

Digital Pathology – Precision Medicine, Pathomics and Decision Support

Joel Saltz MD, PhD

Chair and Professor Department of Biomedical Informatics

Professor Department of Pathology

Cherith Endowed Chair

Stony Brook University

RSNA Session 553

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NO CONFLICTS TO DISCLOSE

Pathology Image Driven Decision Support

- Improve reproducibility in traditional Pathology assessments (e.g. Gleason grade, NSCLC subtypes)
- Precise scoring of well known criteria (tumor infiltrating lymphocytes, mitoses and IHC staining)
- Development of novel computational methods to employ Pathology image information to predict response to cancer treatment and outcomes.

What is the Gleason grade or Gleason score? What do the numbers in the Gleason score mean, for example $3+4=7$ or $3+3=6$?

Pathologists grade prostate cancers using numbers from 1 to 5 based on how much the cells in the cancerous tissue look like normal prostate tissue under the microscope. This is called the *Gleason system*. Grades 1 and 2 are not often used for biopsies – most biopsy samples are grade 3 or higher.

- If the cancerous tissue looks much like normal prostate tissue, a grade of 1 is assigned.
- If the cancer cells and their growth patterns look very abnormal, a grade of 5 is assigned.
- Grades 2 through 4 have features in between these extremes.

Since prostate cancers often have areas with different grades, a grade is assigned to the 2 areas that make up most of the cancer. These 2 grades are added to yield the Gleason score (also called the *Gleason sum*). The highest a Gleason score can be is 10.

Major treatment decisions can hinge on subjective judgements

The ASCO Post

A Gleason 6 Tumor: Is It Cancer, and Should It Be Treated?

cancer**network**

Gleason 6 Prostate Cancer:
Serious Malignancy or
Toothless Lion?

By Herbert Lepor, MD and Nicholas M. Donin, MD

Jan 15, 2014

PROSTATE CANCER

DISCOVERY

"Tumors with a Gleason score of 4 + 3 are more aggressive and predictive of advanced disease at the time of surgery, compared to Gleason 3 + 4 tumors," explains Mark L. Gonzalgo, M.D., Ph.D., assistant professor of urology and oncology. In a recent study, published in the journal Urology, Gonzalgo and urologists Alan W. Partin, M.D., Ph.D., and Patrick C. Walsh, M.D., investigated the relationship between a man's biopsy Gleason score, the Gleason score in the entire prostate (the specimen removed during radical prostatectomy) and the recurrence of PSA among men who were diagnosed with Gleason 7 cancer in a needle biopsy.

BJUI
BJU International

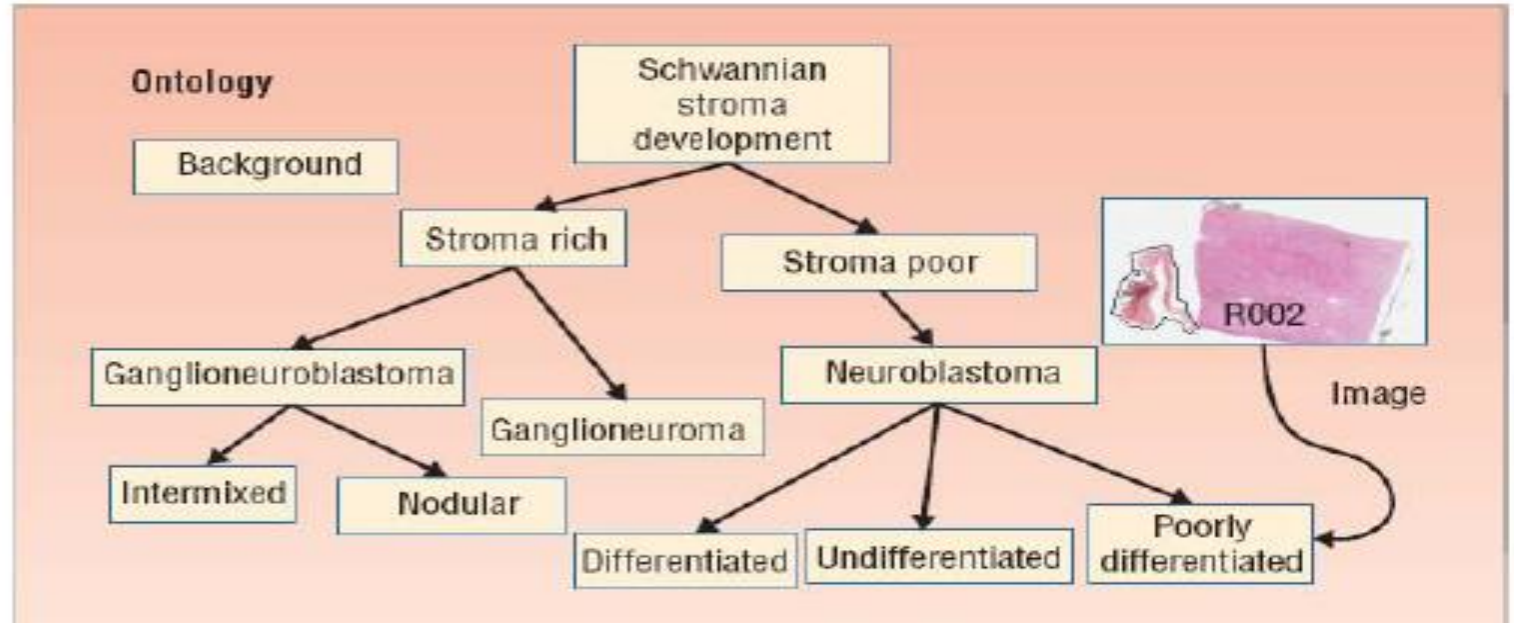
Editorial: Current Gleason score 3 + 4 = 7: has it lost its significance compared with its historical counterpart?

🕒 01 Jun 2016

Early Steps to Pathology Computer Aided Classification 2005-2010

BISTI/NIBIB Center for Grid Enabled Image Analysis - P20 EB000591, PI Saltz

- Analyze images by computer
- Analyze the whole tissue, several slides
- Provide quantitative information to the pathologist
- Reduce inter- and intra-reader variability

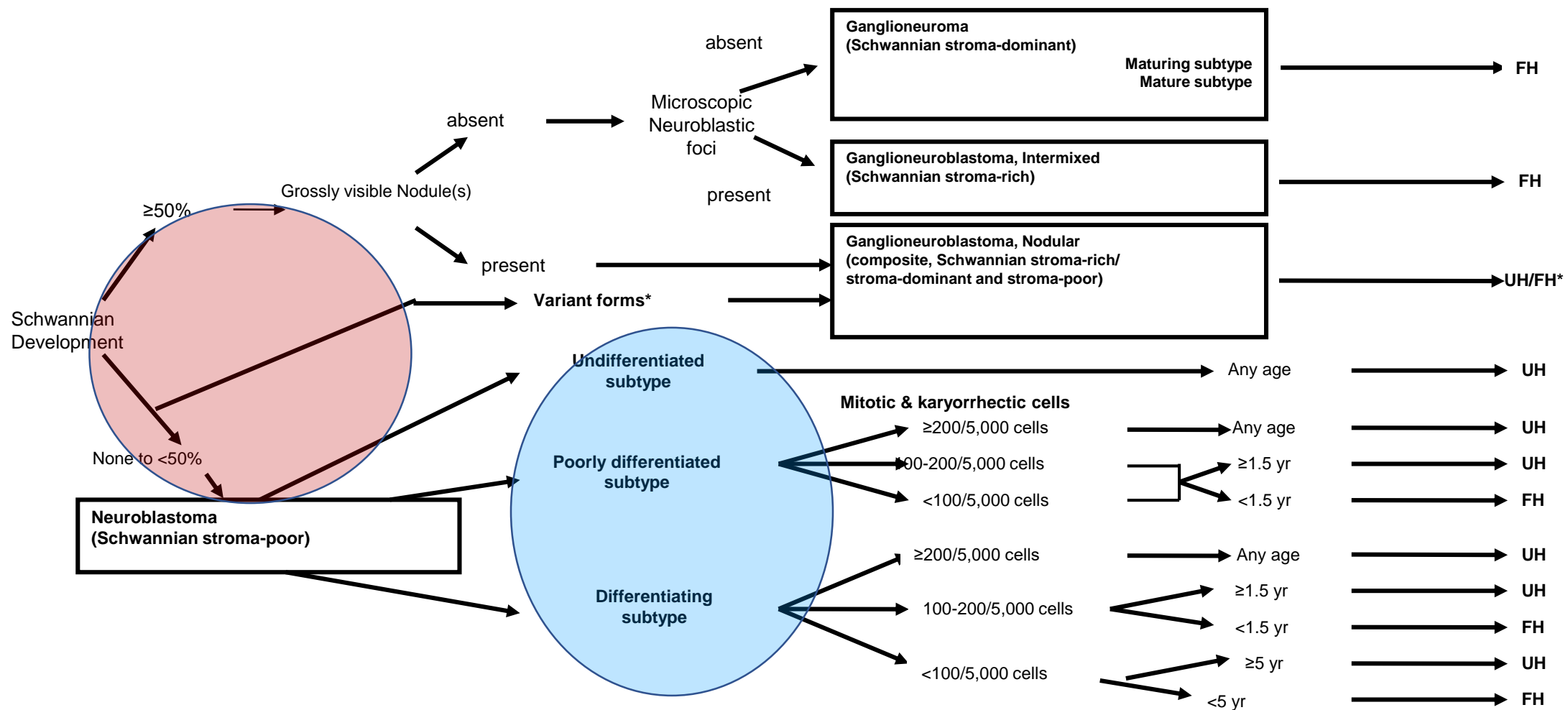


Morphological characterization of tissue used for prognosis

Hiro Shimada, Metin Gurcan, Jun Kong, Lee Cooper Joel Saltz

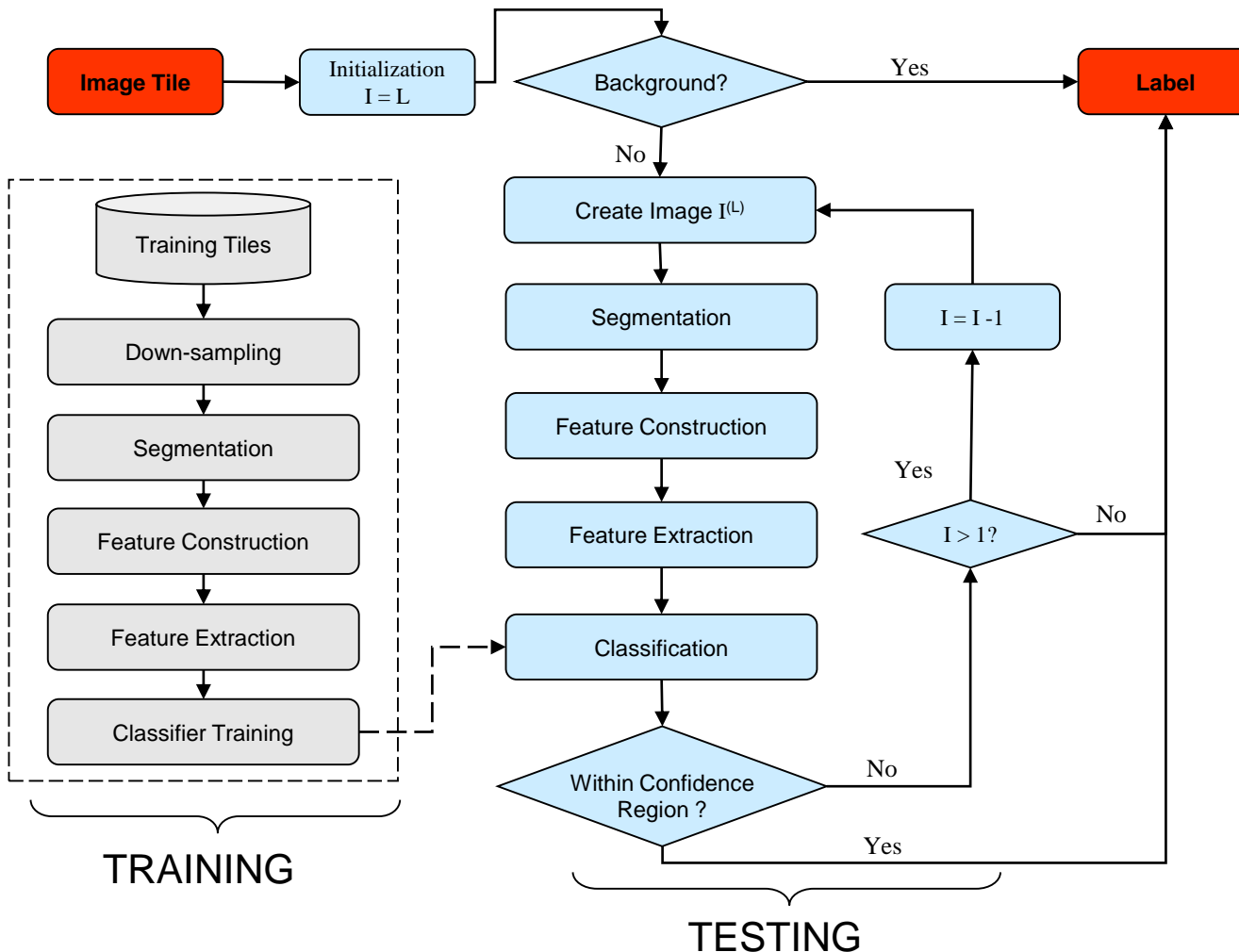
Gurcan, Shamada, Kong, Saltz

Neuroblastoma Classification



FH: favorable histology **UH:** unfavorable histology
 CANCER 2003; 98:2274-81

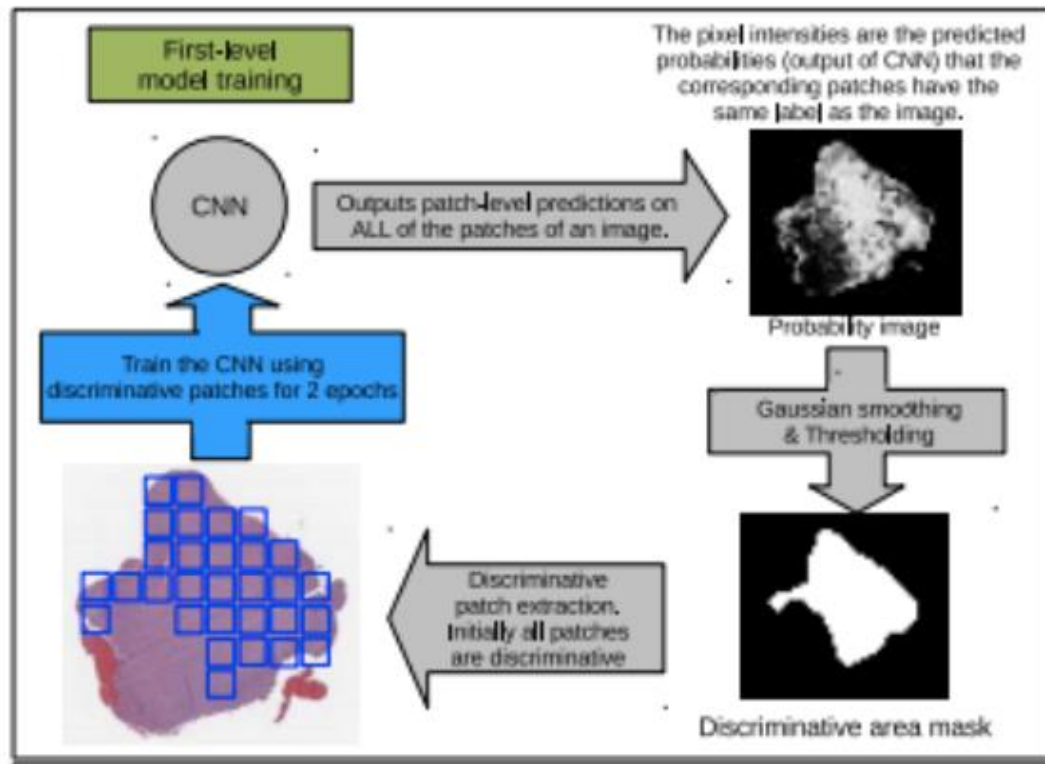
Multi-Scale Machine Learning Based Shimada Classification System



- Background Identification
- Image Decomposition (Multi-resolution levels)
- Image Segmentation (EMLDA)
- Feature Construction (2nd order statistics, Tonal Features)
- Feature Extraction (LDA) + Classification (Bayesian)
- Multi-resolution Layer Controller (Confidence Region)

Patch-Based Convolutional Neural Network for Whole Slide Tissue Image Classification

Le Hou, Dimitris Samaras, Tahsin M. Kurc, Yi Gao, James E. Davis, Joel H. Saltz; The IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 2016, pp. 2424-2433





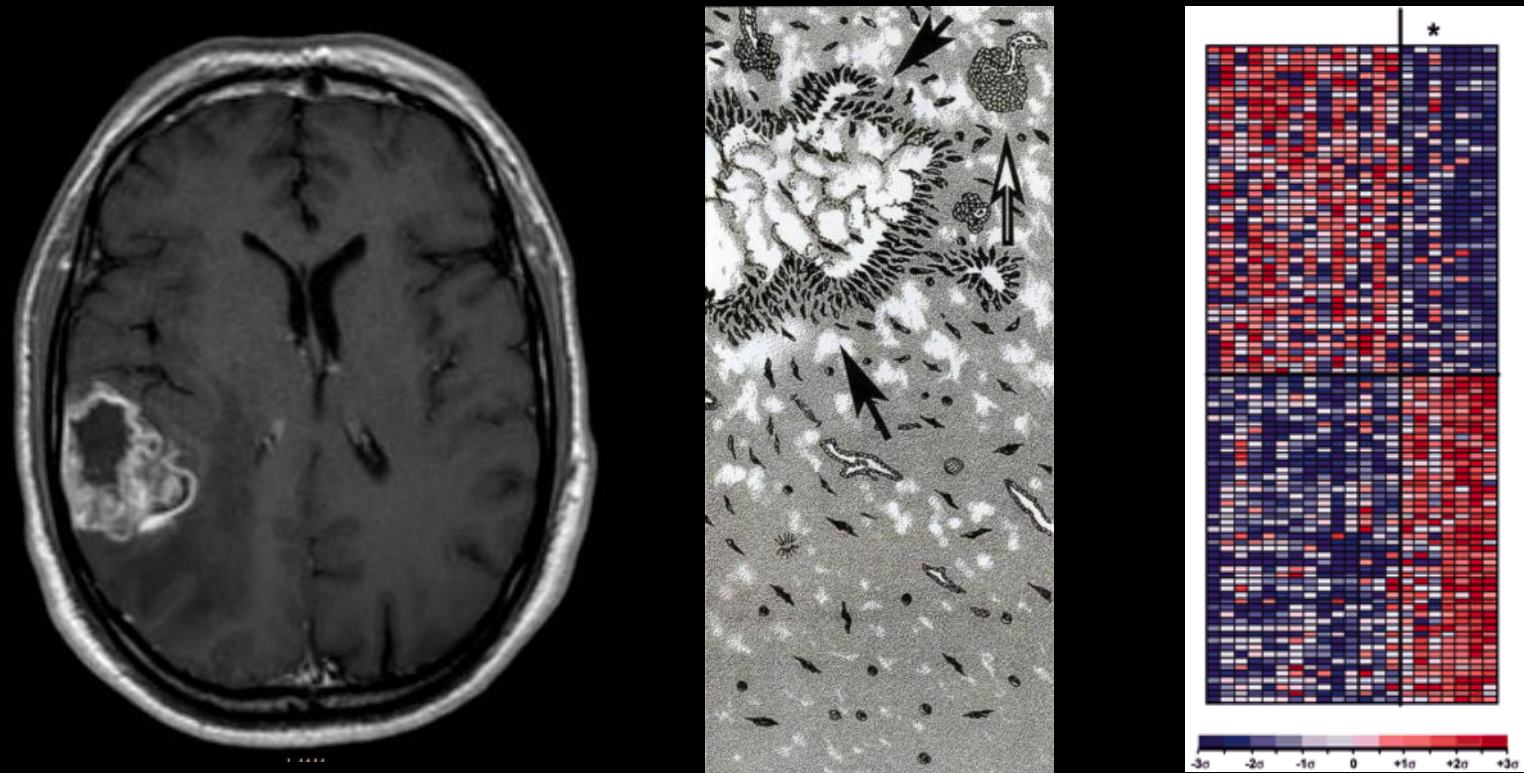
Confusion Matrix: OA is very hard even for pathologists

| | GBM | OD | OA | DA | AA | AO |
|--|-----|----|----|----|----|----|
| Glioblastoma, Grade IV (GBM) | 214 | | 2 | | 1 | |
| <u>Oligodendroglioma</u> , Grade II (OD) | 1 | 47 | 22 | 2 | | 1 |
| <u>Oligoastrocytoma</u> , Grade II & III (OA) | 1 | 18 | 40 | 8 | 3 | 1 |
| Diffuse Astrocytoma, Grade II (DA) | 3 | 9 | 6 | 20 | | 1 |
| Anaplastic Astrocytoma, Grade III (AA) | 3 | 2 | 3 | 3 | 4 | |
| Anaplastic <u>Oligodendroglioma</u> , Grade III (AO) | 2 | 2 | 3 | | | 1 |

Le Hou, Dimitris Samaras, Tahsin Kurc, Yi Gao, Liz Vanner, James Davis, Joel Saltz

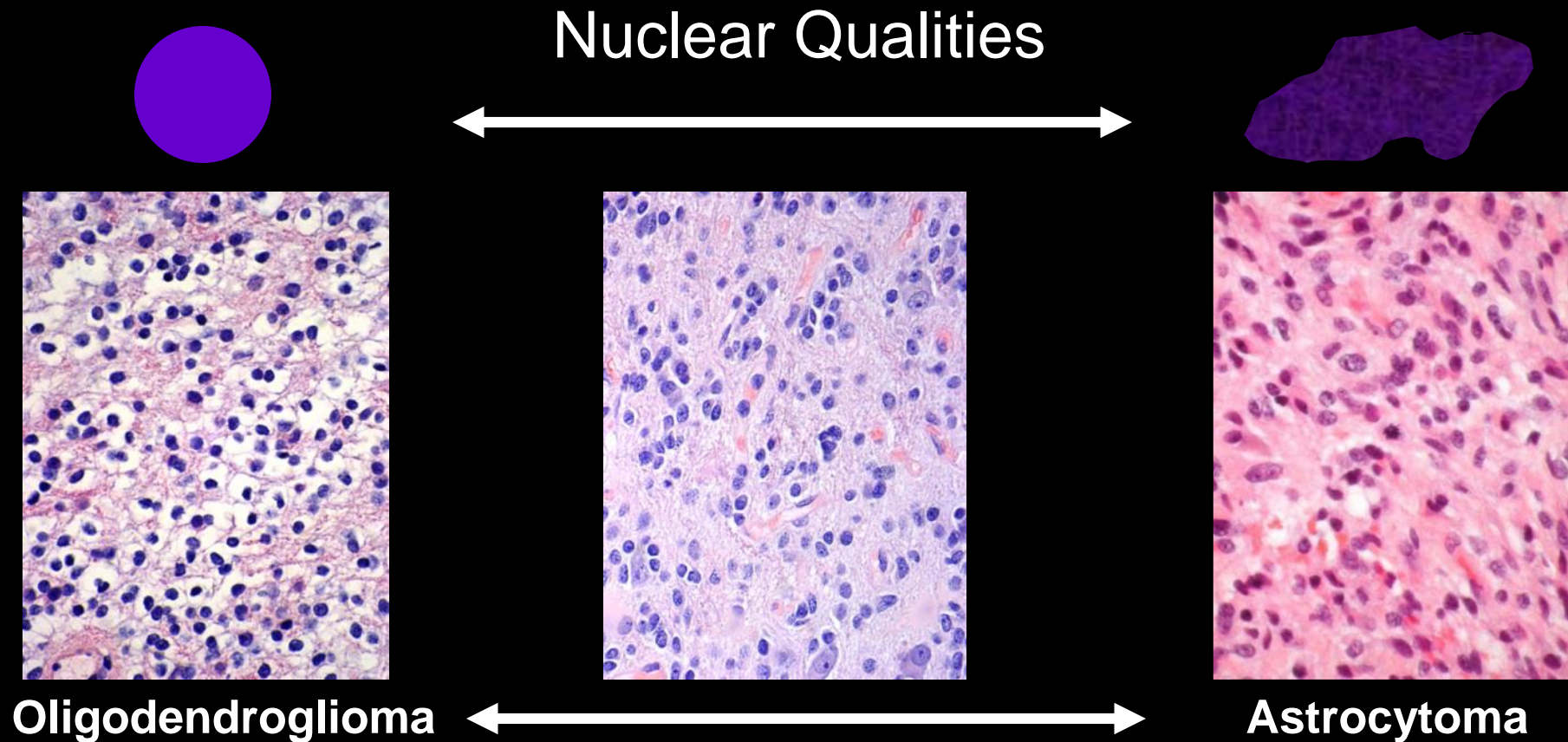
Digital Pathology as Precision Medicine

- Statistical analyses and machine learning to link Radiology/Pathology features to “omics” and outcome biological phenomena
- Image analysis and deep learning methods to extract features from images
- Support queries against ensembles of features extracted from multiple datasets
- Identify and segment trillions of objects – nuclei, glands, ducts, nodules, tumor niches
- Analysis of integrated spatially mapped structural/“omic” information to gain insight into cancer mechanism and to choose best intervention



Quantitative Feature Analysis in Pathology: Emory In Silico
Center for Brain Tumor Research (PI = Dan Brat, PD= Joel
Saltz) 2009 - 2013

Can we use image analysis of TCGA GBMs TO INFORM diagnostic criteria based on molecular or clinical endpoints?



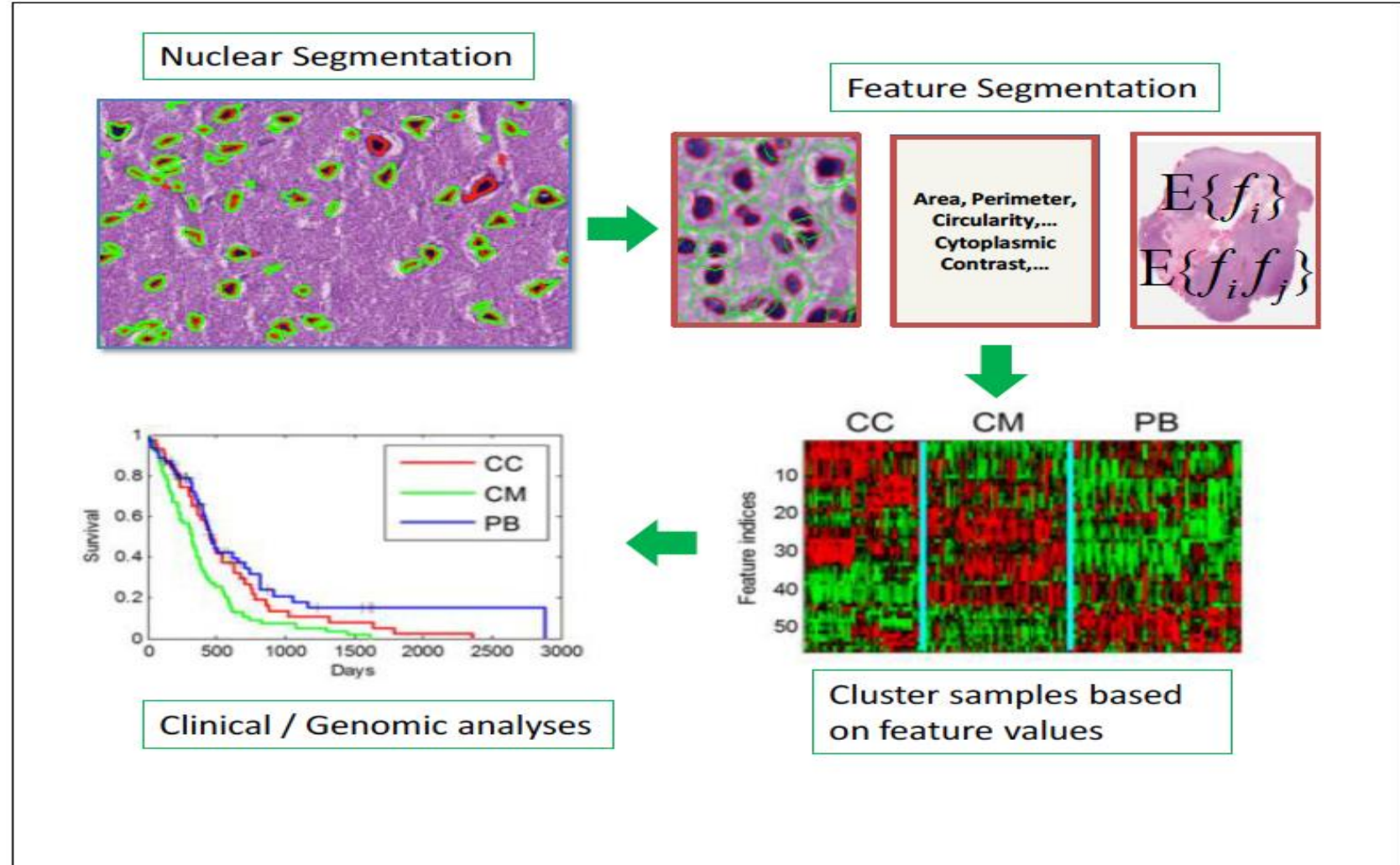
Application: Oligodendroglioma Component in GBM

Integrative Morphology/"omics"

Quantitative Feature Analysis in Pathology: Emory In Silico Center for Brain Tumor Research (PI = Dan Brat, PD= Joel Saltz)

NLM/NCI: Integrative Analysis/Digital Pathology R01LM011119, R01LM009239 (Dual PIs Joel Saltz, David Foran)

Marcus Foundation Grant – Ari Kaufman, Joel Saltz

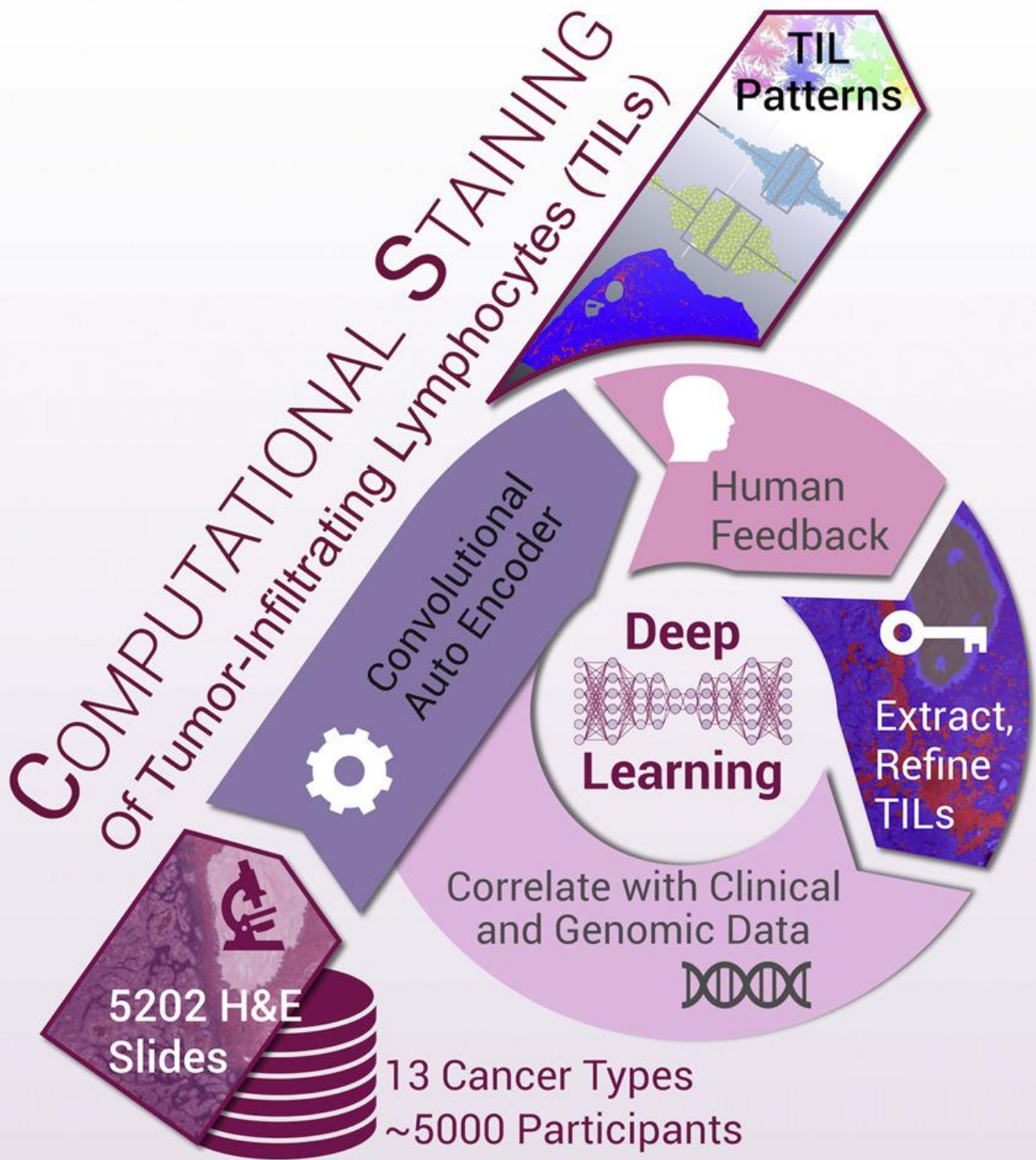


Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images

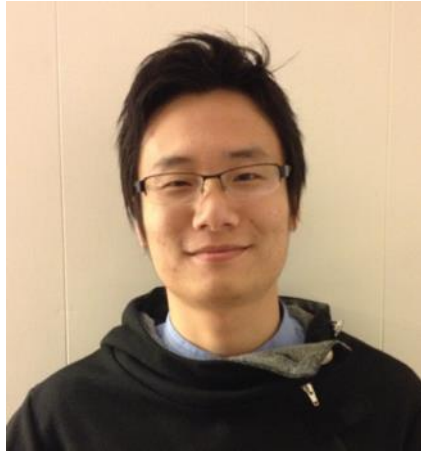
Joel Saltz,^{1,*} Rajarsi Gupta,^{1,4} Le Hou,² Tahsin Kurc,¹ Pankaj Singh,³ Vu Nguyen,² Dimitris Samaras,² Kenneth R. Shroyer,⁴ Tianhao Zhao,⁴ Rebecca Batiste,⁴ John Van Arnam,⁵ The Cancer Genome Atlas Research Network, Ilya Shmulevich,⁶ Arvind U.K. Rao,^{3,7} Alexander J. Lazar,⁸ Ashish Sharma,⁹ and Vésteinn Thorsson^{6,10,*}

[http://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30447-9.pdf](http://www.cell.com/cell-reports/pdf/S2211-1247(18)30447-9.pdf)

- Stony Brook, Institute for Systems Biology, MD Anderson, Emory group
- TCGA Pan Cancer Immune Group – led by ISB researchers
- Deep dive into linked molecular and image based characterization of cancer related immune response



- Deep learning based computational stain for staining tumor infiltrating lymphocytes (TILs)
- TIL patterns generated from 4,759 TCGA subjects (5,202 H&E slides), 13 cancer types
- Computationally stained TILs correlate with pathologist eye and molecular estimates
- TIL patterns linked to tumor and immune molecular features, cancer type, and outcome



Le Hou – Graduate Student
Computer Science



Anne Zhao – Pathology Informatics
Biomedical Informatics, Pathology
(now Surg Path Fellow SBM)



Vu Nguyen– Graduate Student
Computer Science

Deep Learning and Lymphocytes: Stony Brook Digital Pathology Trainee Team



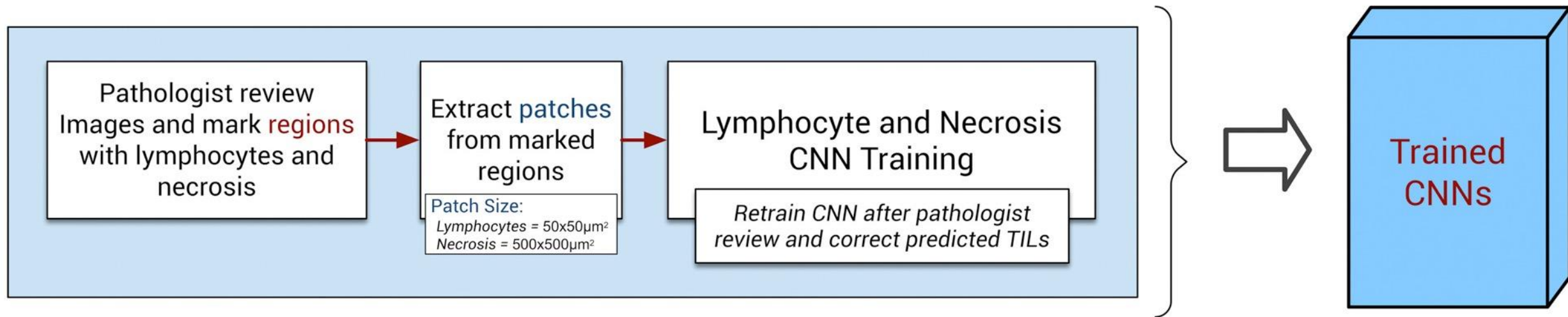
Raj Gupta – Pathology Informatics
Biomedical Informatics, Pathology

Importance of Immune System in Cancer Treatment and Prognosis

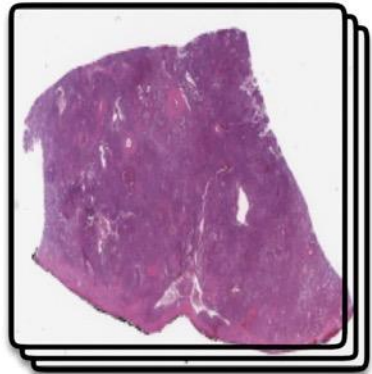
- Tumor spatial context and cellular heterogeneity are important in cancer prognosis
- Spatial TIL densities in different tumor regions have been shown to have high prognostic value – they may be superior to the standard TNM classification
- Immune related assays used to determine Checkpoint Inhibitor immune therapy in several cancer types
- Strong relationships with molecular measures of tumor immune response – results to soon appear in TCGA Pan Cancer Immune group publications
- TIL maps being computed for SEER Pathology studies and will be routinely computed for data contributed to TCIA archive
- Ongoing study to relate TIL patterns with immune gene expression groups and patient response

Training, Model Creation

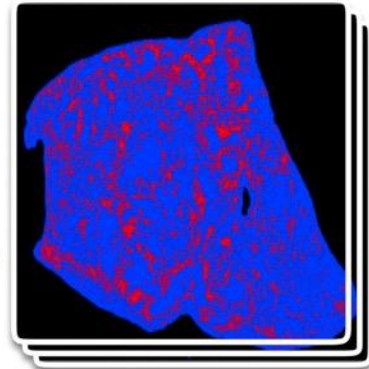
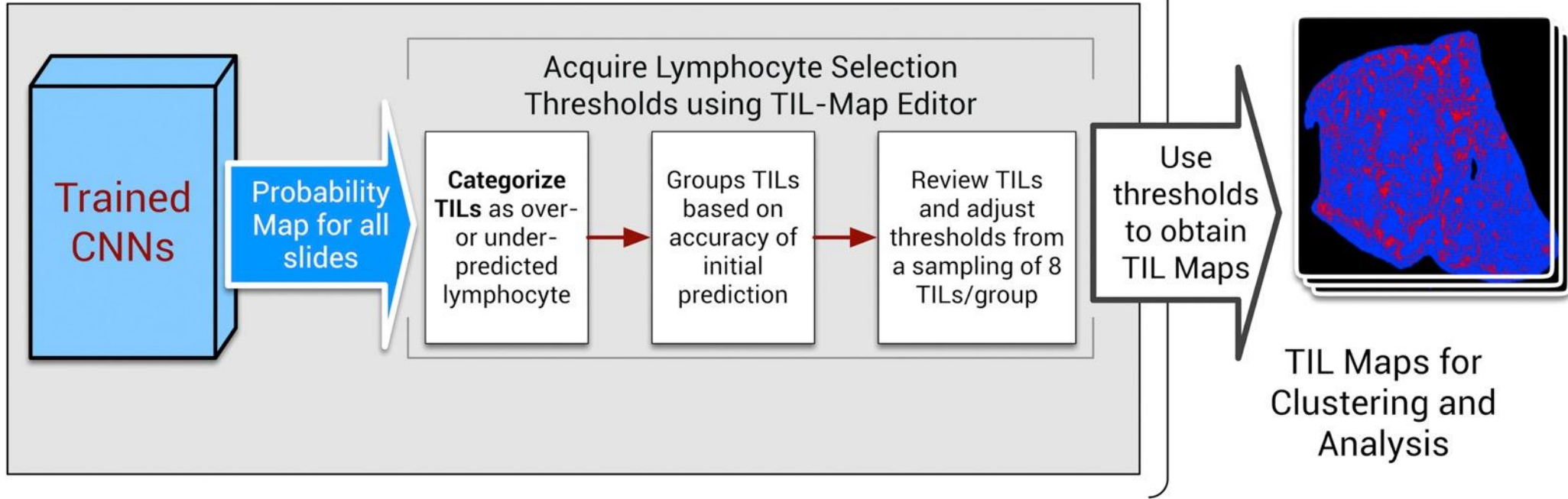
- Algorithm first trained on image patches
- Several cooperating deep learning algorithms generate heat maps
- Heat maps used to generate new predictions
- Companion molecular statistical data analysis pipelines



Training, threshold adjustment, quality control

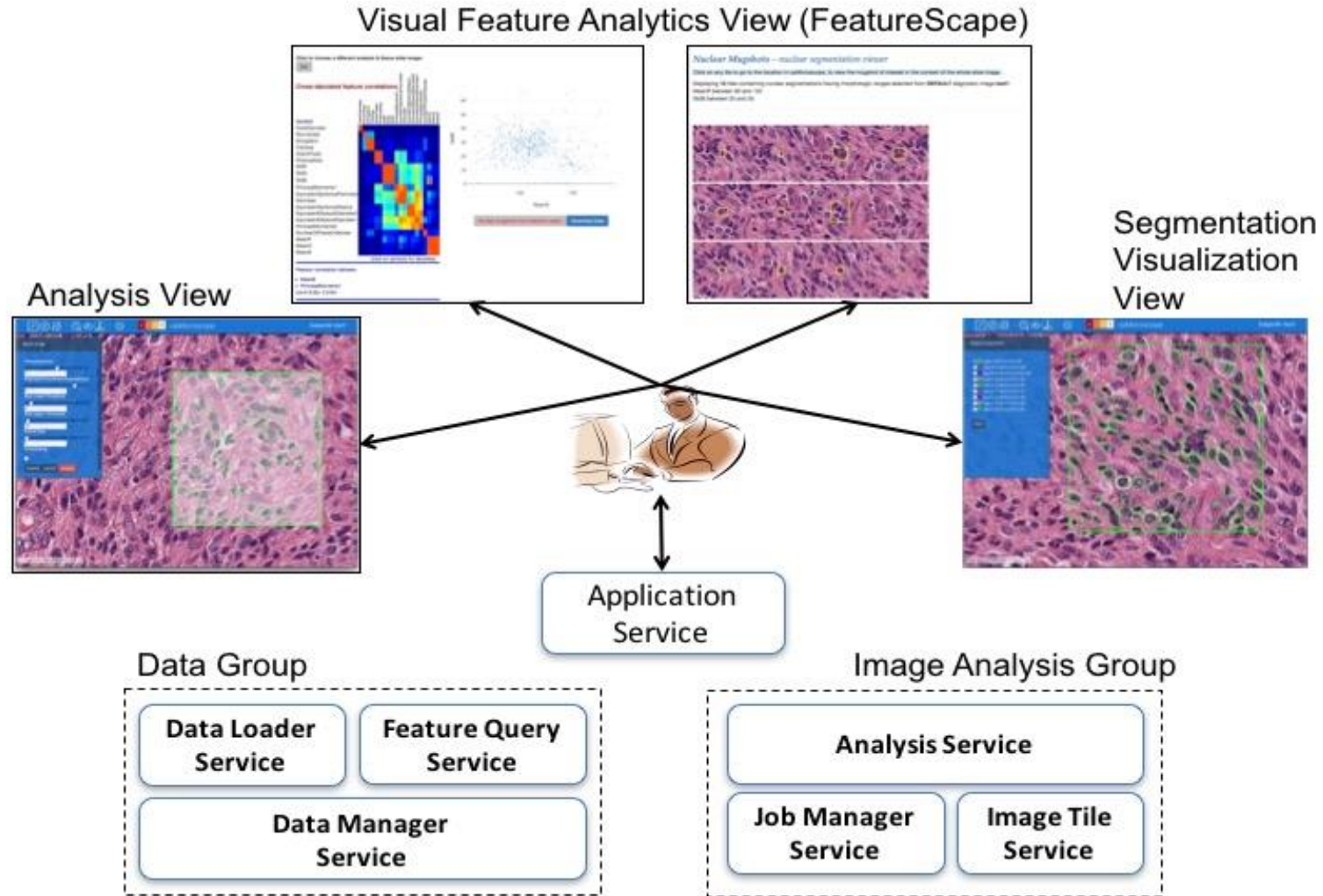


Unlabeled set of WSI H&E Images (5455 images, 13 cancer types)

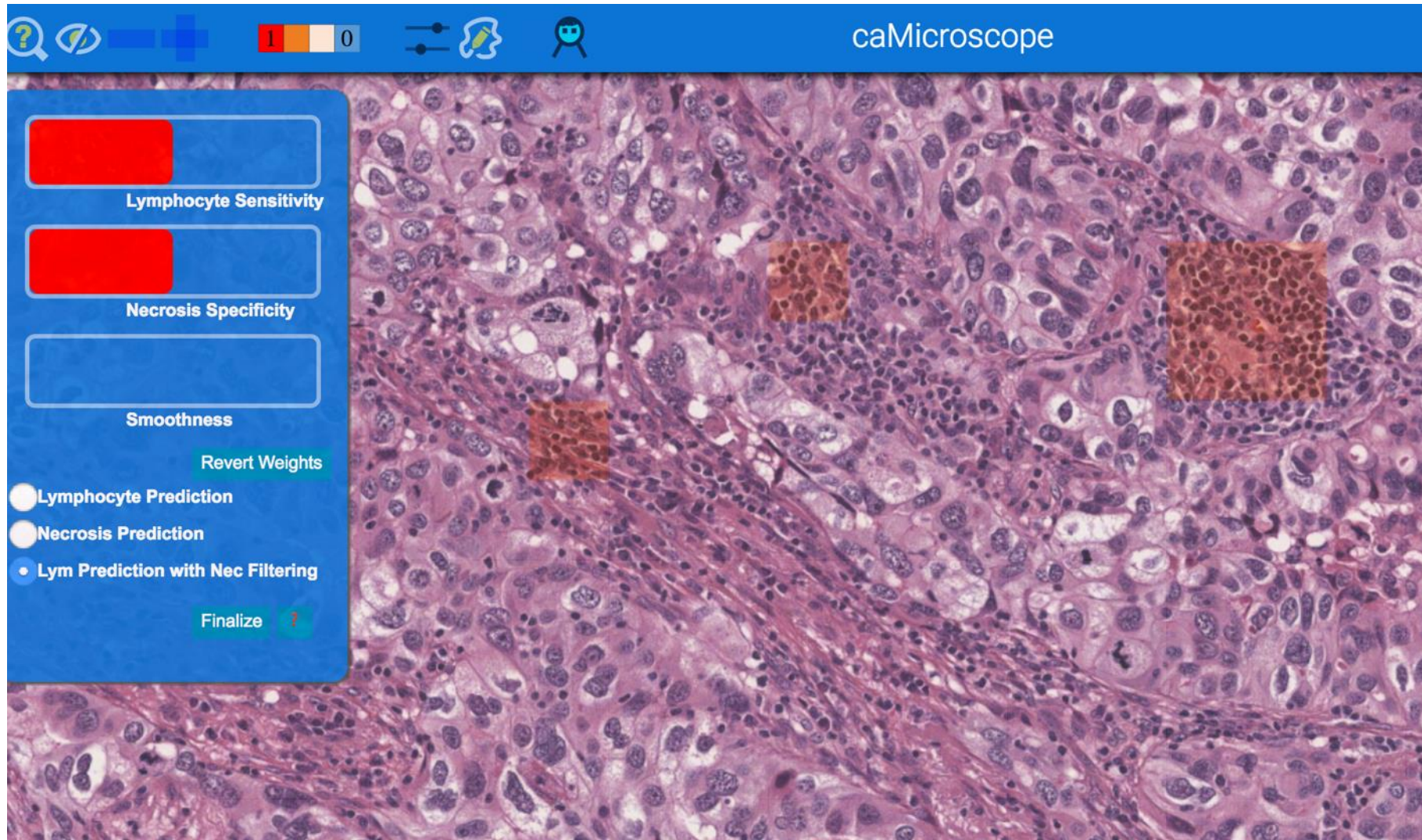


TIL Maps for Clustering and Analysis

Tools: Quantitative Imaging Pathology - QuIP Tool Set



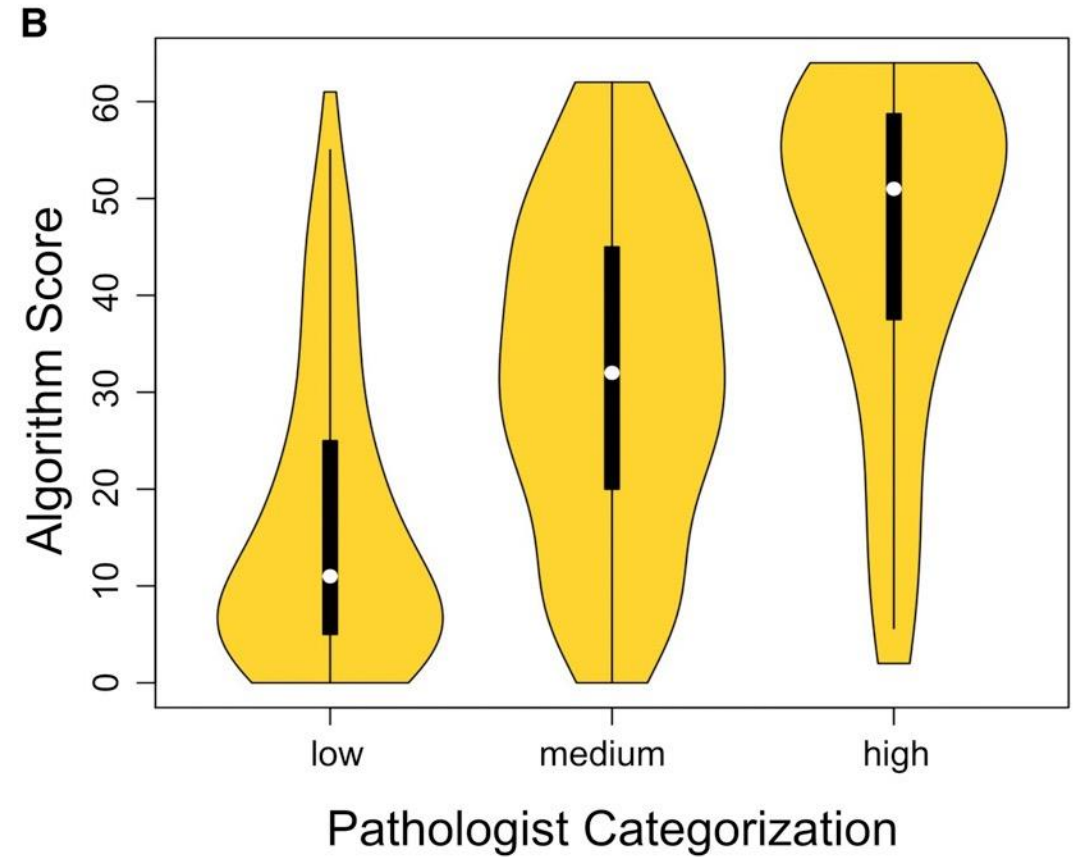
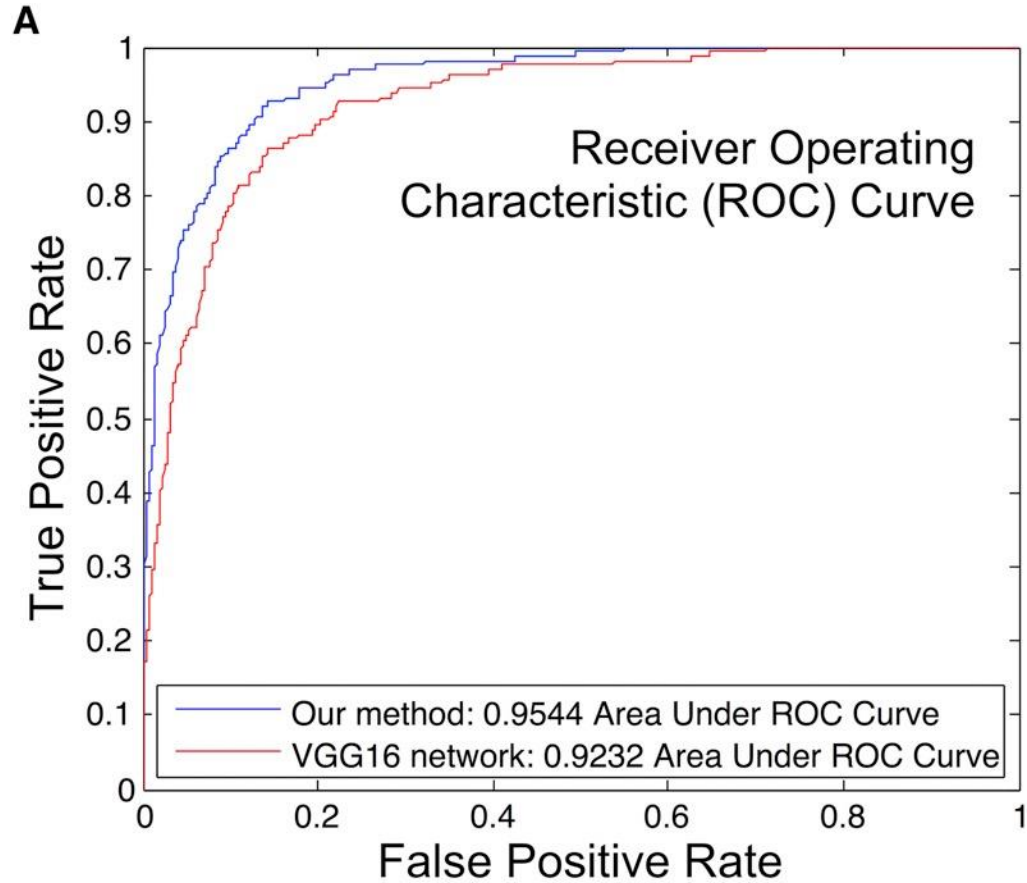
Interactive Deep Learning Training Tool



The screenshot displays the caMicroscope interface. At the top, a blue header bar contains a navigation menu with icons for help, zoom, pan, a color calibration bar (labeled '1' and '0'), a brush tool, and a user profile icon. The text 'caMicroscope' is positioned on the right side of this bar. The main area is a histology image with several regions highlighted in brown, indicating predicted areas of interest. On the left, a blue sidebar contains three progress bars: 'Lymphocyte Sensitivity' (filled with red), 'Necrosis Specificity' (filled with red), and 'Smoothness' (empty). Below these are three radio buttons: 'Lymphocyte Prediction' (unselected), 'Necrosis Prediction' (unselected), and 'Lym Prediction with Nec Filtering' (selected). At the bottom of the sidebar are two buttons: 'Revert Weights' and 'Finalize ?'.

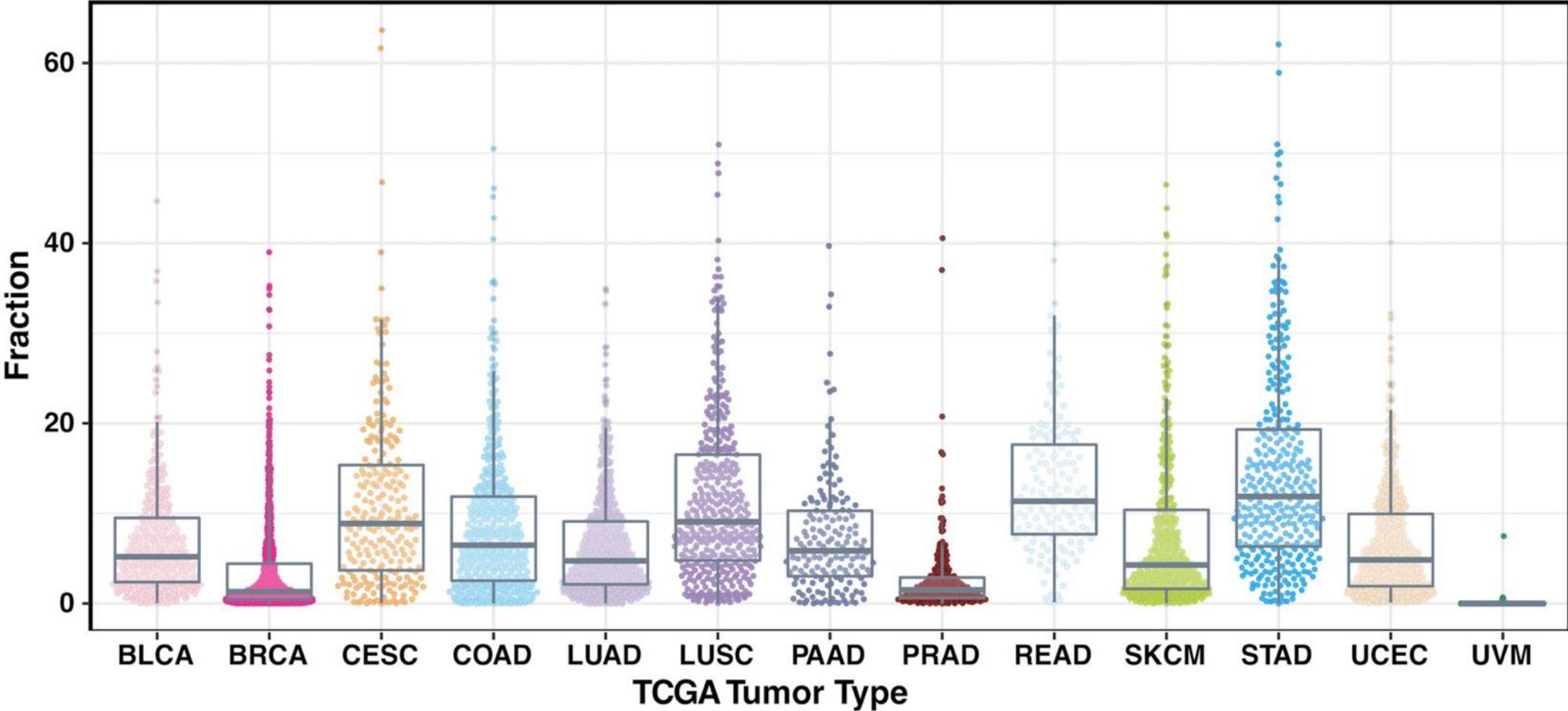
Validation – Stratified sampling from 5K whole slide images

Arvind Rao, expert in spatial biostatistics (U Michigan)



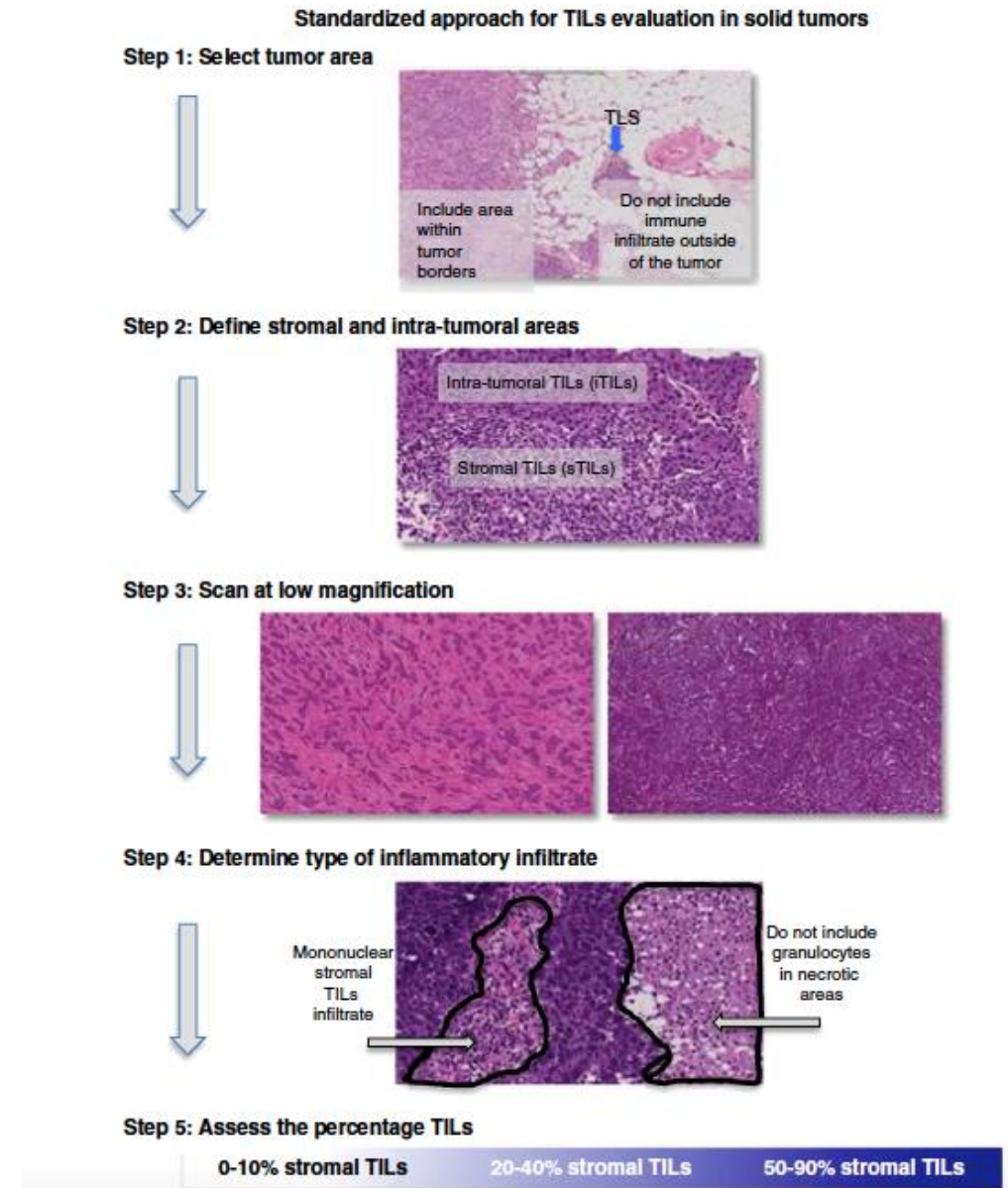
Quantitative Assessment of TIL Fractions

A

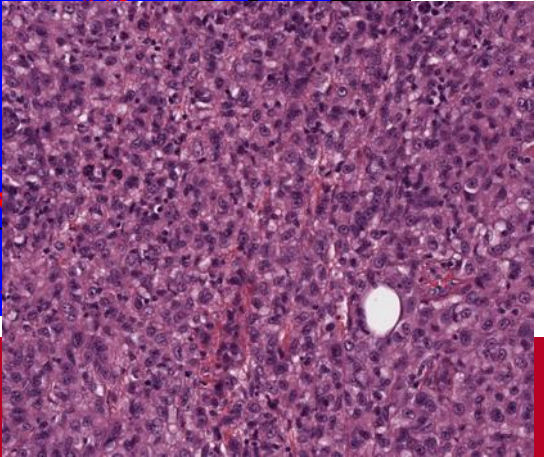
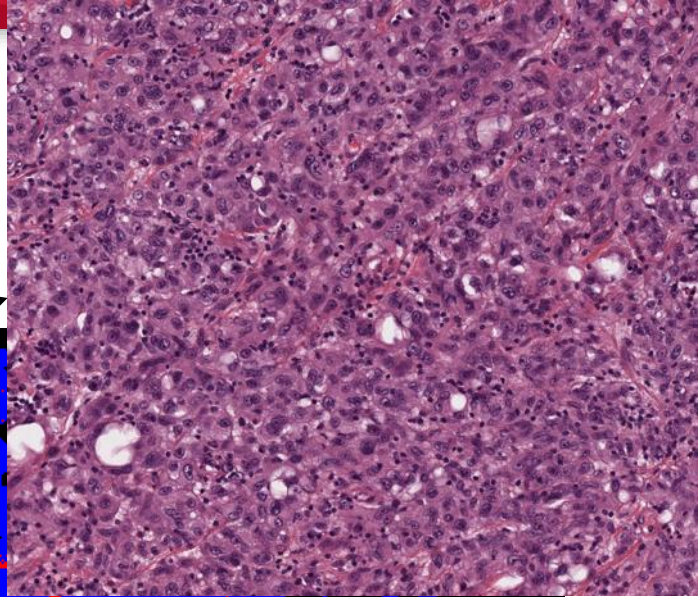
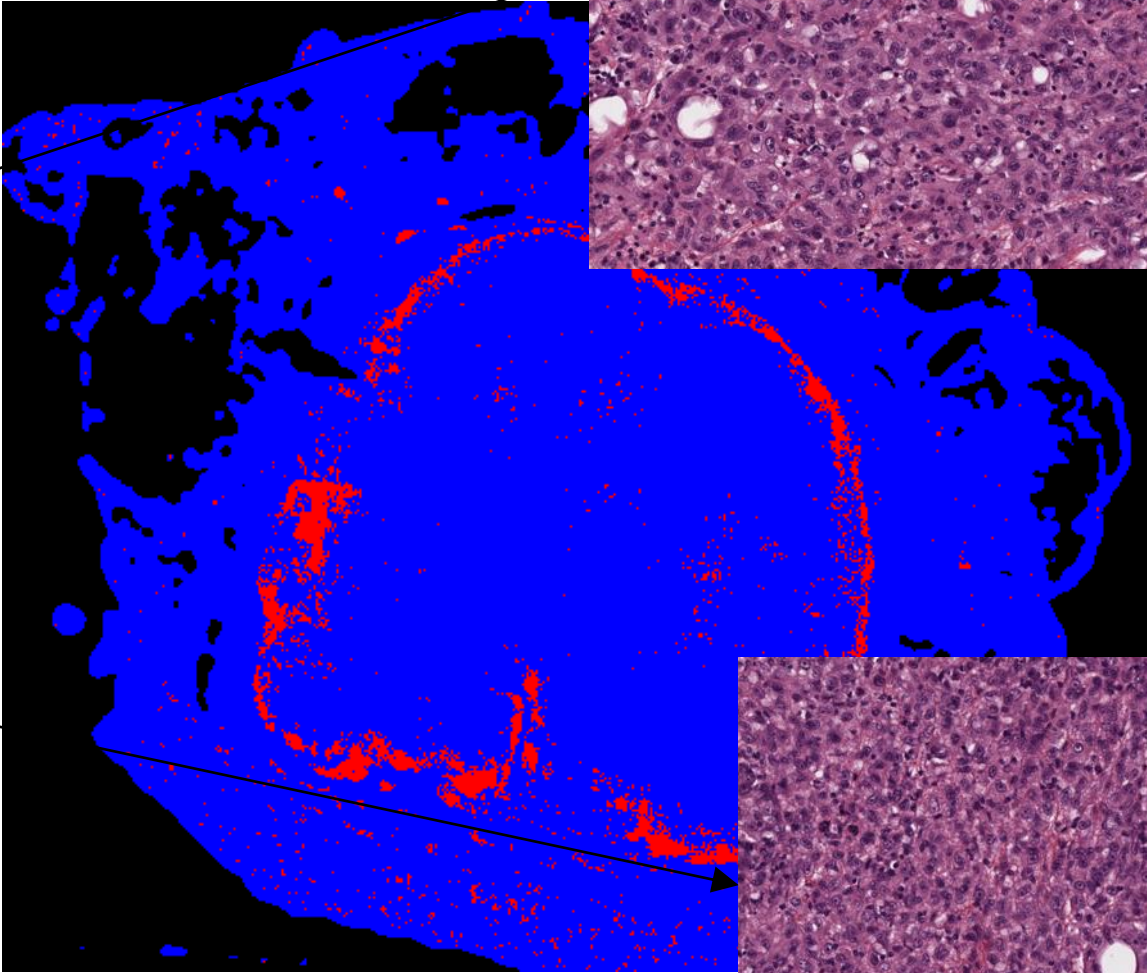
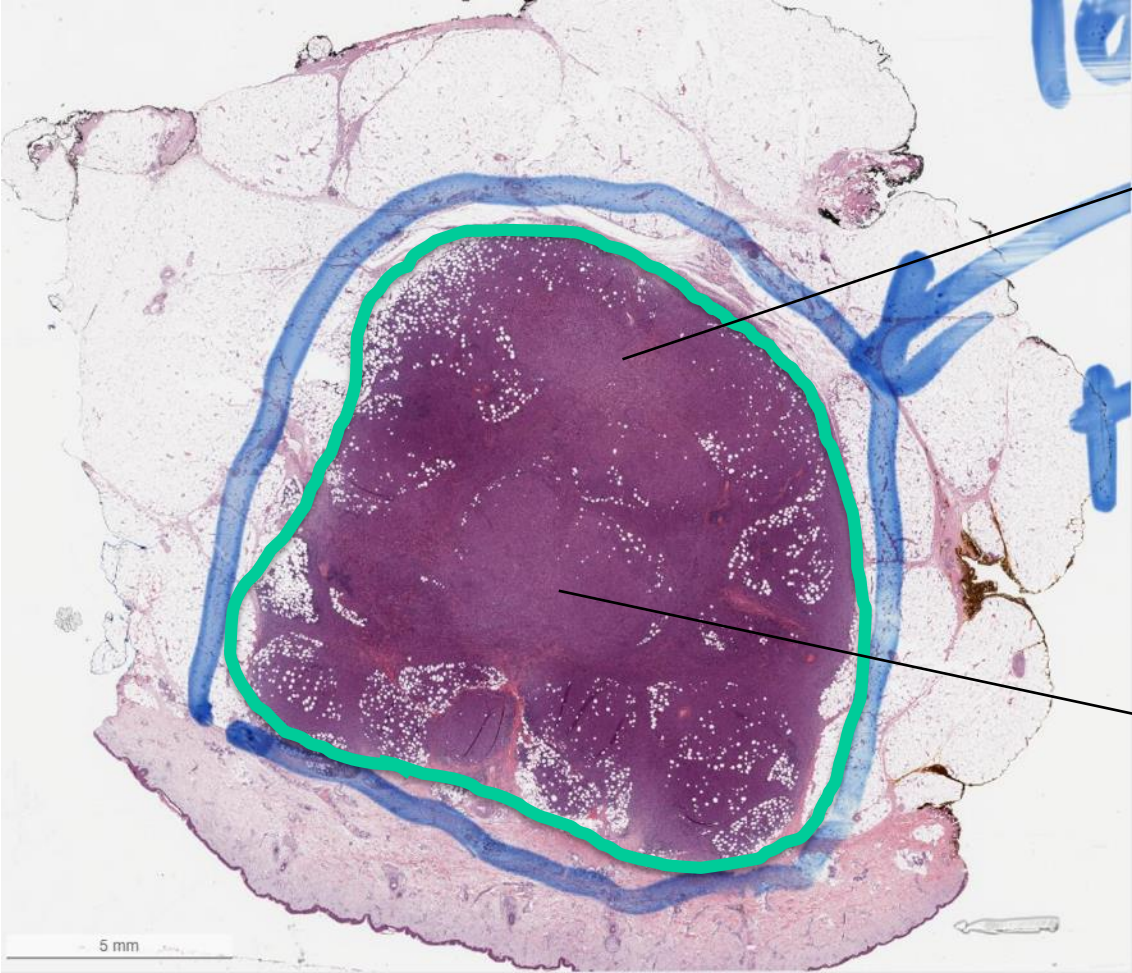


Characterization of TIL Pattern and Relationship to Molecular Immune Subtype

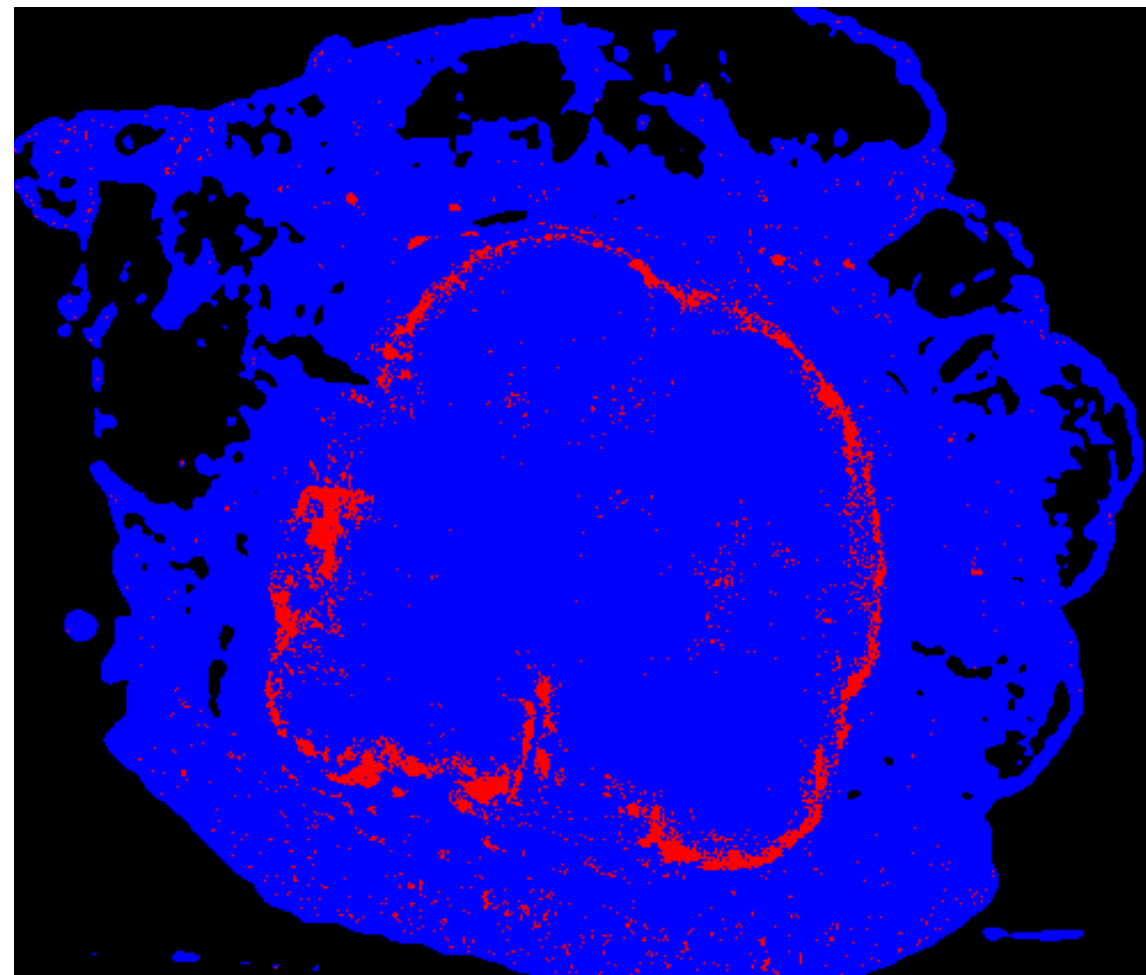
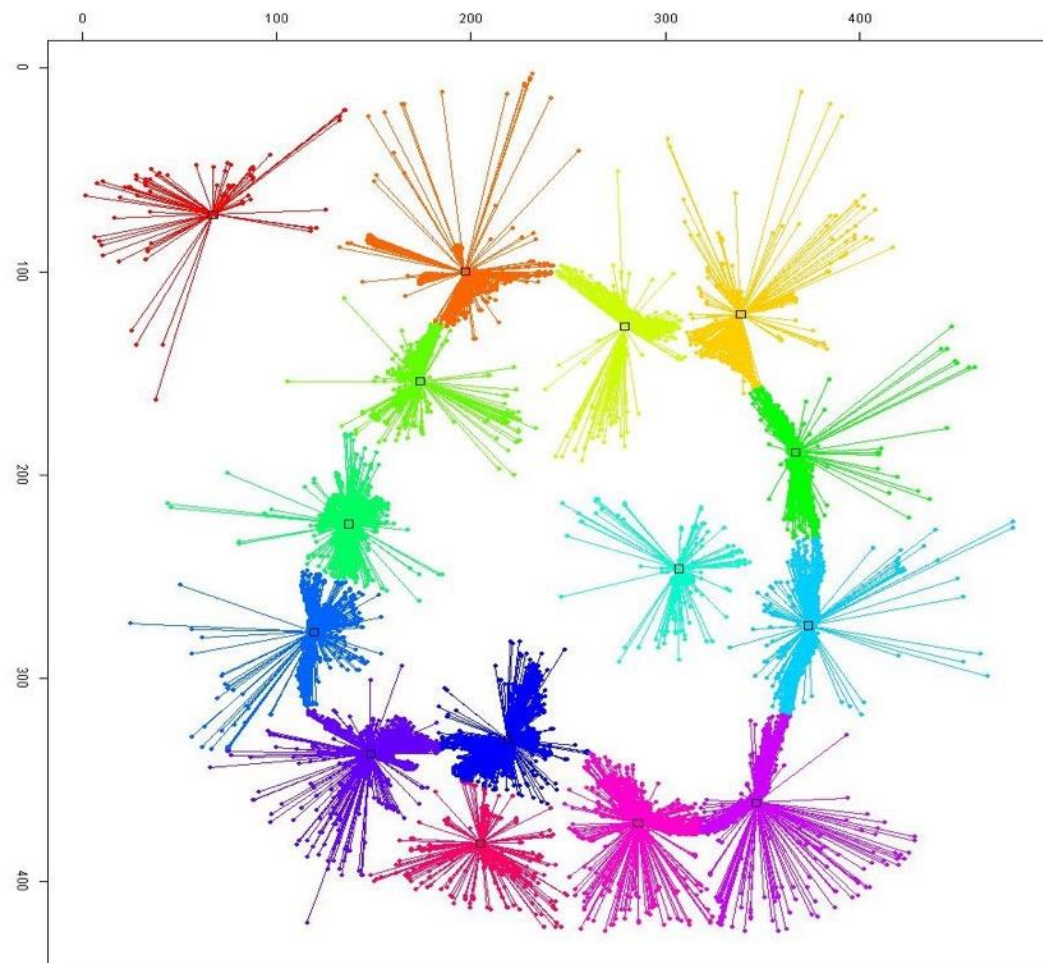
- The **pattern** of immune infiltrate
- Division of immune infiltrate between different compartments
- Does it surround tumor region? Present in tumor, invasive margin?
- Assessing Tumor-infiltrating Lymphocytes in Solid Tumors:
- A Practical Review for Pathologists and Proposal for a Standardized Method From the International Immunooncology Biomarkers Working Group – part 1 and 2 - Adv Anat Pathol Volume 24, Number 5, September 2017 (figure to right from that reference)



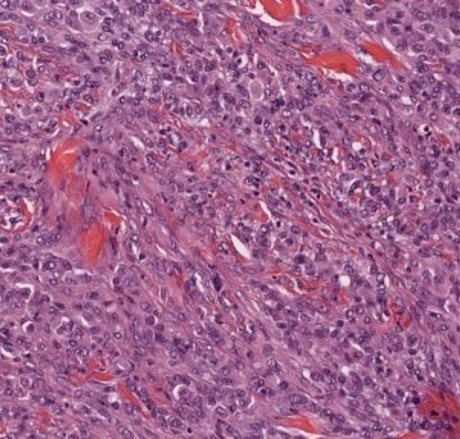
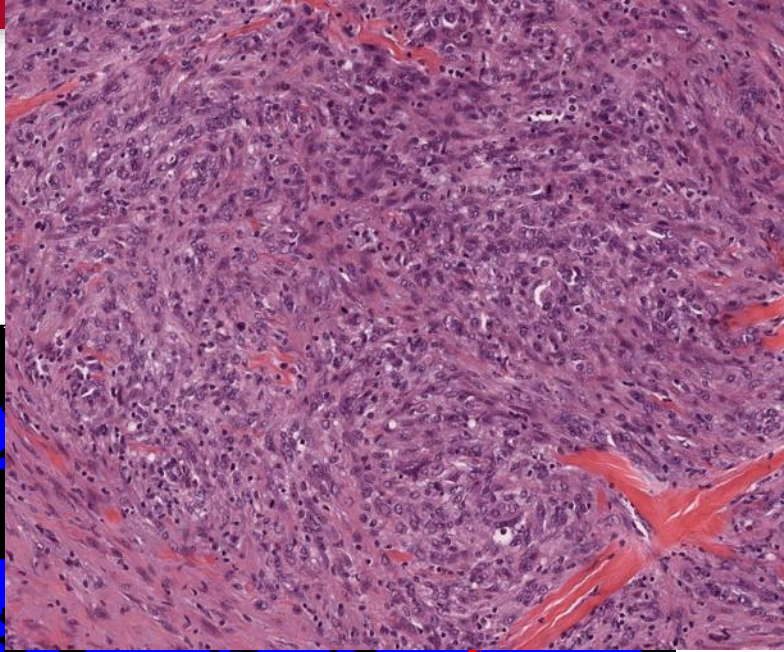
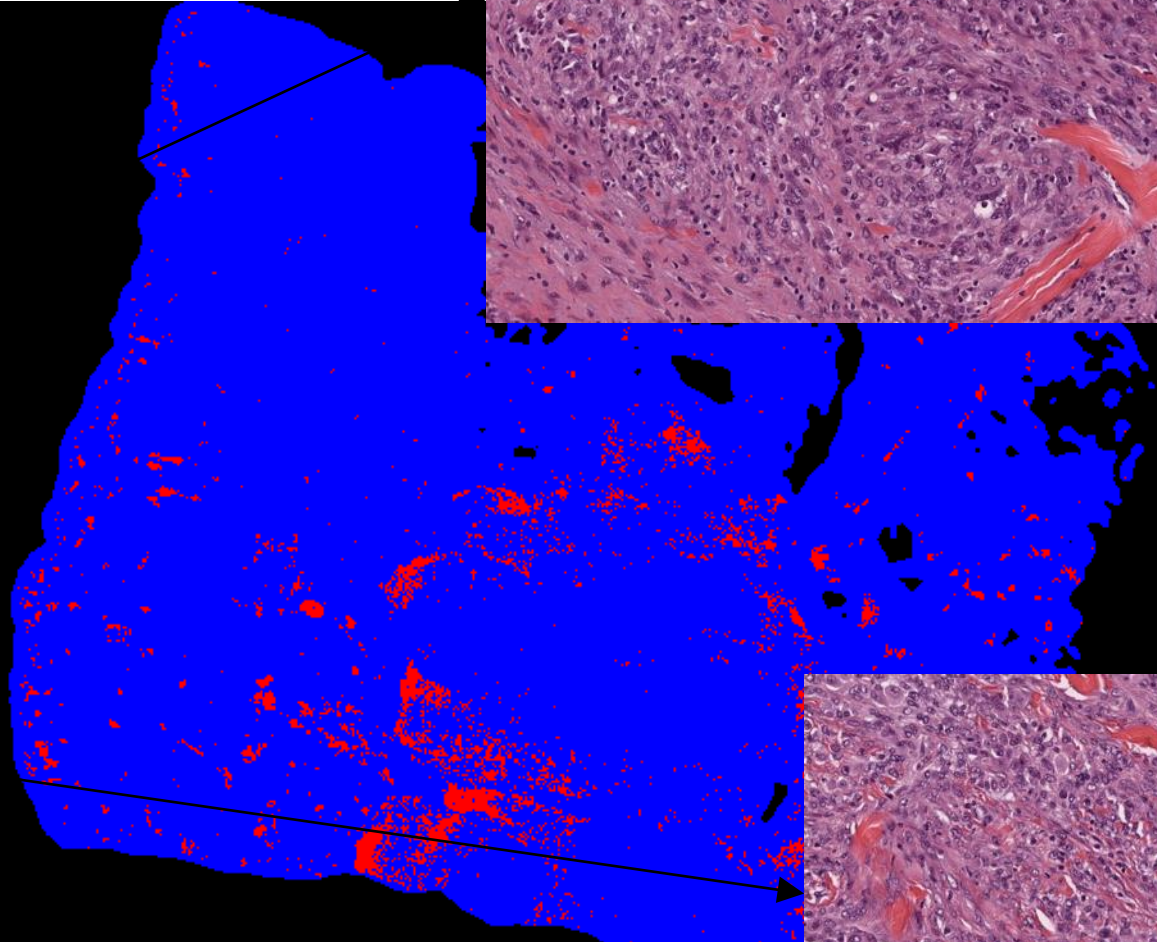
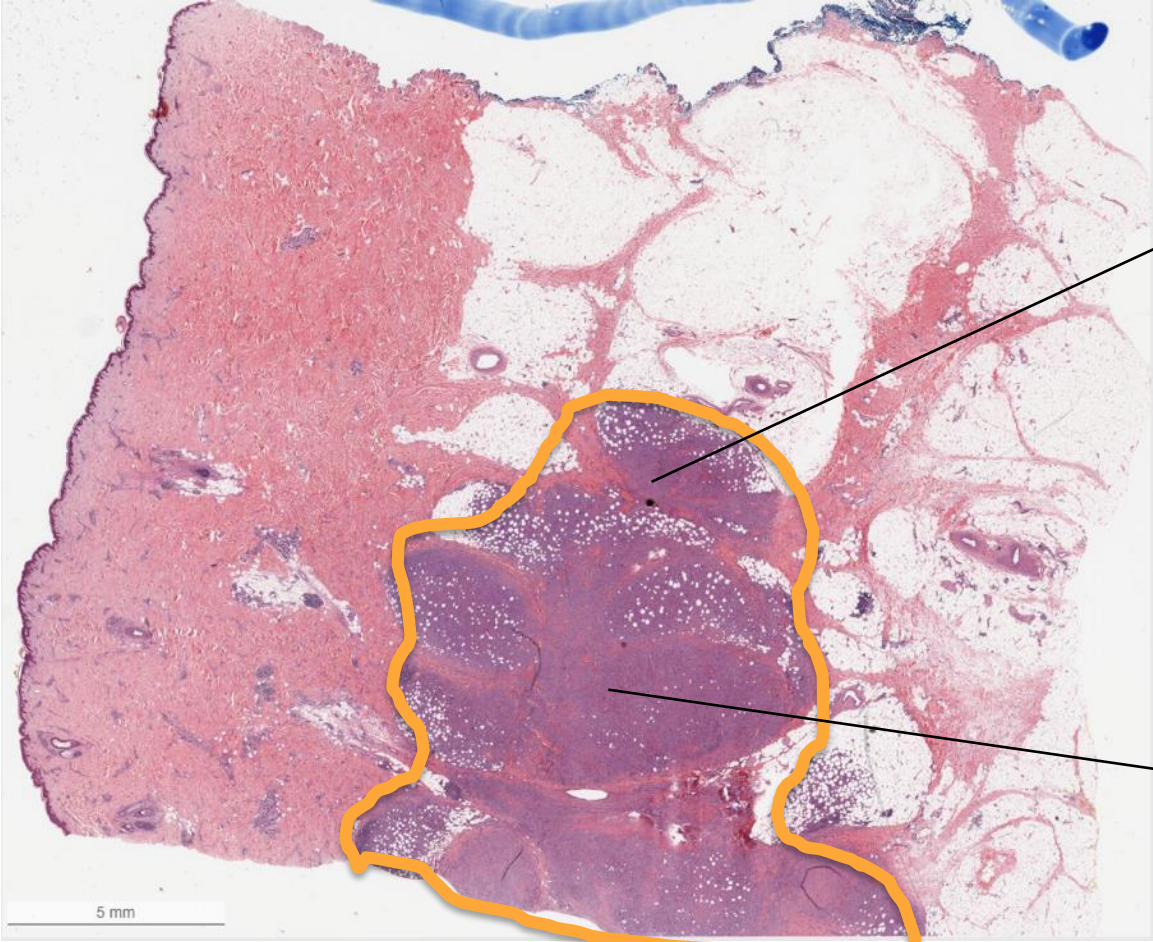
SKCM TCGA-D3-A2JF-06Z-00-DX1



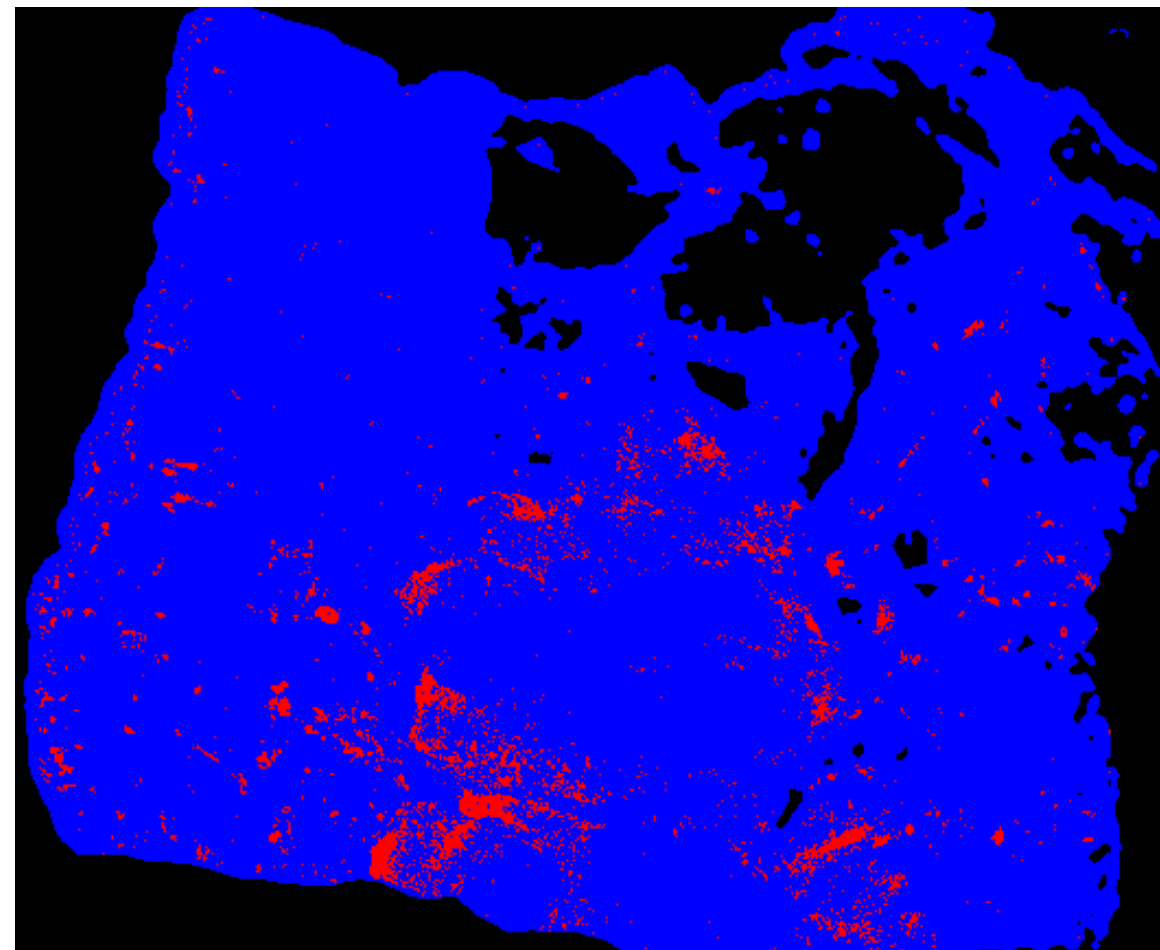
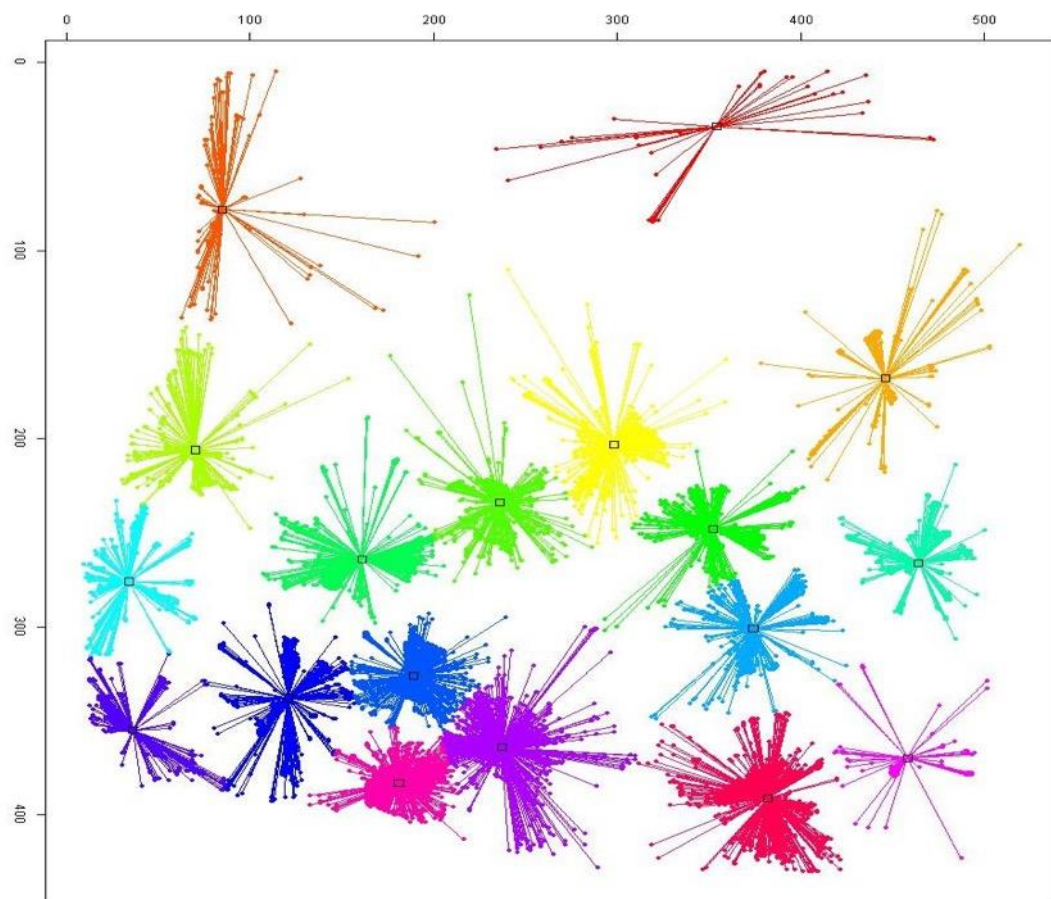
SKCM TCGA-D3-A2JF-06Z-00-DX1



SKCM TCGA-D3-A2JA-06Z-00-DX1



SKCM TCGA-D3-A2JA-06Z-00-DX1



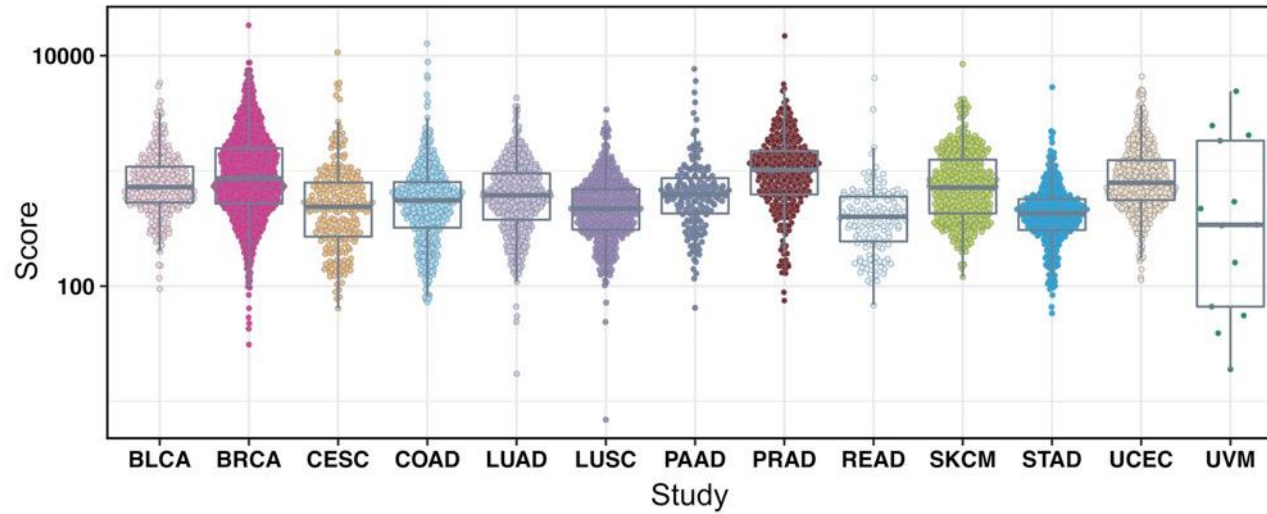
TIL Pattern Descriptions

Qualitative (Alex Lazar, Raj Gupta)

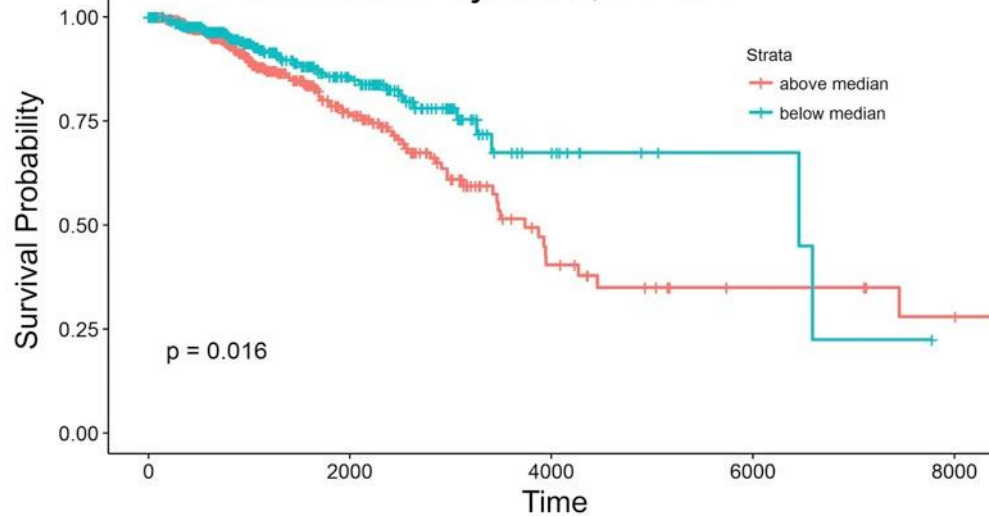
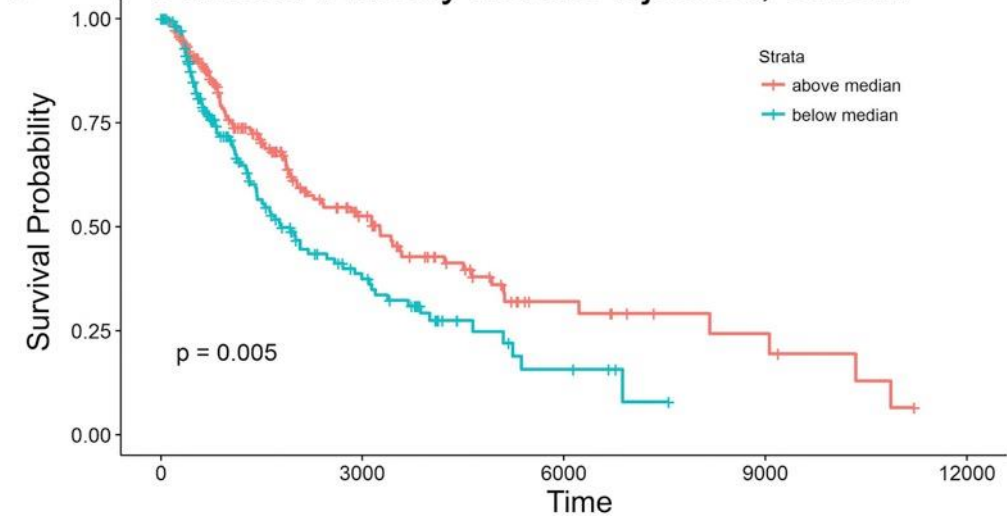
- **“Brisk, diffuse”** diffusely infiltrative TILs scattered throughout at least 30% of the area of the tumor (1,856 cases);
- **“Brisk, band-like”** - band-like boundaries bordering the tumor at its periphery (1,185);
- **“Nonbrisk, multi-focal”** loosely scattered TILs present in less
- than 30% but more than 5% of the area of the tumor (1,083);
- **“Non-brisk, focal”** for TILs scattered throughout less than 5% but greater than 1% of the area of the tumor (874);
- **“None”** < 1% TILS - in 143 cases

Quantitative – Arvind Rao

- Agglomerative clustering
- Cluster indices representing cluster number, density, cluster size, distance between clusters
- Traditional spatial statistics measures
- R package clusterCrit by Bernard Desgraupes - Ball-Hall, Banfield-Raftery, C Index, and Determinant Ratio indices

A Ball-Hall Index by Tumor Type

B

| Index | Tumor Type | p-value |
|---------------------------|------------|----------|
| Ball Hall Adjusted | BRCA | 0.007223 |
| C index Adjusted | LUAD | 0.002552 |
| Banfield Raftery Adjusted | PRAD | 0.013075 |
| Det Ratio Adjusted | PRAD | 0.012113 |
| Banfield Raftery Adjusted | SKCM | 0.001349 |

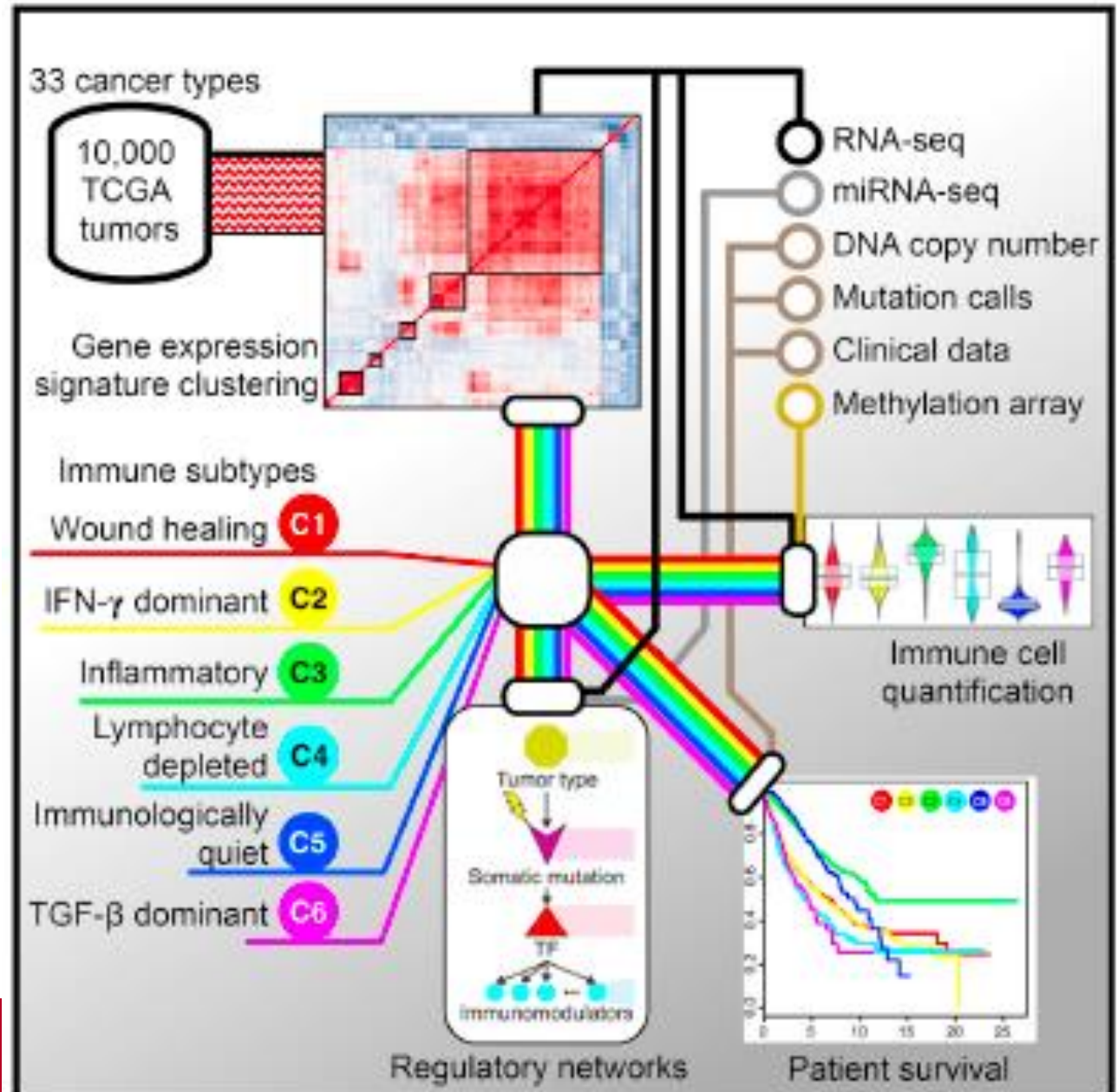
C Ball-Hall Index Adjusted, BRCA

D Banfield-Raftery Index Adjusted, SKCM


Immunity

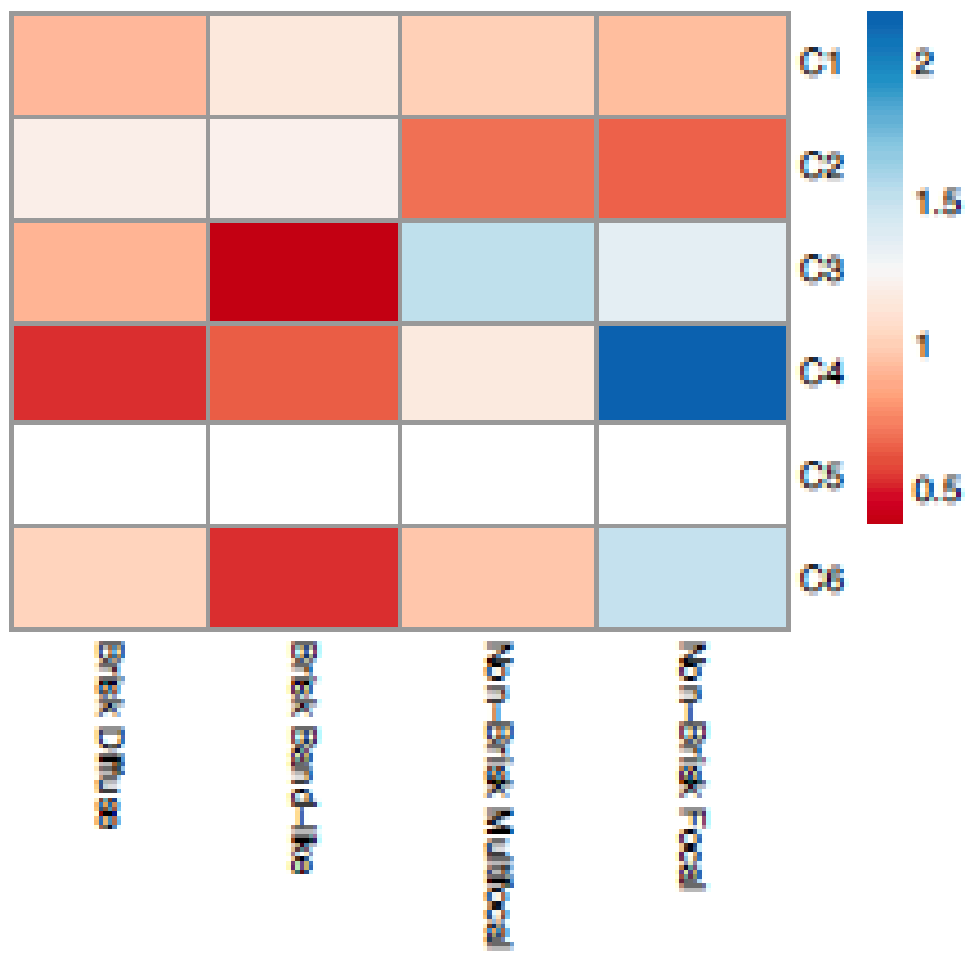
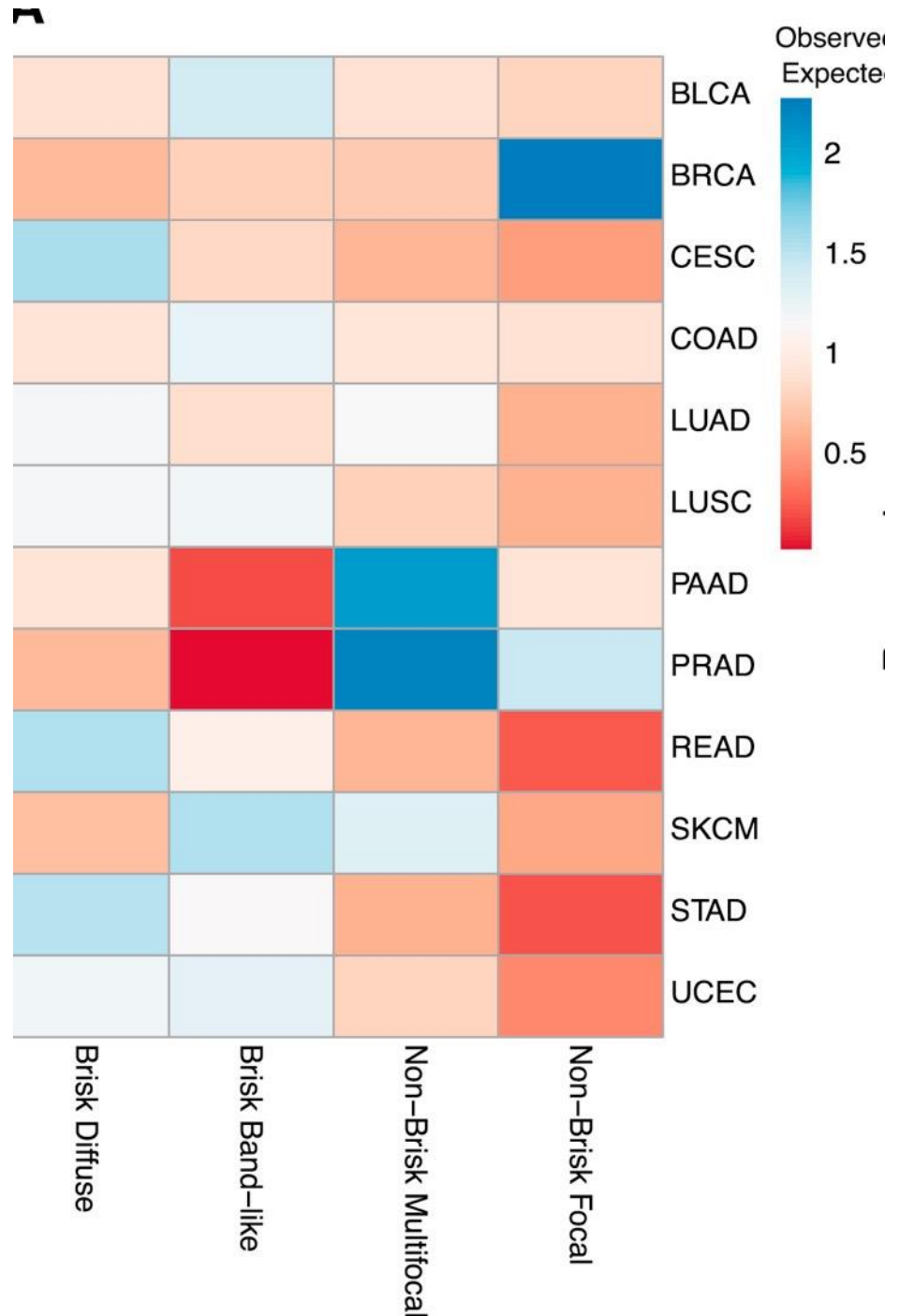
The Immune Landscape of Cancer

- Six identified immune subtypes span cancer tissue types and molecular subtypes
- Immune subtypes differ by somatic aberrations, microenvironment, and survival
- Multiple control modalities of molecular networks affect tumor-immune interactions
- These analyses serve as a resource for exploring immunogenicity across cancer types

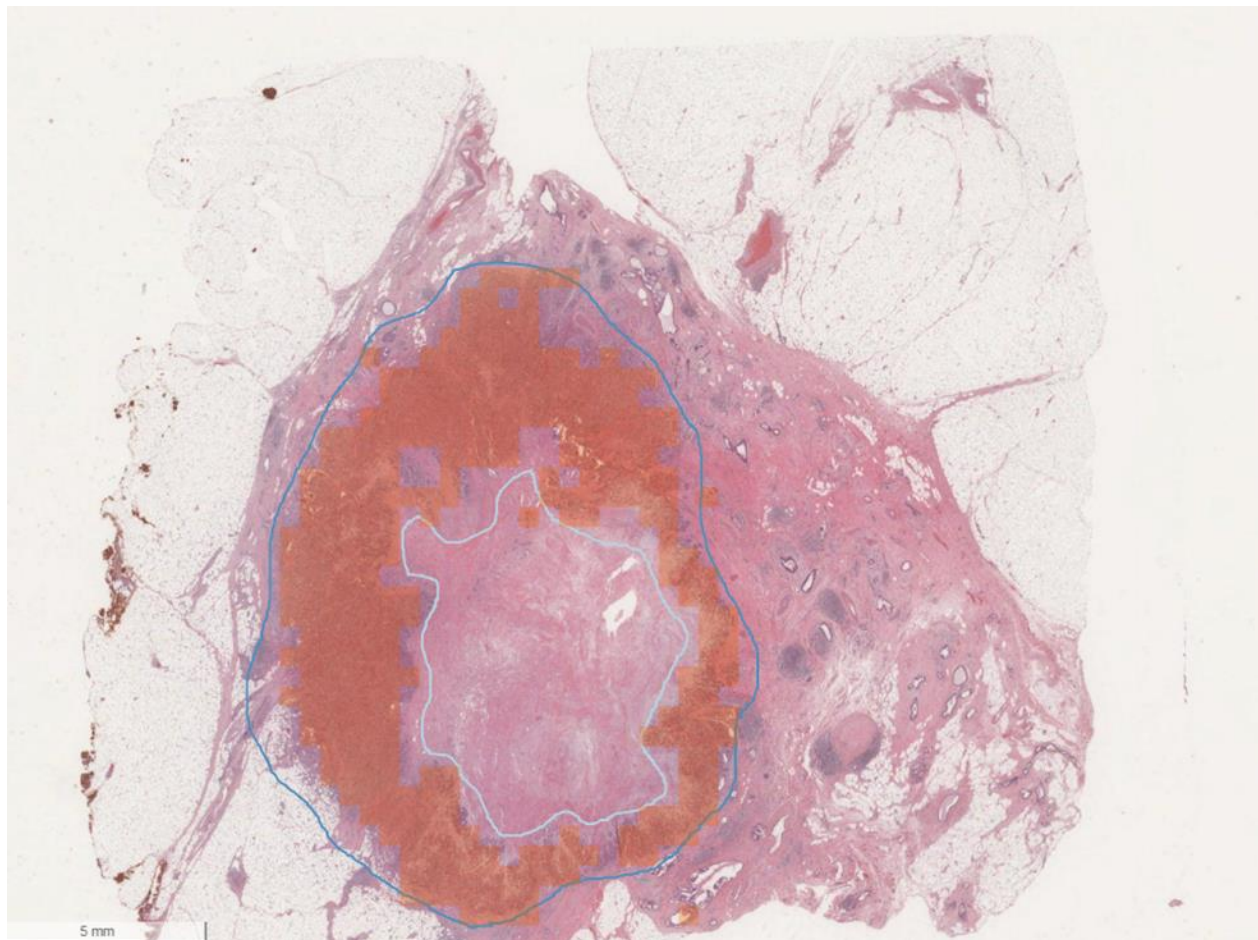
[http://www.cell.com/immunity/fulltext/S1074-7613\(18\)30121-3](http://www.cell.com/immunity/fulltext/S1074-7613(18)30121-3)



Spatial Patterns vs TCGA Tumor, Molecular Subtypes

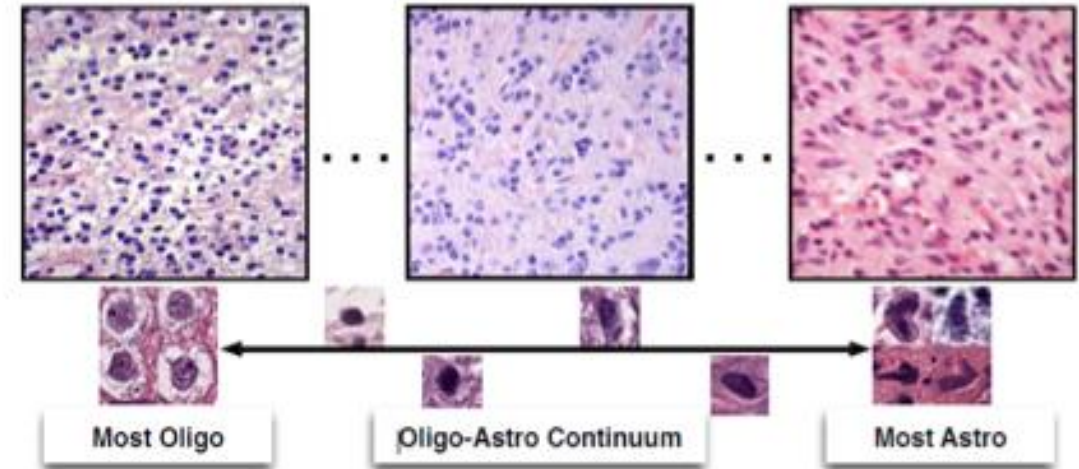


New Results: CNN – Tumor Segmentation

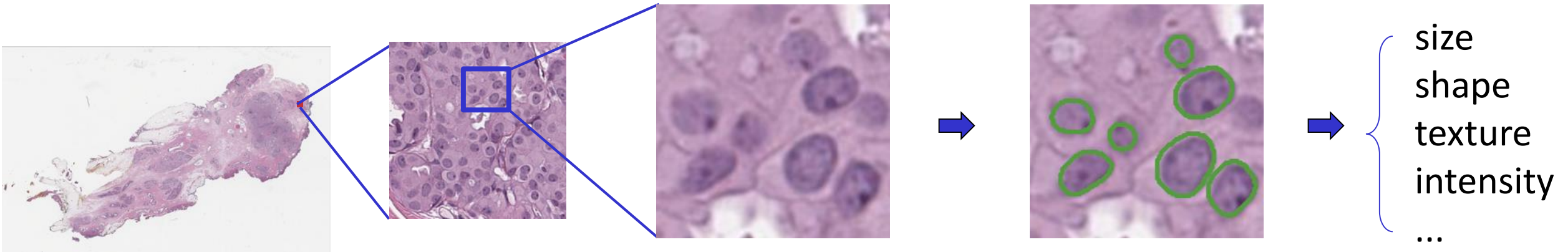


Pathomics – Nuclear Features

- Cell morphology and architectural patterns of tumor growth are critical in cancer diagnosis
- The nucleus-level features, such as size, shape and intensity, are used in cancer diagnosis and classification of cancer subtypes



Nuclear Pathomics Features

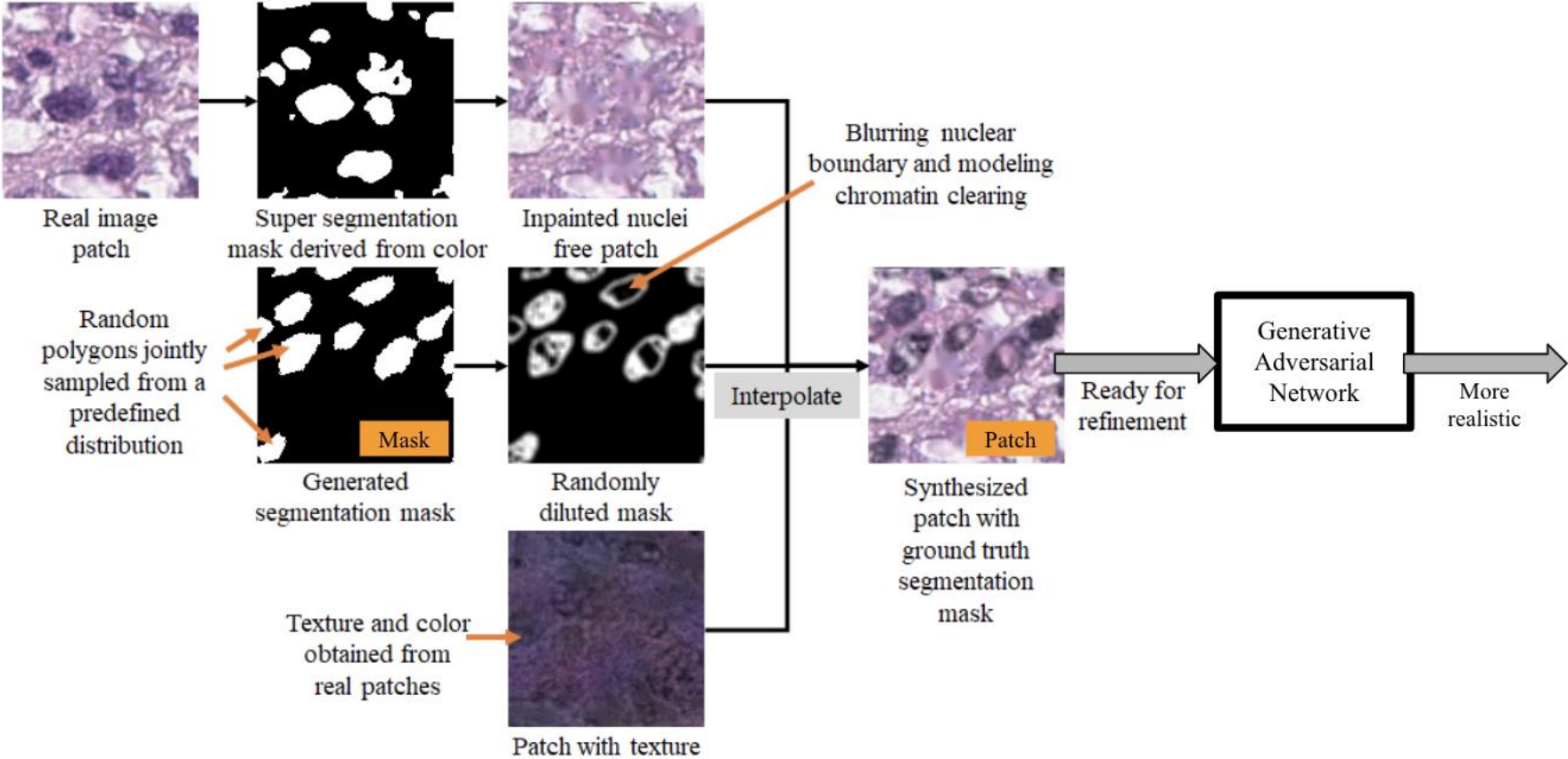


- H&E stained tissue slides: Nuclei are colored blue/purple
- Nucleus segmentation is applied to delineate the boundary of the nuclei
- Nucleus-level features are extracted from segmented object for downstream quantitative analyses

Nuclear Segmentation/Labeling Methods Development

- Baseline – traditional numerical methods: level set/mean shift
- Convolutional Neural Network nuclear segmentation algorithms
- GAN based CNN nuclear segmentation algorithm designed to minimize training requirements
- Deep learning based nuclear classification methods

Deep Learning: Synthetic Tissue/GAN based Nuclear Segmentation Algorithm



Using Machine Learning to Critique Segmentation Results

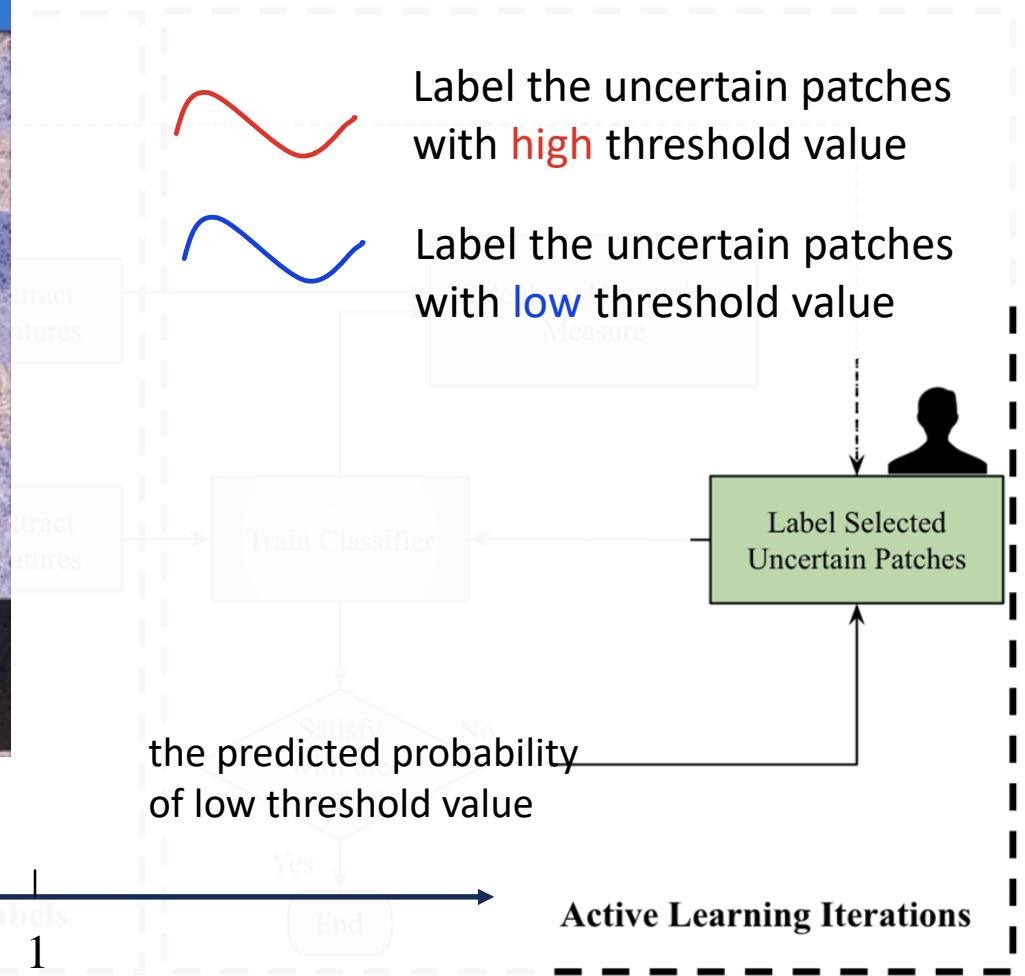
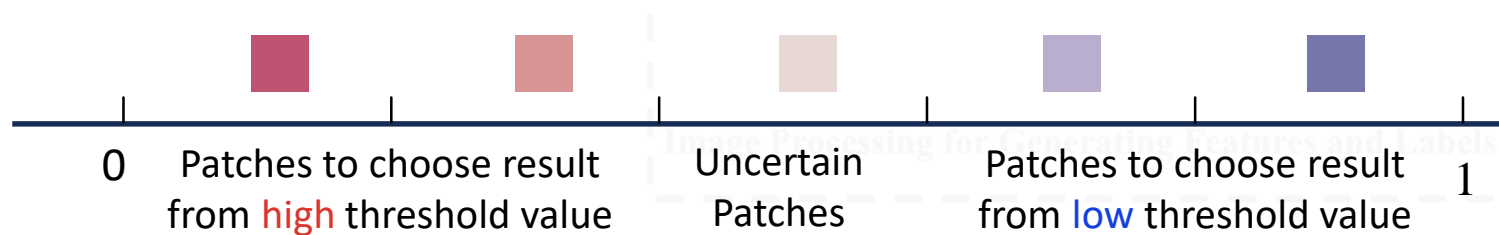
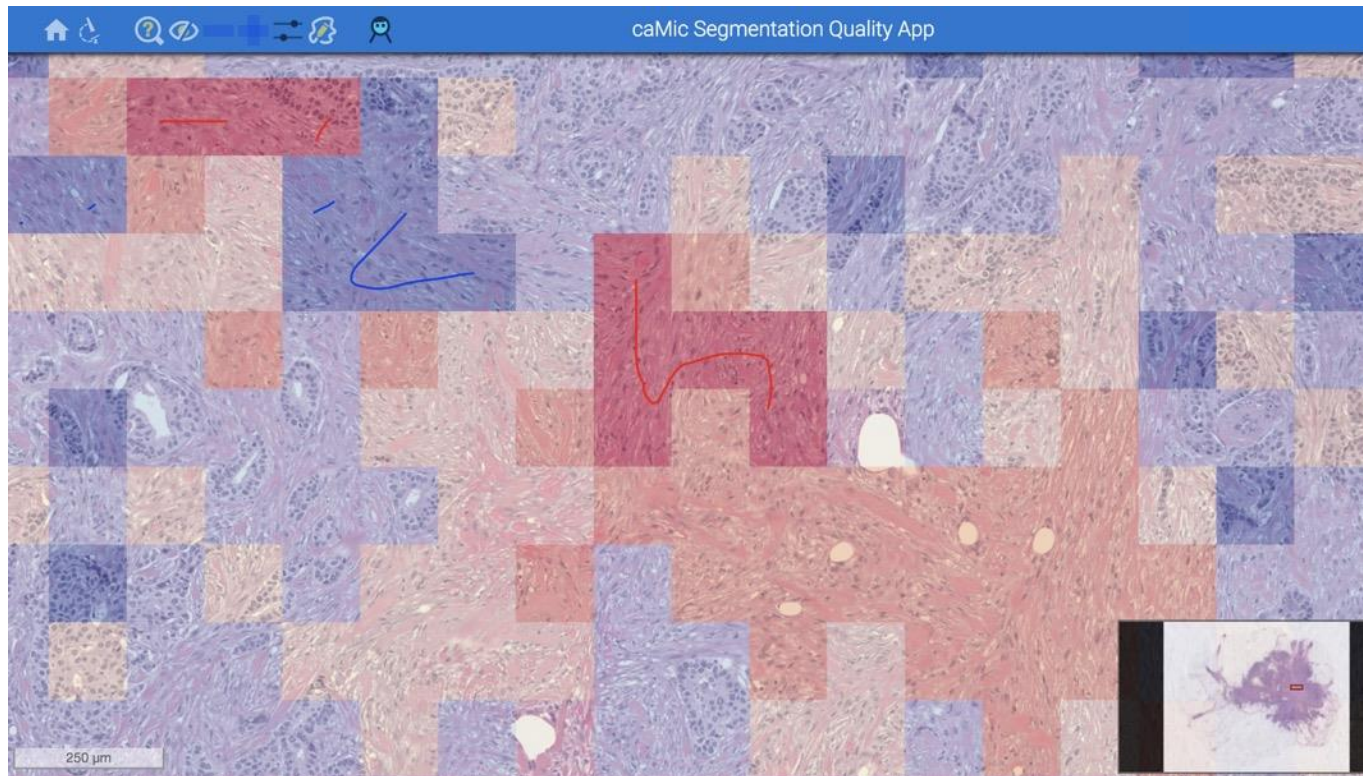
- Automatically select **low & high gain values** for each tissue region

- Investigate **machine learning algorithms**:
 - Random Forests
 - Support Vector Machine
 - Convolutional Neural Network

- Investigate impact of **active learning process**

- **PhD Thesis – Si Wen co supervised by Joel Saltz and Tahsin Kurc**

ACTIVE Learning



- NCI Quantitative Imaging for Pathology (QuIP): Stony Brook, Emory, MD Anderson, Institute for Systems Biology, Oak Ridge
- NCI SEER Pathology: Stony Brook, Emory, Rutgers, University of Kentucky (three Cancer registries)
- Cancer Imaging Archive: Arkansas, Stony Brook, Emory (Stony Brook leads Pathology component)
- Virtual Tissue Repository: Led by NCI SEER; Stony Brook, Emory
- TIES Research Network - Integrated Pathology text and imaging: Pittsburgh, Stony Brook main sites, 6+ other sites (Stony Brook leads digital Pathology)

Tools to Analyze Morphology and Spatially Mapped Molecular Data - U24 CA180924

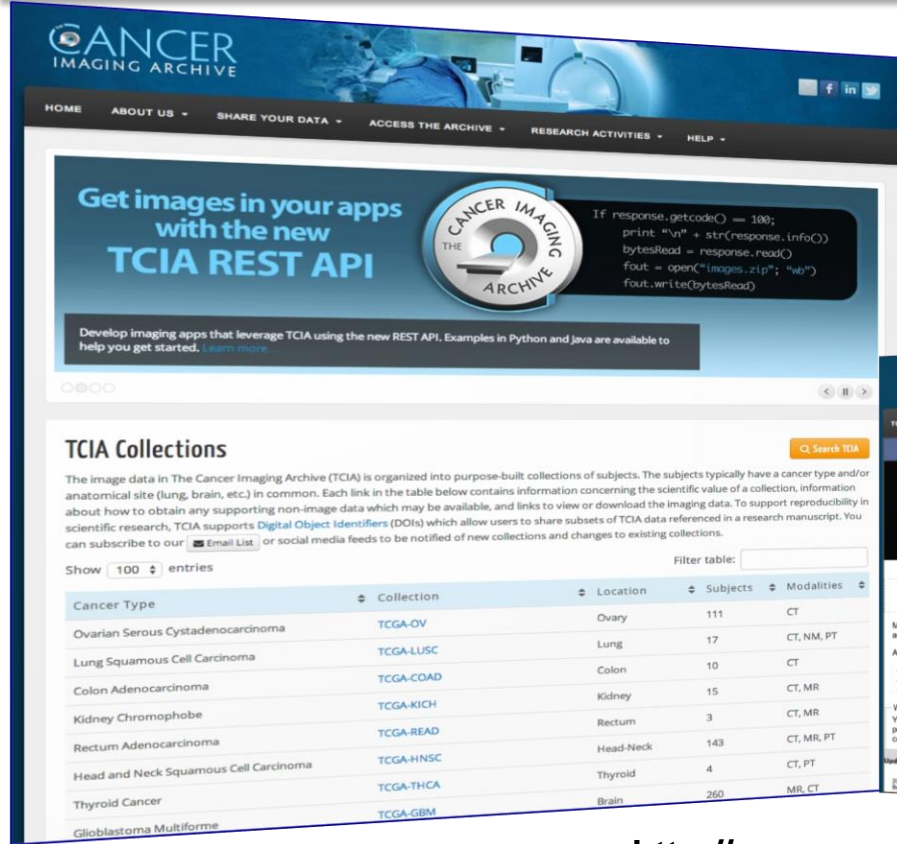
- **Specific Aim 1** Analysis **pipelines** for multi-scale, integrative image analysis.
- **Specific Aim 2: Database** infrastructure to manage and query Pathomics features.
- **Specific Aim 3:** HPC software that **targets clusters, cloud computing, and leadership scale systems.**
- **Specific Aim 4:** Develop **visualization** middleware to relate Pathomics feature and image data and to integrate Pathomics image and “omic” data.

Methods and tools for integrating pathomics data into cancer registries

Saltz, Sharma, Foran and Durban

- Enhance SEER registry data with machine learning based classifications and quantitative pathomics feature sets.
- The New Jersey State Cancer Registry, Georgia and Kentucky State Cancer Registries
- Prostate Cancer, Lymphoma and NSCLC
- Repository of high-quality digitized pathology images for subjects whose data is being collected by the registries.
- Extract computational features and establish deep linkages with registry data, thus enabling the creation of information-rich, population cohorts containing objective imaging and clinical attributes

Cancer Imaging Archive – Integration of Pathology and Radiology for Community Clinical Studies

Get images in your apps with the new TCIA REST API

```

    IF response.getStatusCode() == 100;
    print "\n" + str(response.info())
    bytesRead = response.read()
    fout = open("images.zip", "wb")
    fout.write(bytesRead)
  
```

Develop imaging apps that leverage TCIA using the new REST API. Examples in Python and Java are available to help you get started. [Learn more](#)

TCIA Collections

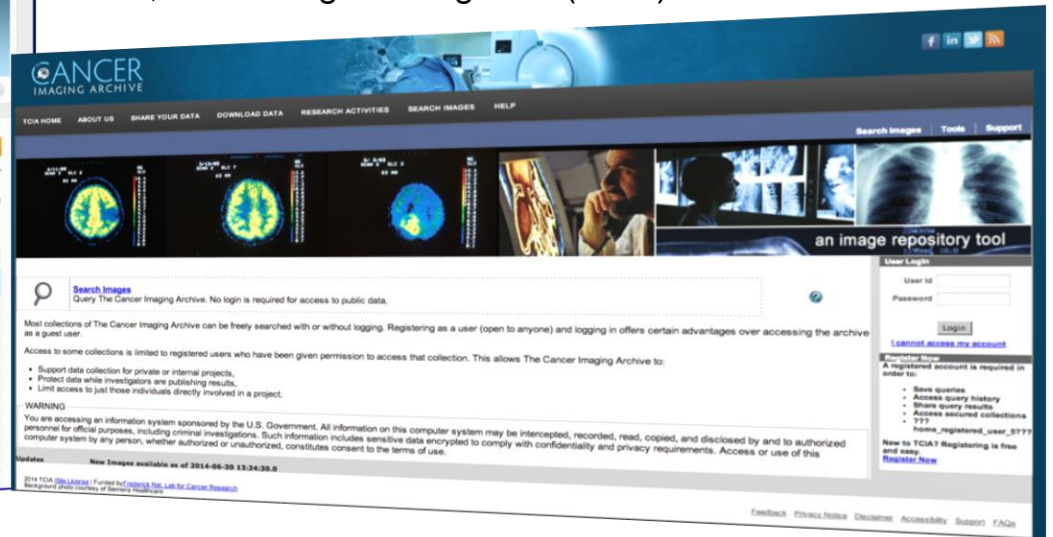
The image data in The Cancer Imaging Archive (TCIA) is organized into purpose-built collections of subjects. The subjects typically have a cancer type and/or anatomical site (lung, brain, etc.) in common. Each link in the table below contains information concerning the scientific value of a collection, information about how to obtain any supporting non-image data which may be available, and links to view or download the imaging data. To support reproducibility in scientific research, TCIA supports Digital Object Identifiers (DOIs) which allow users to share subsets of TCIA data referenced in a research manuscript. You can subscribe to our [Email List](#) or social media feeds to be notified of new collections and changes to existing collections.

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| Cancer Type | Collection | Location | Subjects | Modalities |
|---------------------------------------|------------|-----------|----------|------------|
| Ovarian Serous Cystadenocarcinoma | TCGA-OV | Ovary | 111 | CT |
| Lung Squamous Cell Carcinoma | TCGA-LUSC | Lung | 17 | CT, NM, PT |
| Colon Adenocarcinoma | TCGA-COAD | Colon | 10 | CT |
| Kidney Chromophobe | TCGA-KICH | Kidney | 15 | CT, MR |
| Rectum Adenocarcinoma | TCGA-READ | Rectum | 3 | CT, MR |
| Head and Neck Squamous Cell Carcinoma | TCGA-HNSC | Head-Neck | 143 | CT, MR, PT |
| Thyroid Cancer | TCGA-THCA | Thyroid | 4 | CT, PT |
| Glioblastoma Multiforme | TCGA-GBM | Brain | 260 | MR, CT |

TCIA encourages and supports the cancer imaging open science community by hosting and managing **Findable Accessible, Interoperable, and Reusable (FAIR)** images and related data.

Clark, et al. J Digital Imag 26.6 (2013): 1045-1057.



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2014 TCIA (PIL) Logo Funded by NCI/NIH, NIH, Lab for Cancer Research
 Background photo courtesy of Stony Brook University

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<http://www.cancerimagingarchive.net/>

TCIA sustainment and scalability

Platforms for quantitative imaging informatics in precision medicine

Prior, Saltz, Sharma -- U24CA215109-01

- Identify quantitative imaging phenotypes across scale through the use of Radiomic/Pathomic analyses
- Well-curated data for algorithm testing and validation.
- Integrative Radiology/Pathology Image-Omics studies
- Extend TCIA to support its rapidly growing user community and continue to promote research reproducibility and data reuse in cancer precision medical research.

Thanks!



Now this is not the end. It is not even the beginning of the end. But it is, perhaps, the end of the beginning.

(Winston Churchill)

izquotes.com

ITCR Team

Stony Brook University

Joel Saltz
Tahsin Kurc
Yi Gao
Allen Tannenbaum
Erich Bremer
Jonas Almeida
Alina Jasniewski
Fusheng Wang
Tammy DiPrima
Andrew White
Le Hou
Furqan Baig
Mary Saltz
Raj Gupta

Emory University

Ashish Sharma
Adam Marcus

Oak Ridge National Laboratory

Scott Klasky
Dave Pugmire
Jeremy Logan

Yale University

Michael Krauthammer

Harvard University

Rick Cummings

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