Pathology Whole Slide Image De-Identification

MIDI Workshop Day 2



Panelists

Adam Taylor



David Gutman



Tom Bisson



Format

- Introduction
 - Digital pathology and whole slide imaging in the context of de-identification
 - De-identification validation for WSI and multiplexed tissue imaging in HTAN
- Presentations on recent work
 - David Gutman
 - Tom Bisson
- Panel discussion

Digital pathology and whole slide imaging



De-identification considerations for WSI

Filename

TCGA-V1-A8MU-01Z-00-DX1.2C9CED13-5C2C-4FFB-AB0B-3904BAA4FEFF.svs (864,7 MB)

Slide label



Burnt in text



Image headers/tags

Assay/study metadata

TIFF public tags DateTime 306 (0x132) ASCII: 2020:01:28 14:32:26

Format and metadata diversity

Bioformats supports 162 formats with varying degrees of metadata readability

	Amersham Biosciences Gel	.gel						×	×	*	×	
	Amira Mesh	.am, .amiramesh, .grey, .hx, .labels	•	•	•	•	•	*	*	×	*	
	Amnis FlowSight	.cif					*	×	4	v	×	
	Analyze 7.5	.img, .hdr						×	×	×	×	
	Andor SIF	.sif		*	*	¥	*	×	×	×	×	
	Animated PNG	.png								×	×	
	Aperio AFI	.afi, .svs						×	×		4	
	Aperio SVS TIFF	.svs						×	×			
	Applied Precision CellWorX	.htd, .pnl				¥		×	×		×	
	AVI (Audio Video Interleave)	.avi						~	*	×	×	
	Axon Raw Format	.arf					*	×	×	×	×	
	BD Pathway	.exp, .tif	*					×	*		×	
	Becker & Hickl SPC FIFO	.spc	٠				•	×	×		×	
	Becker & Hickl SPCImage	.sdt						×	×		×	
		1.15										



Multiplexed tissue imaging

We are in an expansionist phase in the development of advanced multiplexed tissue imaging modalities. We should anticipate their adoption in research and clinical environments



Cyclic (CyCIF, MxIF, mIHC)





Increasingly larger, higher dimension and higher resolution data



Accelerate biomedical discoveries by improving methods for scientific *collaboration* and *communication*



Human Tumor Atlas Network

A National Cancer Institute funded Cancer Moonshot Initiative



Project goal(s): Construct 3D atlases of the dynamic cellular, morphological and molecular features of human cancers as they evolve from precancerous lesions to advanced disease.

The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell. 2020. doi:10.1016/j.cell.2020.03.053

HTAN Data Destinations



NATIONAL CANCER INSTITUTE Cancer Research Data Commons



Level 1 and 2 Sequencing =

NIH CRDC CDS authenticated through dbGaP available through Seven Bridges Genomics Cloud

Level 3 and 4 Sequencing =

Available through Synapse, and through Google BigQuery at ISB-CGC (June 2022)

Imaging =

CDS and Imaging Data Commons





Data in the context of additional metadata

Metadata such as 'Sectioning days to index' where sectioning is proximal to imaging provides an attack vector to reconstruct participant date of birth



Data in the context of additional metadata

This effect is multiplied in the case of longitudinal studies



Validation of de-identification in HTAN



Validation of de-identification in HTAN



FAIR data requires communication at scale



Adam Taylor



David Gutman



Tom Bisson

