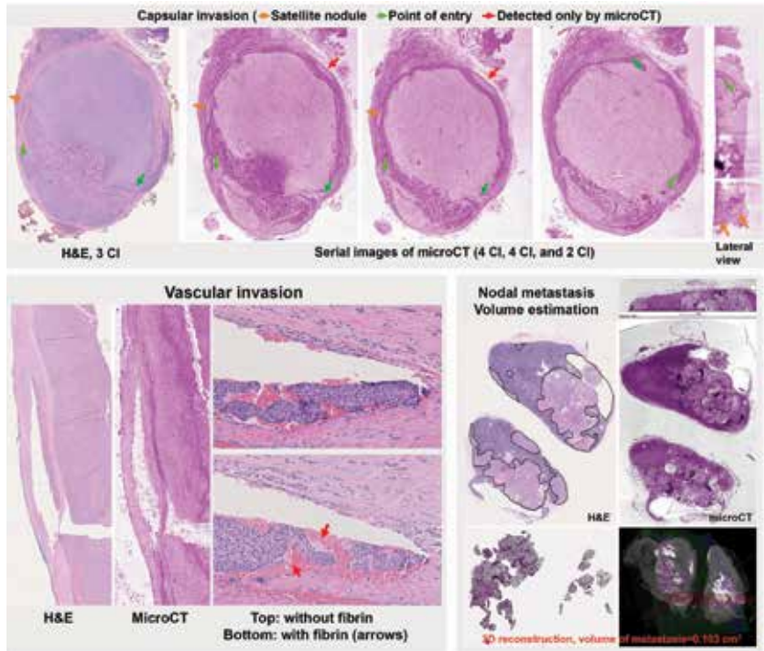
Project Participants

Bin Xu, MD, PhD, Alexei Teplov, Kareem Ibrahim, Takashi Inoue, PhD, Benjamin Stueben, MD, Nora Katabi, MD, Meera R. Hameed, MD, Ronald A. Ghossein, MD, Yukako Yagi, PhD

In the modern era, detailed pathologic characteristics of a thyroid tumor are crucial to achieve an accurate diagnosis and guide treatment decisions. The presence of capsular invasion (CI) distinguishes malignant tumors from their benign counterparts, whereas the presence and extent of vascular invasion (VI) and the size of nodal metastasis (NM) are included in risk stratification to assess the need for radioactive iodine therapy.

In cases with VI and/or CI, WSI of serial H&E slides were obtained and underwent 3D-reconstruction to be compared with the WBI: (1) Satellite tumor nodules beyond tumor capsules were shown to be CI by demonstrating the point of penetration using micro-CT and 3D reconstruction. (2) Additional foci of CI were detected in WBI using micro-CT. (3) VI was best defined as endothelialized tumor embolus within a vascular space. Associated fibrin thrombus was not always present on serially sectioned H&E slides. (4) WBI by micro-CT scanner was able to assess the volume of NM.

WBI by a micro-CT scanner is able to detect CI, VI, and volume of NM in thyroid carcinoma. It has the potential to increase the detection rate of invasion, better define criteria for CI and VI and provide an accurate assessment of the volume of nodal disease.



2019 Projects

Gastrointestinal | Whole Block Imaging (WBI) Utilizing Micro-Computed Tomography (micro-CT) Reveals Pathological Information Not Detected on Regular Histology: A Pilot Study of Rectal Cancer Resection Specimens

Project Participants

Canan Firat, MD, Alexei Teplov, Noboru Kawata, MD, Kareem Ibrahim, Peter Ntiamoah, PhD, Meera R. Hameed, MD, Efsevia Vakiani, MD, PhD, Julio Garcia-Aguilar, MD, PhD, Yukako Yagi, PhD, and Jinru Shia, MD

The continued improvement in pathological evaluation of rectal cancer resection specimens (including increasingly more detailed assessments of mesorectum, circumferential margin, tumor deposits [TDs] and lymph nodes [LNs]) has proven to be beneficial to both the survival rate and quality of life observed in patients with this cancer. Micro-CT WBI is a newly emerged 3-dimensional modality that can assess the paraffin tissue's microarchitecture. The aim of this pilot study is to explore whether micro-CT imaging can further enhance the pathologic evaluation of rectal cancer resection specimens.

Wholemount blocks and H&E sections were prepared from rectal cancer resection specimens. Whole slide imaging (WSI) of the H&E sections and WBI via micro-CT of the corresponding paraffin blocks were performed. Detailed annotations on the WSI served as training tools for the recognition of the histologic patterns on the WBI. Comparative analyses of WSI versus WBI were then carried out to determine whether WBI revealed additional information beyond what was ascertained from the H&E.

A total of 80 wholemount blocks and their corresponding H&E sections from 7 different patients were evaluated. Complementing conventional histology, WBI provided a 3rd dimension that allowed visualization of the evolution of each of the features both within the same block and through the entire tumor via contiguous blocks. This was particularly informative with regard to the origin of TDs: WBI detected the presence of TDs in 3 of 3 cases; in 1, the origin of TD was traced to the presence of VI, and in another, to the primary cancer. No origin could be detected in the 3rd case.

WBI provides a 3D methodology that can complement conventional histology. In our analysis of rectal cancer resection specimens, micro-CT WBI revealed evidence indicating varied origins of tumor deposits in these cancers. This is clinically and biologically pertinent information that is not ascertainable from the conventional 2D sections. Further studies with additional cases are underway.

Machine Learning and AI | Mitosis Detection with Tiny-YOLO

Project Participants

Kenji Ikemura, MD, Yukako Yagi, PhD

A convolutional neural networks (CNN) model named "You Only Look Once (YOLO)," has gained recognition for its fast and efficient object detection tasks. Tiny-YOLO is a more compact model suited for real-time object detection. It is also used to quickly assess whether or not YOLO can learn a particular task before training it on a larger CNN model such as YOLOv3. In this study we tested the ability of YOLOv3-tiny (a version of tiny-YO -LO) to detect mitoses in histological images.

This study utilizes breast cancer images downloaded from a publicly available repository: https://mitos-atypia- 14.grand-challenge.org/. The training set was composed of 928 histological images at 40x magnification from a WSI scanner. For each image, we made a CSV file with following information: 1) whether or not mitoses exist in the image, 2) the coordinates of each mitotic figure, and 3) the height and width of mitotic figures. The test set is composed of 20 unique H&E slides scanned at our institution on 2 types of WSI scanners (a total of 40 images). The "gold standard" of mitosis is when three out of five pathologists mark the object as mitosis. Tiny- YOLO was configured to have a batch size of 64 and run for 600 epochs. Evaluation of tiny-YOLO was made by calculating sensitivity, precision (positive predictive value), and F-measure = 2*sensitivity* precision/ (sensitivity + precision).

The trained tiny-YOLO tested on the WSI scanner test set had a sensitivity of 20%, precision of 19%, and F-measure of 0.20. Tiny-YOLO tested on a 3DHisTech test set had a sensitivity of 28%, precision of 15%, and F-measure of 0.20. Sample output images shown in Figure 1.

Although our evaluation score appears low, it clearly shows that tiny-YOLO is learning to distinguish mitosis from non-mitosis. From this result, we anticipate that full YOLO architecture can also learn to detect mitosis and with higher performance. Tiny-YOLO was also able to transfer what it learned from one type of WSI Scanner images to another WSI scanner from a different manufacturer. These findings show the potential to generalize learning over different scanners. Moving forward, we plan to expand the data set through image augmentation and add images from various scanners to acquire generalizability.

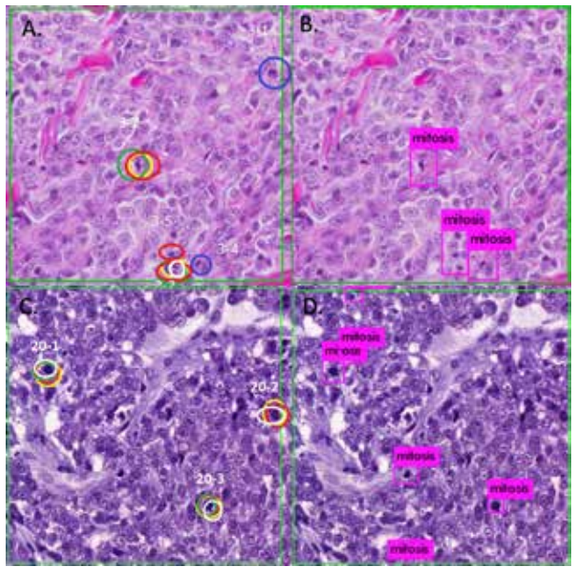


Fig. 1

2019 Projects

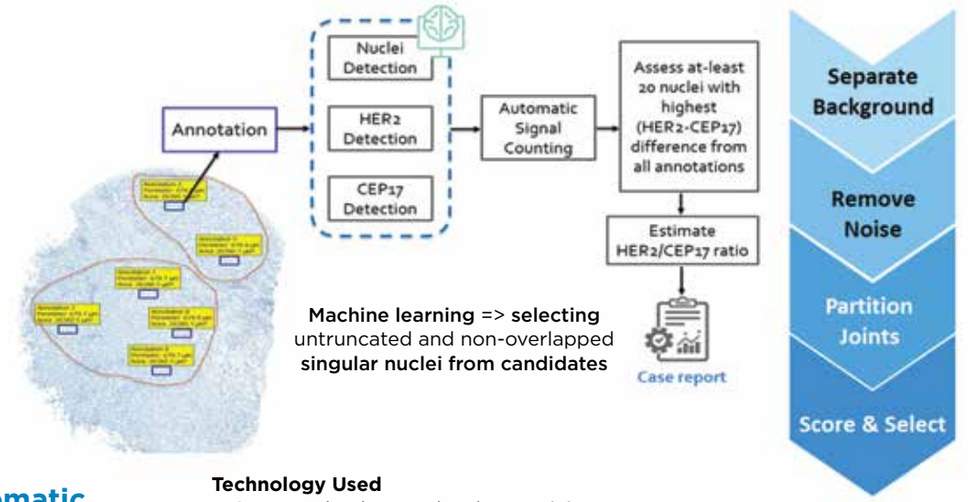
Machine Learning and AI | A Feasibility Study in the Automated Quantification of HER2 Gene Amplification in Breast Cancer Using Chromogenic in Situ Hybridization Whole Slide Images

Project Participants

Dara S. Ross, MD, Marcia Edelweiss, MD, Edi Brogi, MD, Rene N. Serrette, Handy O. Oen, Meera R. Hameed, MD, Matthew G. Hanna, MD, Willard Wong, MD, Hossain Md. Shakhawat and Yukako Yagi, PhD

HER2 gene amplification is seen in approximately 20% of breast cancers (BC). HER2 is a predictive and prognostic bio-marker in BC and accurate assessment of the HER2 status is essential. Immunohistochemistry (IHC), dual-probe fluorescence in situ hybridization (FISH) and dual-probe chromogenic in situ hybridization (CISH) are accepted methods to determine the HER2 amplification status. Advantages of CISH compared to FISH include use of a light microscope, appreciation of morphology and lower cost; however, manual evaluation is labor intensive and time consuming. In this study, we assess the practicability of an automated quantification of HER2 CISH on whole slide images (WSI).

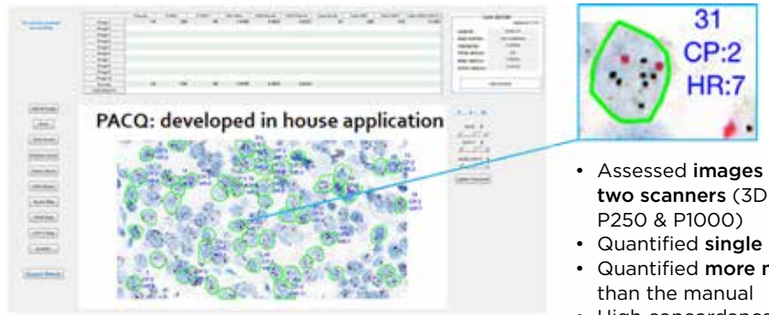
Thirty-five cases of invasive or metastatic BC with prior IHC and/or FISH testing were selected for inclusion in this study. Subsequent manual assessment by dual-probe CISH was performed and categorized. WSIs were then scanned and regions of interest (ROI) containing invasive cells were manually annotated and analyzed with **SHIMARIS PACQ V1.2** (in-house application) for automated dual-probe CISH. The manual CISH results were compared to the automated CISH results. Automated CISH was concordant with manual CISH in 33/35 (94%) cases (Table 1) demonstrating the feasibility of automated HER2 CISH evaluation. Careful assessment of ROI, tissue processing, and signal intensity is necessary and emphasizes the importance of morphologic correlation in CISH. Further study in the automated platform could provide clinical efficiencies and may enable automated analysis in other tumors (i.e. gastric) using HER2 prognostication.



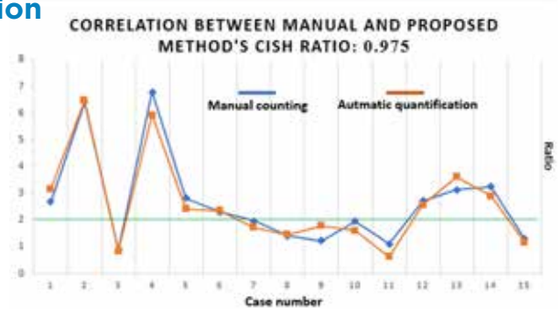
Automatic Quantification Method

Technology Used

- Separate background: color unmixing
- Remove noise: hue and intensity
- Partition: distance transform + watershed
- Score: nuclei => shape & signals => property



Quantification Results



- Assessed **images from two scanners** (3DHistec P250 & P1000)
- Quantified **single nuclei**
- Quantified **more nuclei** than the manual
- High concordance in ratio & **no discrepancy in status**

- Randomly selected 15 cases (10 positive/5 negative diagnosed with IBC)
- **Quantified the 15 cases and compared** with pathologists manual counting

2019 Projects

Development and Evaluation of an Automated 3D Scoring System of Fluorescence in situ Hybridization (FISH) on Formalin-Fixed Paraffin-Embedded (FFPE) Tissues using a Confocal Whole Slide Image Scanner

Project Participants

Ziv Frankenstein, PhD, Naohiro Uraoka, MD, PhD, Kareem Ibrahim, Umut Aypar, PhD, Ruth Aryeequaye, Mamta Rao, Ahmet Dogan, MD, PhD, Meera R. Hameed, MD, Yanming Zhang, MD, Yukako Yagi, PhD

The standard manual scoring of fluorescence in situ hybridization (FISH) analysis of formalin-fixed paraffin-embedded (FFPE) tissues is labor-intensive, time-consuming and subjective. Confocal imaging, which eliminates out-of-focus noise, offers higher resolution and more spatial information than conventional widefield imaging. The purpose of this study was to establish an automated 3D FISH scoring method.

Ten de-identified archival FFPE blocks of malignant lymphoma and Ewing's sarcoma with previous FISH tests using MYC, BCL2, BCL6 and EWSR1 break-apart probes were included in the current study. For each slide, several regions of interest (ROIs) within tumor areas were selected for confocal scanning according to the corresponding H&E and IHC slides. FISH slides were digitized and scanned at seven layers at 0.6 -m intervals. Images were reviewed, and ROIs were defined. Image analysis for 3D FISH scoring was performed with **SHIMARIS PAFQ V1.0** (in-house application) that employs 3D calculations for individual nuclei segmentation, spot detection and distribution of break-apart probe signal patterns, including standard break-apart, and variant patterns due to truncation, and deletion, etc. (Fig. 1). The accuracy of the analysis was compared with clinical manual scoring and with our previous study using a commercially available software (semi-automated).

FISH slides provided high quality data for 3D analysis of spot signals in each nuclei. Using our automated 3D system, individual nuclei segmentation, spot detection and distribution of probes were successfully performed. The average number of segmented individual nuclei are 343.6, 261.1 and 100, using the automated system, the semi-automated method by the commercially available software and the manual procedure, respectively. Using a cut-off of 10%, the percentages of abnormal signal patterns correlated well with the clinical results using manual scoring (Table 1).

We have successfully established an automated method of 3D FISH scoring for FFPE tissue using with confocal scanning. This method is more efficient, accurate and precise than the current standard and commercially available image analysis software. It enables the automated counting of more nuclei, precisely detecting more abnormal signal variations in nuclei and analyzing gigabyte multi-layer stacking imaging data of FFP E tissue samples.

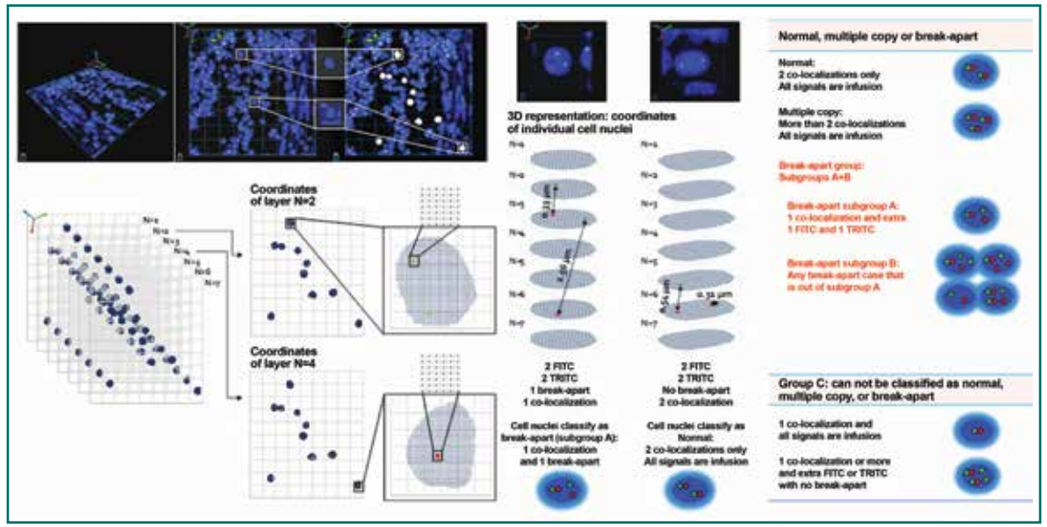


Fig. 1. Segmentation, coordinates representation and nuclei patterns.

	Number of cell nuclei (% from total)*									
Case number: / Break-apart probe:	1 BCL6	2 BCL2	3 EWSR1	4 MYC	5 BCL2	6 BCL6	7 BCL6	8 MYC	9 MYC	10 MYC
Automated algorithm	Negative (1.3)	Negative (8.4)	Positive (81.6)	Negative (2.7)	Positive (60.2)	Negative (7.5)	Positive (74.3)	Positive (71.3)	Negative (3.6)	Negative (7.3)
Image analysis software	Negative (1.2)	Negative (5.3)	Positive (88.4)	Negative (7.5)	Positive (45.0)	Negative (3.3)	Positive (84.7)	Positive (52.7)	Negative (5.5)	Negative (3.1)
Manual procedure	Negative (-)	Negative (-)	Positive (88.0)	Negative (-)	Positive (56.0)	Negative (-)	Positive (68.0)	Positive (74.0)	Negative (-)	Negative (-)

*Percentages are of break apart signal patterns out of normal, multiple copy and break apart patterns (see Fig. 1)

Table 1. 3D FISH counting and scoring of individual cell nuclei.

2019 Projects

Three-Dimensional Vessel Extraction in Whole Block Imaging Using Deep Neural Networks

Project Participants
Takashi Ohnishi, PhD, Alexei Teplov, Noboru Kawata, MD, Benjamin Stueben, MD, Kareem Ibrahim, Peter Ntiamoah, PhD, Canan Firat, MD, Hideaki Haneishi, Meera R. Hameed, MD, Jinru Shia, MD, Yukako Yagi, PhD

In order to more clearly demonstrate the structure of cancerous tissue, components such as vessel structure, depth of invasion, etc., must be examined. Although conventional pathology images only visualize a thin cross section of tissue; micro-computed tomography (micro-CT) allows us to fully analyze the three-dimensional (3D) characteristics of a neoplasm non-invasively. In this study, we applied a flow analysis using deep neural networks. The first iteration of this process was applied to 10 FFPE colorectal tissue blocks that were scanned via micro-CT. The resulting data was then reconstructed into 3D volumetric images for analysis using a VNet. Figure 1 details a schematic of our analytical procedure, which uses WBI from a custom-built micro-CT scanner.

All extractions were successfully conducted. Figure 2 shows an example of the cropped and enlarged images of WBI with extracted vessel region. White triangles on the WBI indicates vessel regions whose size we chose to detect. The shape of extracted vessel regions was smooth, and we could confirm vessel pathways. While it took over 8 hours to manually extract vessel regions, constructed deep neural networks could complete the process in about 10 minutes.

The next step is to improve the networks to measure and extract other structures such as lymph nodes and tumor lesions. In the future, our analysis method might easily understand patterns of invasion and help to guide the therapeutic decisions.

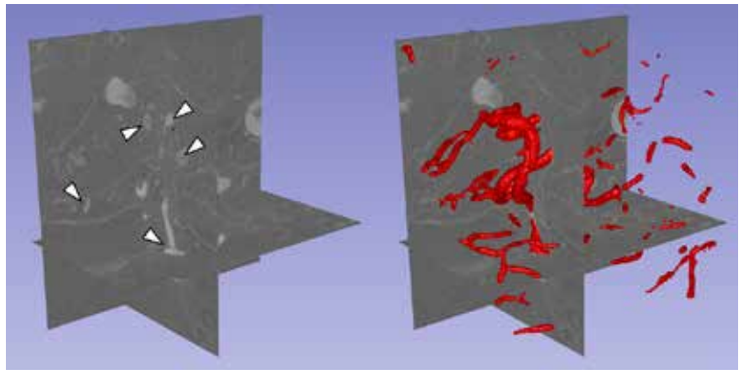


Fig. 2. Cropped and enlarged images of WBI with extracted vessel region

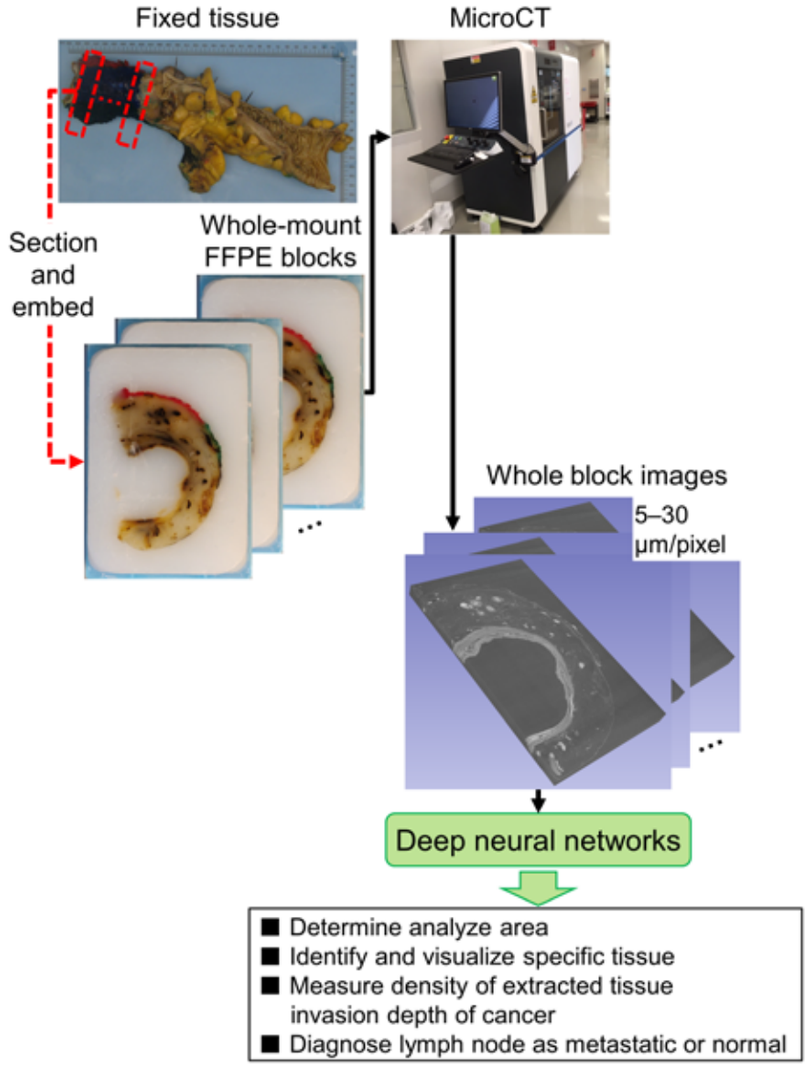


Fig. 1. Analytical procedure using WBI from a custom-built micro-CT scanner

Invited Presentations

Yagi, Yukako. “Pathology Digital Imaging: Beyond Pathology,” Keynote. Third International Symposium on Multimodal Medical Engineering (MME) Chiba University, Japan. January 29, 2019

Yagi, Yukako. “Future Direction of Digital & Computational Pathology,” Keynote. 5th Digital Pathology & AI Congress: ASIA. Tokyo, Japan. April 2, 2019

Yagi, Yukako. “Introduction and Welcome. The Warren Alpert Center’s Digital Imaging Laboratory,” The Second Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Yagi, Yukako. “Multi-Modality Imaging,” Digital Pathology & AI Congress: USA, New York, NY. June 13, 2019

Yagi, Yukako. “Future Direction of Digital & Computational Pathology,” The 12th Kure International Medical Forum (K-INT). Kure, Japan. July 27, 2019

Yagi, Yukako. “Another Direction of Digital & Computational Pathology,” The 18th General Meeting of The Japanese Society of Digital Pathology, Tokyo, Japan. August 31, 2019

Yagi, Yukako. “Present Stage of Scanner Integration into Routine Pathology Diagnostics,” European Congress of Pathology, Nice, France. September 9, 2019

Yagi, Yukako. “Discussion and Proposal for a Digital Pathology White Paper,” ASHI/BANFF (American Society for Histocompatibility and Immunogenetics/ Banff Foundation for Allograft Pathology) Joint Scientific Meeting, Pittsburgh, PA. September 23, 2019

Yagi, Yukako. “Practical Standardization in Digital & Computational Pathology– Harmonization and Standardization of Pathological Imaging.” AI Analysis Symposium, National Cancer Center, Japan. February 20, 2019

Posters

Frankenstein, Z. Automated Scoring of FISH Using a Confocal Whole Slide Image Scanner. The Second Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Ibrahim, K. Toward an Automated Scoring Algorithms of Fluorescence in Situ Hybridization (FISH) on Formalin-Fixed Paraffin-Embedded (FFPE) Tissues Using a Confocal Whole Slide Image Scanner and Image Analysis Software. The Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Joshi, H. New Dimension to Multimodality Data Management System. The Second Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Shakhawat, HM. An Automatic System to Quantify the HER2 Amplification in Invasive Breast Cancers from CISH Whole Slide Images. Pathology Informatics Summit 2019, Pittsburgh, PA. May 5-9, 2019

Shakhawat HM. Automatic Quantification of HER2 Gene Amplification in Invasive Breast Cancer Using Chromogenic in Situ Hybridization (CISH) and Computational Pathology. The Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Teplov, A. Whole Block Imaging (WBI) by Micro-CT: of Lung Carcinoid Tumors: Morphometric 3-Dimensional Analysis of Spread Through Air Spaces (STAS). The Annual Warren Alpert Center for Digital & Computational Pathology Spring Symposium, New York, NY. May 8, 2019

Publications

Fu X, Klepeis V, Yagi Y. (2018). Evaluation of an Automated Tissue Sectioning Machine for Digital Pathology. *Diagnostic Pathology*, 4(1)

Hanna MG, Reuter VE, Hameed MR, Tan LK, Chiang S, Sigel C, Hollmann T, Giri D, Samboy J, Moradel C, Rosado A, Otilano JR III, England C, Corsale L, Stamelos E, Yagi Y, et al. (2019). Whole Slide Imaging Equivalency and Efficiency Study: Experience at a Large Academic Center. *Modern Pathology*, 32, 916–928

Hanna MG, Reuter VE, Samboy J, England C, Corsale L, Fine SW, Agaram NP, Stamelos E, Yagi Y, Hameed M, Klimstra DS, Sirintrapun SJ. Implementation of Digital Pathology Offers Clinical and Operational Increase in Efficiency and Cost Savings. *Archives of Pathology & Laboratory Medicine*: December 2019, Vol. 143, No. 12, pp. 1545-1555

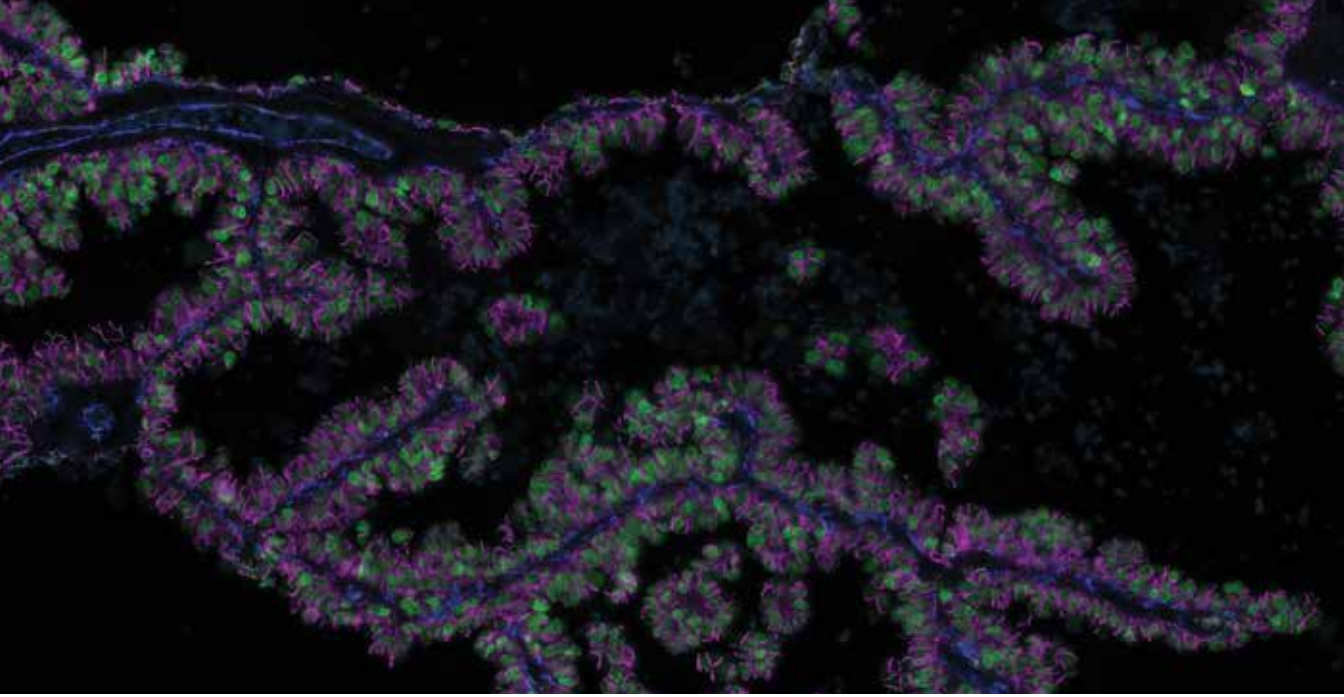
Shakhawat HM, Hanna MG, Uraoka N, Nakamura T, Edelweiss M, Brogi E, Hameed MR, Yamaguchi M, Ross DS, Yagi Y. (2019). Automatic Quantification of HER2 Gene Amplification in Invasive Breast Cancer from Chromogenic in Situ Hybridization Whole Slide Images. *Journal of Medical Imaging*, 6(4), 047501

Tabata K, Uraoka N, Benhamida J, Hanna MG, Sirintrapun SJ, Gallas BD, Gong Q, Aly RG, Emoto K, Matsuda KM, Hameed MR, Klimstra DS, Yagi Y. Validation of Mitotic Cell Quantification Via Microscopy and Multiple Whole-Slide Scanners. *Diagnostic Pathology*, June 26, 2019;14(1):65

Teplov A, Tabata K, Fu X, Uraoka N, Roehrl MHA, Ntiamoah P, Humm JL, Sirintrapun SJ, Murray MP, Shia J, Travis WD, Brogi E, Hameed MR Yagi Y. (2019). Development of Standard Operating Procedure (SOP) of Micro-computed tomography (micro-CT) in Pathology. *Diagnostic Pathology*, 5(1)

Thank you to the Department of Pathology, Radiology and Medical Physics, the Josie Robertson Surgical Center, the Warren Alpert Center for Digital and Computational Pathology, Nikon, 3DHistech, Dainippon Seiki, Tokyo Institute of Technology, Dokkyo Medical University Hospital, Shizuoka Cancer Center, Chiba University and all of our research partners and supporters

Happy Holidays



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