## Extreme Scale, Tissue Analytics and Al

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> Workshop on Clusters, Clouds, and Data for Scientific Computing September 2022

# **Application Challenges**

- Al Pathologist: Answer nuanced questions about patients and disease categories
- Big Picture Clinical Goal: Predict outcome and response to treatment using all available image, clinical, molecular data

# Answers to Nuanced Questions

- Difficult cases require involved back and forth discussions
- Current AI methods select between a small number of alternatives
- New AI methods should be able to select between hundreds of alternatives and to provide nuanced reasoning with visual and verbal examples



## **Applications context – Cancer**





**Slide Scanner – GT450** – Roughly 1 minute to acquire a (roughly) 10 Gigapixel image

**Tray of glass slides** – generally a Pathologist needs to examine many slides for each patient

# Example GBM (Brain Tumor) Image



## Brain Tumor Classification – CVPR 2016



## **Combining Information from Patches**



## **Brain Tumor Classification Results**

#### Methods Accuracy

VGG16 features + BoW + SVM	0.667
Patch-CNN + Voting	0.710
Patch-CNN + Max-pooling	0.710
Our method	0.771
Pathologists' Agreement [M. Gupta 2015] (on a similar dataset)	0.7-0.8

Confusion Matrix: OA is very hard even for pathologists	GBM	OD	OA	DA	AA	AO
Glioblastoma, Grade IV (GBM)	214		2		1	
Oligodendroglioma, Grade II (OD)	1	47	22	2		1
Oligoastrocytoma, 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 Oligodendroglioma, Grade III (AO)	2	2	3			1

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

Glioma is

The most common brain cancer

deaths in people under age 20

· The leading cause of cancer-related

691 Google Scholar citations; PaigeAI FDA cleared clinical application using closely related method



# The Promise of Self Supervised Learning

- Large language models are trained on huge quantities of text using methods that include filling in masked words, predicting next sentence
- These models are now able to generate sophisticated responses to questions
- Many open issues but see next example of nuanced question involving lymphomas



#### what lymphomas resemble hodgkins disease but do not have reed sternberg cells

- There are several types of lymphomas that can resemble Hodgkin's disease but do not have Reed-Sternberg cells. Reed-Sternberg cells are large, abnormal lymphocytes that are the hallmark of classical Hodgkin's lymphoma.
- Some of the lymphomas that can mimic Hodgkin's disease but lack Reed-Sternberg cells include:
- Nodular lymphocyte-predominant Hodgkin's lymphoma: This is a rare type of Hodgkin's lymphoma that accounts for about 5% of all cases. It is characterized by the presence of large, popcorn-shaped lymphocytes called "L&H cells" that resemble normal B cells.
- T-cell/histiocyte-rich large B-cell lymphoma: This is a subtype of diffuse large B-cell lymphoma that can mimic classical Hodgkin's lymphoma. It is characterized by the presence of scattered large B cells, surrounded by a background of small T cells and histiocytes.



## ChatGPT

- Anaplastic large cell lymphoma: This is a type of non-Hodgkin's lymphoma that can mimic Hodgkin's disease. It is characterized by the presence of large, anaplastic lymphocytes that express CD30, a marker also seen in Hodgkin's disease.
- Mediastinal large B-cell lymphoma: This is a subtype of diffuse large B-cell lymphoma that often presents as a large mass in the mediastinum (the area between the lungs). It can mimic Hodgkin's disease due to the presence of fibrosis and the presence of some large, atypical lymphoid cells.



# Image based self supervised learning

- Generate and solve various visual puzzles
- Reassemble jigsaw puzzles
- Fill in masked regions
- Recognize warped, distorted, noisy images

Unsupervised Learning of Visual Representations by Solving Jigsaw Puzzles

Mehdi Noroozi and Paolo Favaro

https://arxiv.org/pdf/1603 .09246.pdf



# Self Supervision in Pathology

- Gigapixel Images
- Images can have millions of cells, many tens of thousands + of glands, crypts ducts
- Models need to learn syntax and semantics of tissue
- We are doing this, starting out with generating a model using self supervised training using whole slide images and cell density
- Fine tuned codes have above SOTA performance on classification and segmentation tasks





Saarthak Kapse Stony Brook Jingwei Zhang Stony Brook



#### Precise Location Matching Improves Dense Contrastive Learning in Digital Pathology

Jingwei Zhang<sup>1\*</sup>, Saarthak Kapse<sup>1\*</sup>, Ke Ma<sup>2</sup>, Prateek Prasanna<sup>1</sup>, Maria Vakalopoulou<sup>3</sup>, Joel Saltz<sup>1</sup>, and Dimitris Samaras<sup>1</sup>



# Self Supervised Learning in Pathology



- Deep learning based pipelines adapted to carry out scientific tasks
- Characterize detailed composition and structure of tissue – Radiology, Pathology and molecular composition
  - Predict outcome, treatment response, steer treatment
  - "Real World" large population research studies
  - Scientific studies involving disease mechanism



# Applications of AI based Tumor Infiltrating Lymphocyte Analysis Methods (TILS)

Lymphocytes are immune cells

Immune therapy has become ubiquitous

Many clinical studies involving many types of cancer

Spatial patterns of distribution of TILs maps to ascertain the functional immune status of the tumor microenvironment

Combine diagnostic criteria and TILs to stratify patients, guide clinical management, and select therapy (e.g. immunotherapy)





# Teaching Algorithms to Recognize Immune Cells in Confusing Contexts

Deep Learning-Based Mapping of Tumor Infiltrating Lymphocytes in Whole Slide Images of 23 Types of Cancer

Shahira Abousamra<sup>1\*</sup>, Rajarsi Gupta<sup>2</sup>, Le Hou<sup>1</sup>, Rebecca Batiste<sup>3</sup>, Tianhao Zhao<sup>3</sup>, Anand Shankar<sup>4</sup>, Arvind Rao<sup>4</sup>, Chao Chen<sup>2</sup>, Dimitris Samaras<sup>1</sup>, Tahsin Kurc<sup>2</sup> and Joel Saltz<sup>2</sup>



TIL positive – Red TIL confounders - Green



Tumor TIL Analyses

High-resolution detection and classification of tumor cells, lymphocytes, and stromal cells in the entirety of whole slide images



#### The American Journal of Pathology Volume 190, Issue 7, July 2020, Pages 1491-1504



## Utilizing Automated Breast Cancer Detection to Identify Spatial Distributions of Tumor-Infiltrating Lymphocytes in Invasive Breast Cancer

Han Le \*  $\stackrel{\circ}{\sim}$  ⊠, Rajarsi Gupta <sup>†, ‡</sup>, Le Hou \*, Shahira Abousamra \*, Danielle Fassler <sup>‡</sup>, Luke Torre-Healy <sup>†</sup>, Richard A. Moffitt <sup>†, ‡</sup>, Tahsin Kurc <sup>†</sup>, Dimitris Samaras \*, Rebecca Batiste <sup>‡</sup>, Tianhao Zhao <sup>‡</sup>, Arvind Rao <sup>§</sup>, Alison L. Van Dyke <sup>¶</sup>, Ashish Sharma <sup>II</sup>, Erich Bremer <sup>†</sup>, Jonas S. Almeida \*\*, Joel Saltz <sup>†</sup>

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# Qualitative evaluation of lymphocyte distribution enables interpretable risk identification

Score	0	1	2	3
Intratumoral strength				
Peritumoral strength				
TIL deserts				num_risky_
TIL forests				
Lymphoid aggregates				
		an in the bar		# Events: 74

Metric	Level	TCGA BRCA Hazard Ratio
	1	0.62
Intratumoral strength	2	0.27
	3	0.19
TIL deserts	Present	2.0 **
TIL forests	Present	0.56 *
	1	2.07
Peritumoral	2	1.14
	3	0.61

num_risky_features	0 (N=135)	reference						
	1 (N=76)	(0.89 – 5.4)					C	0.089
	2 (N=79)	2.9 (1.21 – 6.9)	F		-			0.017 *
	3 (N=103)	3.8 (1.72 – 8.2)		F				<0.001 ***
	4 (N=112)	3.9 (1.77 – 8.4)		F		-		<0.001 ***
# Events: 74; Global p-valu AIC: 782.57; Concordance	ue (Log–Rank): 0.0 Index: 0.62	0015835	: 1	2		5		10

# Presence of multiple risky features stably correlates with risk in new data set



#### **UNC-CBCS - Validation dataset**

High Risk Features	<2 (N=123)	ref	8					
	2+ (N=278)	1.8 (1 - 3.2)	<b></b>		•			*
# Events: 76; Glob AIC: 878.42; Conc	al p–value (Log ordance Index:	–Rank): 2.51x 0.55	10-3	1.5	2	2.5	3	3.5
			( <b>b</b> )					
High Risk Features	<2 (N=123)	ref						
	2+ (N=278)	1.9 (1.1 - 3.4)						*
Stage	Stage I (N=419)	ref						
	Stage II (N=506)	5.0 (2.1 – 11.6)	)	-				***
	Stage III (N=140)	9.6 (3.9 – 23.8)	1		,	-		***
	Stage IV (N=27)	2.5 (0.3 - 21.2)	) <b></b>					
# Events: 76; Glo AIC: 850.62; Cor	bal p-value (Lo ncordance Index	og-Rank): 7.6x (: 0.68	<b>10-08</b> 0.5	1 2	5	10	20	

## **Collaboration with SEER Registries to Bring AI Pathology to Surveillance and to Create Real World Clinical Research Datasets**



## Participating SEER Registries: New Jersey, Kentucky, Georgia, New York

#### **ORIGINAL ARTICLE**

J Pathol Inform 2022, 13:5

An expandable informatics framework for enhancing central cancer registries with digital pathology specimens, computational imaging tools, and advanced mining capabilities

David J Foran<sup>1</sup>, Eric B Durbin<sup>2</sup>, Wenjin Chen<sup>3</sup>, Evita Sadimin<sup>1</sup>, Ashish Sharma<sup>4</sup>, Imon Banerjee<sup>4</sup>, Tahsin Kurc<sup>5</sup>, Nan Li<sup>4</sup>, Antoinette M Stroup<sup>6</sup>, Gerald Harris<sup>6</sup>, Annie Gu<sup>4</sup>, Maria Schymura<sup>7</sup>, Rajarsi Gupta<sup>5</sup>, Erich Bremer<sup>5</sup>, Joseph Balsamo<sup>5</sup>, Tammy DiPrima<sup>5</sup>, Feiqiao Wang<sup>5</sup>, Shahira Abousamra<sup>8</sup>, Dimitris Samaras<sup>8</sup>, Isaac Hands<sup>9</sup>, Kevin Ward<sup>10</sup>, Joel H Saltz<sup>5</sup>

# Complex AI Pipelines Spatial Contexts -- Cell Detection and Classification

- Classification accuracy is frequently context sensitive
- Training on new tissue types and new cell categories is time consuming
- Method detects and classifies nuclei
- Training requires "dotting" nuclei

Multi-Class Cell Detection Using Spatial Context Representation

Shahira Abousamra, David Belinsky, John Van Arnam, Felicia Allard, Eric Yee, Rajarsi Gupta, Tahsin Kurc, Dimitris Samaras, Joel Saltz, Chao Chen Stony Brook University Stony Brook, NY 11794, USA







# Pipeline encompasses cell detection, cell classifier and learning category specific spatial statistics



# **Extreme Scale Deployments**

#### Understanding and leveraging the I/O patterns of emerging machine learning analytics

Ana Gainaru<sup>1</sup>, Dmitry Ganyushin<sup>1</sup>, Bing Xie<sup>1</sup>, Tahsin Kurc<sup>2</sup>, Joel Saltz<sup>2</sup>, Sarp Oral<sup>1</sup>, Norbert Podhorszki<sup>1</sup>, Franz Pöschel<sup>4</sup>, Axel Huebl<sup>3</sup>, and Scott Klasky<sup>1</sup>

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- Middleware for managing image and model data to optimize memory hierarchy performance in complex training and prediction tasks
- Collaboration with ORNL to explore impact using ADIOS and tumor infiltrating lymphocyte tasks



# Observations

- Algorithms designed to do specific things -> generalized trainable algorithms
- Self supervision, multi-modal friendly methods such as transformers
- Multi-modal/Multi-task learning
- Combination of very large data, need for self-supervision, multi-modal integration creates a perfect storm for exascale (and beyond) computing requirements
- Analyses typically carried out with <100,000 whole slide images (usually much smaller) – large institutions now have 10M+ whole slide image datasets
- Need for extreme scale system software to control complexity, validate pipelines and to optimize performance

## **Stony Brook Multi-Modal Deep Learning Faculty**



#### Dimitis Samaras, Chao Chen, Tahsin Kurc, Prateek Prasanna, Raj Gupta

## **SEER UG3 Team**

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