

THE 4TH SOLID SYMPOSIUM · LONDON · 2026

THE NEXT CHAPTER FOR DATA ON THE WEB

Halcyon

Digital Pathology Whole-Slide Imaging
Research Life-cycle Management

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S P E A K E R

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ROLE

Director for Applied Informatics
Biomedical Informatics, Stony Brook
University

W3C AC Representative, Stony Brook

Co-editor — W3C Linked Web Storage
Protocol

CREDENTIALS

PhD - Biomedical Informatics (in progress)
Stony Brook University

M.Sc. - Computer & Systems Engineering,
Rensselaer Polytechnic Institute

B.S. - Computer & Systems Engineering,
Rensselaer Polytechnic Institute

30+ years - programming, databases,
networking, OS

INTERESTS

AI and medical imaging

Scalable linked-data systems

Data visualization

Standards-based, open research
infrastructure

THE PROBLEM

A single pathology slide is huge.



40 GB

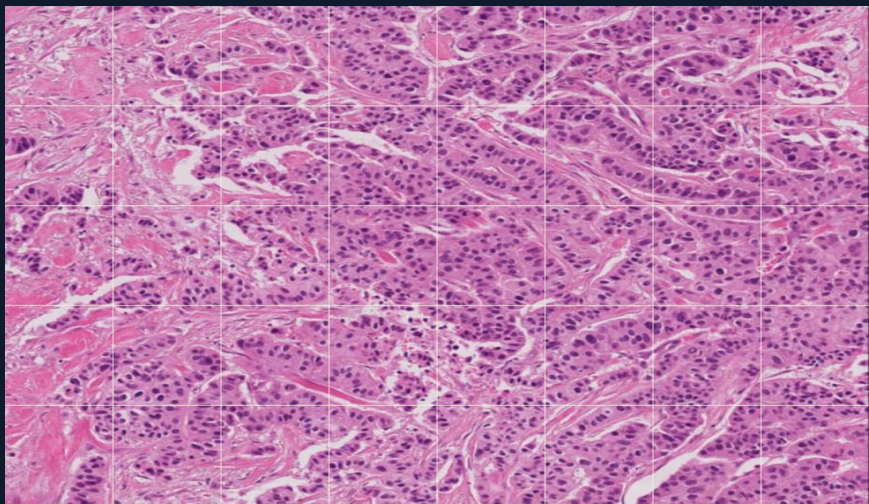
uncompressed size of a single whole-slide image

Research life cycle of a pathology image



Every stage generates data that must be linked back to the source image.

You can't send the whole image. Tile it.

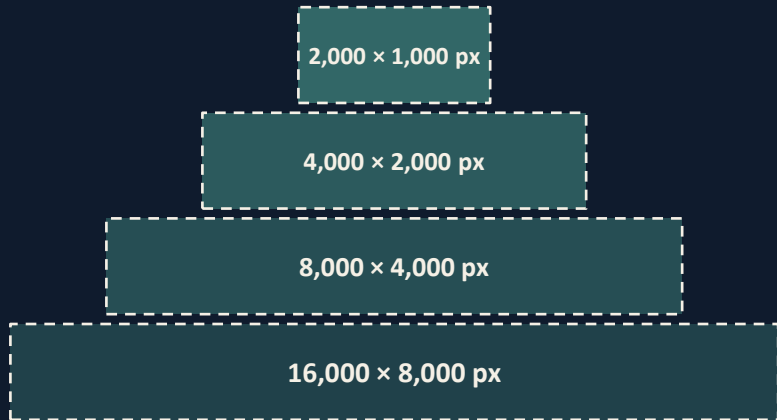


The browser requests only the tiles it needs for the current viewport and zoom level.

IIIF Protocol

- International Image Interoperability Framework, the standard used across digital libraries and pathology.

Image pyramids

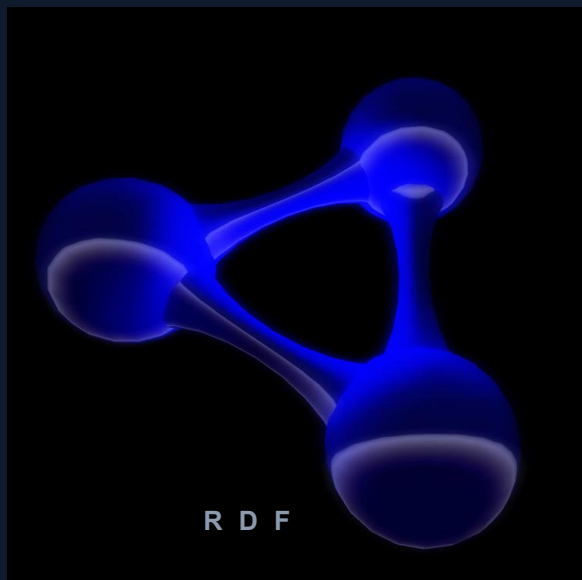


- Level 0 · full resolution
16,000 × 8,000 px
- Level 1
8,000 × 4,000 px
- Level 2
4,000 × 2,000 px
- Level 3 · overview
2,000 × 1,000 px

Each zoom level is a pre-computed, independently addressable layer.

A P P R O A C H

So how do you build this?



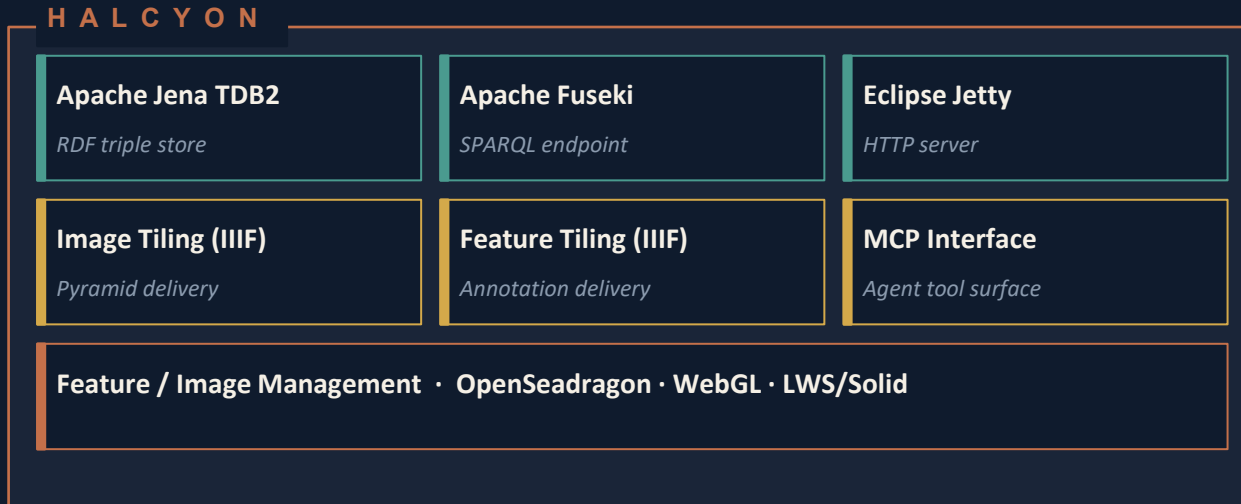
T h e a n s w e r

RDF all the way down.



Every tile, every annotation, every
model output -
addressable, linkable, queryable.

Halcyon · components



Many ways to index 2-D and 3-D spaces

SPACE-FILLING CURVES

Linear index, strong locality

- Geohash
- HHCode
- Z-order curve
- **Hilbert curve**

TREE-BASED

Recursive partition of space

- Quadtree
- Octree
- kd-tree
- BSP-tree
- m-tree

R-TREE FAMILY

Bounding-box overlap queries


- R-tree
- R+ tree
- R* tree
- Hilbert R-tree
- X-tree
- UB-tree

GeoSPARQL — spatial queries over RDF

The OGC standard that lets you write SPARQL queries like

EXAMPLE QUERY

```
SELECT ?feature WHERE {
  ?feature geo:asWKT ?wkt .
  FILTER(
    geof:sfWithin(?wkt, $region)
  )
}
```



HALCYON

Search docs

- Installing
- Image Annotation Toolbar
- Annotations**
- Building
- Authorization
- About

```
@prefix dc: <http://purl.org/dc/terms/> .
@prefix exif: <http://www.w3.org/2003/12/exif/ns#> .
@prefix geo: <http://www.opengis.net/ont/geosparql#> .
@prefix hal: <https://halcyon.is/ns/> .
@prefix prov: <http://www.w3.org/ns/prov#> .
@prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
@prefix sno: <http://snomed.info/id/> .
@prefix so: <https://schema.org/> .
@prefix xsd: <http://www.w3.org/2001/XMLSchema#> .

<urn:md5:a923c8367e61792f531e65d966d4cb78>
  a so:ImageObject;
  exif:height "82984"^^xsd:int;
  exif:width "112231"^^xsd:int .

[ a geo:FeatureCollection;

  dc:creator "http://orcid.org/0000-0003-0223-1059";
  dc:date "2023-11-09T19:48:15.406625700Z"^^xsd:dateTime;
  dc:description "Nuclear segmentation of TCGA cancer types";
  dc:publisher <https://ror.org/01882y777> , <https://ror.org/05qghxh33>;
  dc:references <https://doi.org/10.1038/s41597-020-0528-1>;
  dc:title "cnn-nuclear-segmentations-2019";
  prov:wasGeneratedBy [ a prov:Activity;
    prov:used <urn:md5:a923c8367e61792f531e65d966d4cb78>;
    prov:wasAssociatedWith <https://github.com/SBU-BMI/quip_cnn_segmentation/releases>;
  ];

  rdfs:member [ a geo:Feature;
    geo:hasGeometry [ geo:asWKT "POLYGON ((69379 61479, 69378 61480, 69373 61480, 69373 61479, 69379 61479))"^^xsd:string;
    hal:classification sno:48512009;
    hal:measurement [ hal:classification sno:48512009;
      hal:hasProbability "1.0"^^xsd:float;
    ];
  ];

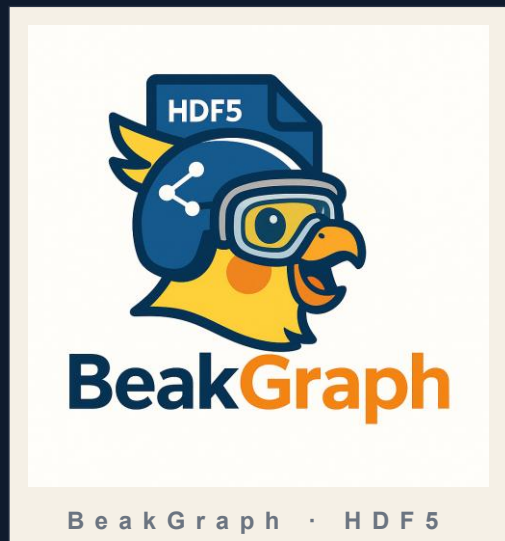
  rdfs:member [ a geo:Feature;
    geo:hasGeometry [ geo:asWKT "POLYGON ((87135 28142, 87134 28143, 87133 28142, 87135 28142))"^^xsd:string;
    hal:classification sno:48512009;
    hal:measurement [ hal:classification sno:48512009;
      hal:hasProbability "1.0"^^xsd:float;
    ];
  ];

];
```

Geometry becomes a queryable property of any resource — slides, annotations, model outputs.

BeakGraph

Apache Jena graph implementation · RDF HDT packed in HDF5



APACHE JENA

Drop-in graph

Implements the Jena Graph interface — use it anywhere Jena runs.

RDF HDT

Compressed triples

Header · Dictionary · Triples. Small on disk, queryable without expansion.

HDF5 CONTAINER

Chunked, portable

One self-describing file. Random access, version-able, widely supported.

Inside a BeakGraph HDF5 file

Object Attribute Info: General Object Info

Attribute Creation Order: Creation Order NOT Tracked

Number of attributes = 1

Name	Type	Array Size	Value{f50[...]}
numQuads	64-bit integer	Scalar	10854248

HDFView root - D:\beakgraph\dest\compressed
User property file - C:\Users\Ench Bremet\hd\New3 3.2

BeakGraph

BeakGraph is an [Apache Jena](#) Graph Implementation of [RDF HDT](#) technology pumped into a [HDF5](#) file and extended to support a full RDF Dataset.

Building

Configuration file generation for native-image (already generated for current source code. Only needed if extensive changes have been made)

```
java -Xmx1G6 -agentlib:native-image-agent-config-output-dir=src/main/resources/META-INF/native-image -ja
```

Native Command-line

```
mvn -Pcmdlinenative clean package
```

Jar Command-line

```
mvn -Pcmdlinejar clean package
```

Core Library Jar Library

```
mvn -Plib clean package
```

Dictionary, triples, and spatial indexes — all as HDF5 datasets, browsable with standard tooling.

The screenshot shows a web browser window with the URL `http://localhost:8888/sparql/index.html`. The page title is "SPARQL Endpoint" and it features the BeakGraph logo. A query is entered in the "Query" field:

```

1 PREFIX
2 select *
3 where {?s ?p ?o}
4 limit 1000
    
```

Below the query, the results are displayed in a table view. The table has three columns: `s`, `p`, and `o`. The results are numbered 1 through 19. The table content is as follows:

s	p	o
1<http://localhost:8888/HalcyonStorage/nasa/eso2320a.tif>	as:updated	"2026-02-25T14:25:19.171419Z"^^xsd:dateTime
2<http://localhost:8888/HalcyonStorage/nasa/eso2320a.tif>	as:mediaType	image/tiff
3<http://localhost:8888/HalcyonStorage/nasa/eso2320a.tif>	sdo:size	"4467780336"^^xsd:integer
4<http://localhost:8888/HalcyonStorage/nasa/eso2320a.tif>	owl:sameAs	<file:///D:/HalcyonStorage/nasa/eso2320a.tif>
5<http://localhost:8888/HalcyonStorage/nasa/eso2320a.tif>	rdf:type	lws:DataResource
6<http://localhost:8888/HalcyonStorage/utah/hdf5/features4.ttl.h5>	as:updated	"2026-04-13T18:24:20.476006500Z"^^xsd:dateTime
7<http://localhost:8888/HalcyonStorage/utah/hdf5/features4.ttl.h5>	as:mediaType	application/vnd.hdfgroup.hdf5
8<http://localhost:8888/HalcyonStorage/utah/hdf5/features4.ttl.h5>	sdo:size	"716399"^^xsd:integer
9<http://localhost:8888/HalcyonStorage/utah/hdf5/features4.ttl.h5>	owl:sameAs	<file:///D:/HalcyonStorage/utah/hdf5/features4.ttl.h5>
10<http://localhost:8888/HalcyonStorage/utah/hdf5/features4.ttl.h5>	rdf:type	lws:DataResource
11<http://localhost:8888/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>	as:updated	"2025-08-21T21:45:24.552914400Z"^^xsd:dateTime
12<http://localhost:8888/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>	as:mediaType	image/png
13<http://localhost:8888/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>	sdo:size	"134042032"^^xsd:integer
14<http://localhost:8888/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>	owl:sameAs	<file:///D:/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>
15<http://localhost:8888/HalcyonStorage/utah/Stack2-With-IHC/Stack2.png>	rdf:type	lws:DataResource
16<http://localhost:8888/HalcyonStorage/utah/hdf5/features1.ttl.h5>	as:updated	"2026-04-13T18:24:24.931672400Z"^^xsd:dateTime
17<http://localhost:8888/HalcyonStorage/utah/hdf5/features1.ttl.h5>	as:mediaType	application/vnd.hdfgroup.hdf5
18<http://localhost:8888/HalcyonStorage/utah/hdf5/features1.ttl.h5>	sdo:size	"567583"^^xsd:integer
19<http://localhost:8888/HalcyonStorage/utah/hdf5/features1.ttl.h5>	owl:sameAs	<file:///D:/HalcyonStorage/utah/hdf5/features1.ttl.h5>



Linked Web Storage: /

[Storage Description](#) | [Turtle](#) | [JSON-LD](#) | [SPARQL Endpoint](#)

[/beakgraph.ttl.gz](#)

[/hdf5](#)

[/nasa](#)

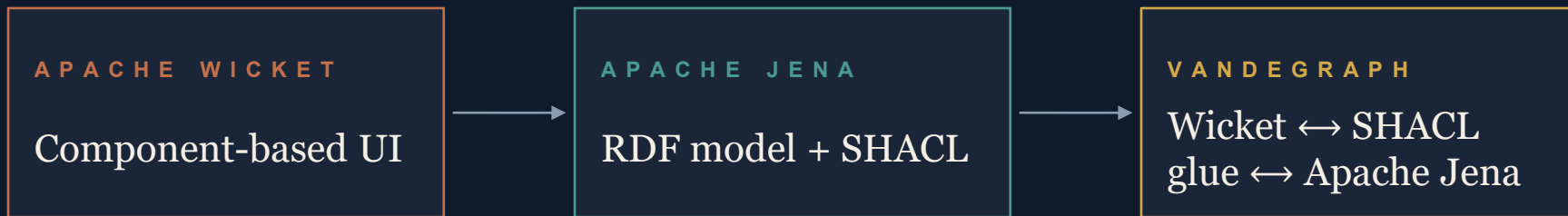
[/tcga](#)

[/utah](#)

LWS containers expose Turtle, JSON-LD, and a SPARQL endpoint at every level.

Vandegraph

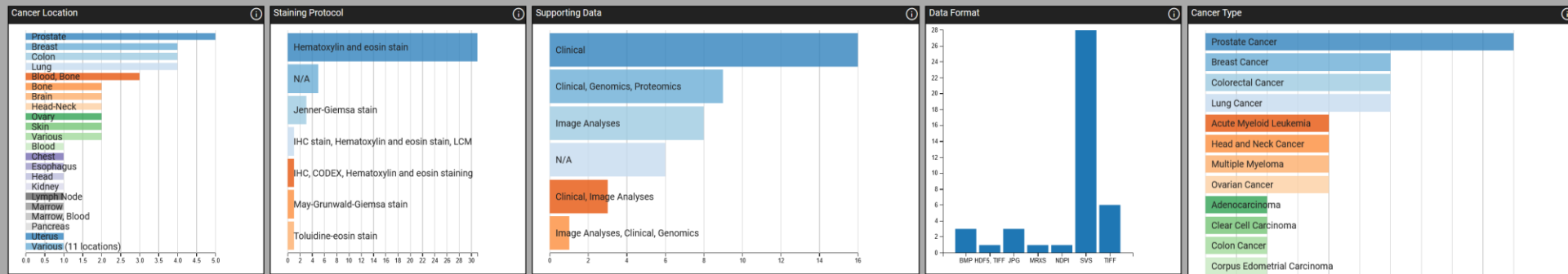
How Halcyon renders SHACL-defined forms with Apache Wicket and Jena.



A SHACL shape becomes a Halcyon form. No hand-coded UI per entity type.

Collection — summary dashboard

Search



Collection Data Table

CSV PDF Excel Print

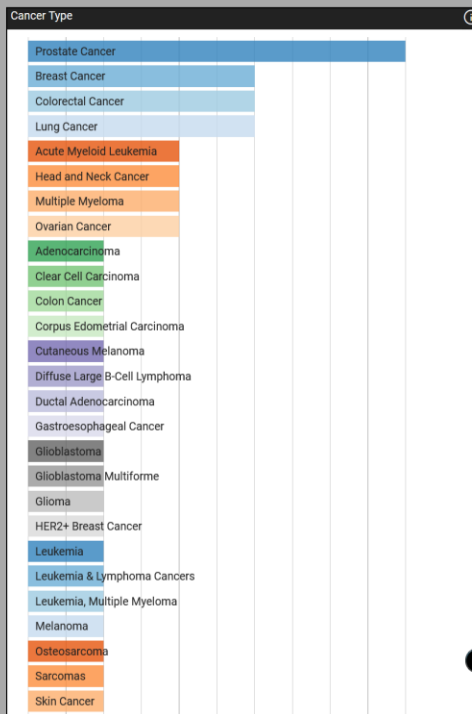
Collection	Visualize Data	Cancer Type	Location	Species	Data Format	Supporting Data	Protocol	Image Type	Pixel Aspect Ratio	Magnification	Size (GB)	Access	Updated
AML-Cytomorphology_LMU	View	Acute Myeloid Leukemia	Blood	Human	TIFF	Image Analyses	N/A	Photomicrograph	(0.290,0.290)mpp	100x	11	Public	2019-10-28
Bone-Marrow-Cytomorphology	View	Leukemia & Lymphoma Cancers	Marrow	Human	JPG	N/A	May-Grunwald-Giemsa stain	Photomicrograph	(0.086,0.086)mpp	40x	6.8	Public	2021-12-06
C-NMC 2019	View	Leukemia	Blood, Bone	Human	BMP	N/A	Jenner-Giemsa stain	Raster			10.44	Public	2019-05-28
CATCH	View	Skin Cancer	Skin	Canine	SVS	Image Analyses	Hematoxylin and eosin stain	Whole slide image	(0.253,0.253)mpp		522	Public	2022-01-13
CMB-CRC	View	Colorectal Cancer	Colon	Human	SVS	Clinical	Hematoxylin and eosin stain	Whole slide image	(0.252,0.252)mpp	40x	13.8	Public	2022-08-12
CMB-GEC	View	Gastroesophageal Cancer	Esophagus	Human	SVS	Clinical	Hematoxylin and eosin stain	Whole slide image	(0.252,0.252)mpp	40x	0.103	Saltz Lab	2022-08-12

Species

Human

Public

Collection Access



Facets, histograms, and the slide table — all driven by SPARQL under the hood.

SPARQL endpoint — embedded in Halcyon

The screenshot shows a web browser window with the URL `localhost:8888/sparql`. The page title is "SPARQL Endpoint". A navigation bar at the top includes links for Home, Security, Containers, Images, SPARQL, User, Help, and Logout. Below the navigation bar, the "SPARQL Endpoint" section contains a query editor with a single query:

```

1 PREFIX
19 select *
20 where {graph ?g {?s ?p ?o}}
21 limit 200
    
```

Below the query editor, the results are displayed in a table view. The table has four columns: `s`, `p`, `o`, and `g`. The results show 11 rows of data, each representing a triple from the graph. The table view includes a "Table" tab, a "Response" tab, and a status bar indicating "200 results in 0.058 seconds". The table also has a "Simple view" checkbox, an "Ellipse" checkbox (checked), a "Filter query results" input field, and a "Page size" dropdown set to 50.

s	p	o	g
1<https://localhost:8888/ldp/zarr/>	rdf:type	ldp:Container	hal:CollectionsAndResources
2<https://localhost:8888/ldp/zarr/>	rdf:type	ldp:BasicContainer	hal:CollectionsAndResources
3<https://localhost:8888/ldp/zarr/>	dct:title	zarr	hal:CollectionsAndResources
4<https://localhost:8888/ldp/zarr/>	ldp:contains	<https://localhost:8888/ldp/zarr/4495402.zarr/>	hal:CollectionsAndResources
5<https://localhost:8888/ldp/zarr/4495402.zarr/>	rdf:type	ldp:NonRDFSource	<https://localhost:8888/ldp/zarr/4495402.zarr/>
6<https://localhost:8888/ldp/zarr/4495402.zarr/>	rdf:type	so:ImageObject	<https://localhost:8888/ldp/zarr/4495402.zarr/>
7<https://localhost:8888/ldp/zarr/4495402.zarr/>	dct:title		<https://localhost:8888/ldp/zarr/4495402.zarr/>
8<https://localhost:8888/ldp/zarr/4495402.zarr/>	dct:modified	"2024-12-05 16:50:06" ^{^^xsd:dateTime}	<https://localhost:8888/ldp/zarr/4495402.zarr/>
9<https://localhost:8888/ldp/zarr/4495402.zarr/>	hal:fileLastModified	"1733351170470" ^{^^xsd:long}	<https://localhost:8888/ldp/zarr/4495402.zarr/>
10<https://localhost:8888/ldp/zarr/4495402.zarr/>	hal:validFile	"true" ^{^^xsd:boolean}	<https://localhost:8888/ldp/zarr/4495402.zarr/>
11<https://localhost:8888/ldp/zarr/4495402.zarr/>	exif:width	"921600" ^{^^xsd:integer}	<https://localhost:8888/ldp/zarr/4495402.zarr/>

The same SPARQL surface the UI uses is exposed to the researcher directly.

Resource graph — interactive view

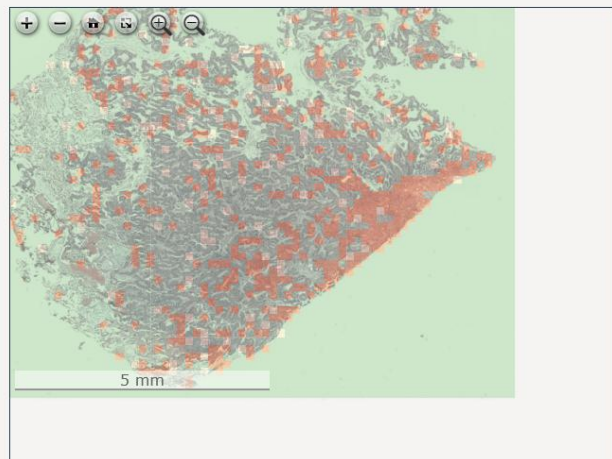
The screenshot displays a web application interface for a resource graph. On the left side, there is a list of 25 URIs, each preceded by a blue checkmark icon. The list includes various identifiers such as <http://www.w3.org/2003/12/exit/ms#Resolution>, <http://www.w3.org/ns/auth/act#accessTo>, and <https://halcyon.is/ns/file/act#Modified>. A 'Predicate' link is visible above the list. The main area on the right shows a large, complex network graph with many nodes and edges. Some nodes are highlighted in blue, corresponding to the URIs in the list. The graph has a hierarchical or clustered structure. At the bottom of the graph area, there is a smaller, simplified version of the graph.

Every node is a URI you can click and follow.

VIEWER

Match Pan Match Zoom

Match Pan Match Zoom



Match Pan Match Zoom

Match Pan Match Zoom



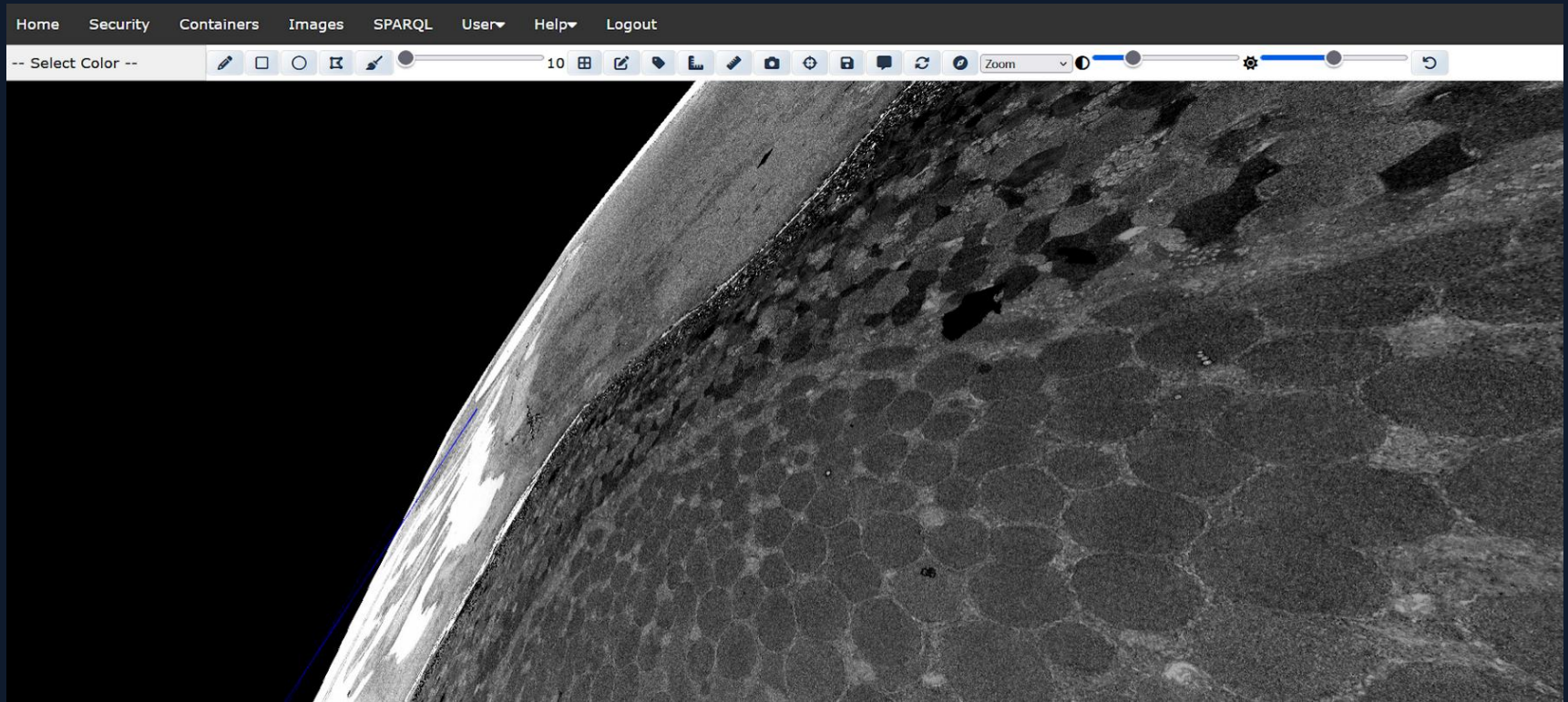
VIEWER

Zephyr

A new WebGL image viewer with annotation tools.

- **WEBGL RENDERING** Hardware-accelerated, smooth pan and zoom across gigapixel tiles.
- **IIIF-NATIVE** Consumes standard IIIF tile pyramids — no proprietary image server.
- **ANNOTATION TOOLS** Freehand, polygon, rectangle, point — every shape is RDF when saved.
- **SHACL-DRIVEN UI** Annotation class palette is generated from the active shape graph.

RUNNING SYSTEM · COMPARISON



Multiple slides, same viewport, synchronized pan & zoom.

Tissue at low magnification

00-DX1.2ad0b8f6-684a-41a7-b568-26e97675cce9.svs

- Liver structure (body structure)
- Heart structure (body structure)
- Liver pate (substance)
- Brain structure (body structure)
- Stizostedion vitreum vitreum (organism)
- Golgi complex (cell structure)
- Mitochondrion (cell structure)
- Lymphocyte (cell)
- Necrosis (morphologic abnormality)

Annotation class palette on the left is generated directly from SHACL shapes.

IIIF — streamed tile pyramid

The screenshot shows a web browser window with the following elements:

- Browser tab: H Halcyon
- Address bar: localhost8888/zephyrx277
- Navigation menu: Home, Security, Containers, Images, SPARQL, Users, Help, Logout
- Viewer toolbar: Includes icons for pan, zoom, and other navigation functions. A zoom slider is set to 10x.
- Legend (left sidebar):
 - Liver structure (body structure) - light blue square
 - Heart structure (body structure) - white square
 - Liver pate (substance) - dark blue square
 - Brain structure (body structure) - cyan square
 - Stizostedion vitreum vitreum (organism) - teal square
 - Golgi complex (cell structure) - blue square
 - Mitochondrion (cell structure) - purple square
 - Lymphocyte (cell) - green square
 - Necrosis (morphologic abnormality) - yellow square
- Image URL: 00-DX1.2ad0b8f6-684a-41a7-b568-26e97675cce9.svs
- Main image: A histological section of a lymphocyte cell, showing a large nucleus with a prominent nucleolus and surrounding cytoplasm. The image is rendered as a tiled pyramid, with the visible region being a small portion of the whole.

At 40x the viewer pulls only the tiles covering the visible region.

Annotation class editor

The screenshot shows a web browser window with the URL `localhost8888/user/colorclasses78`. The page has a dark navigation bar with links: Home, Security, Containers, Images, SPARQL, User, Help, Logout. Below the navigation bar, there are three blue buttons: Save, Delete, and Reset. A dropdown menu labeled "Choose One" is visible. The main content area has a form with a "name" field containing "Raj's fav color classes" and a "delete" link. Below the form, it says "Showing 1 to 5 of 9" with navigation links. A table displays a list of classes with their corresponding colors and delete links.

Class	Color	delete
Liver structure (body structure) <http://snomed.info/id/10200004>		delete
Brain structure (body structure) <http://snomed.info/id/12738006>		delete
Liver pate (substance) <http://snomed.info/id/227014008>		delete
Lymphocyte (cell) <http://snomed.info/id/56972008>		delete
Heart structure (body structure) <http://snomed.info/id/80891009>		delete

Create, edit, and color-code the classes researchers will draw.

Annotation classes with SNOMED bindings

Home Security Containers Images SPARQL User Help Logout

Save Delete Reset

Choose One

name [delete](#)

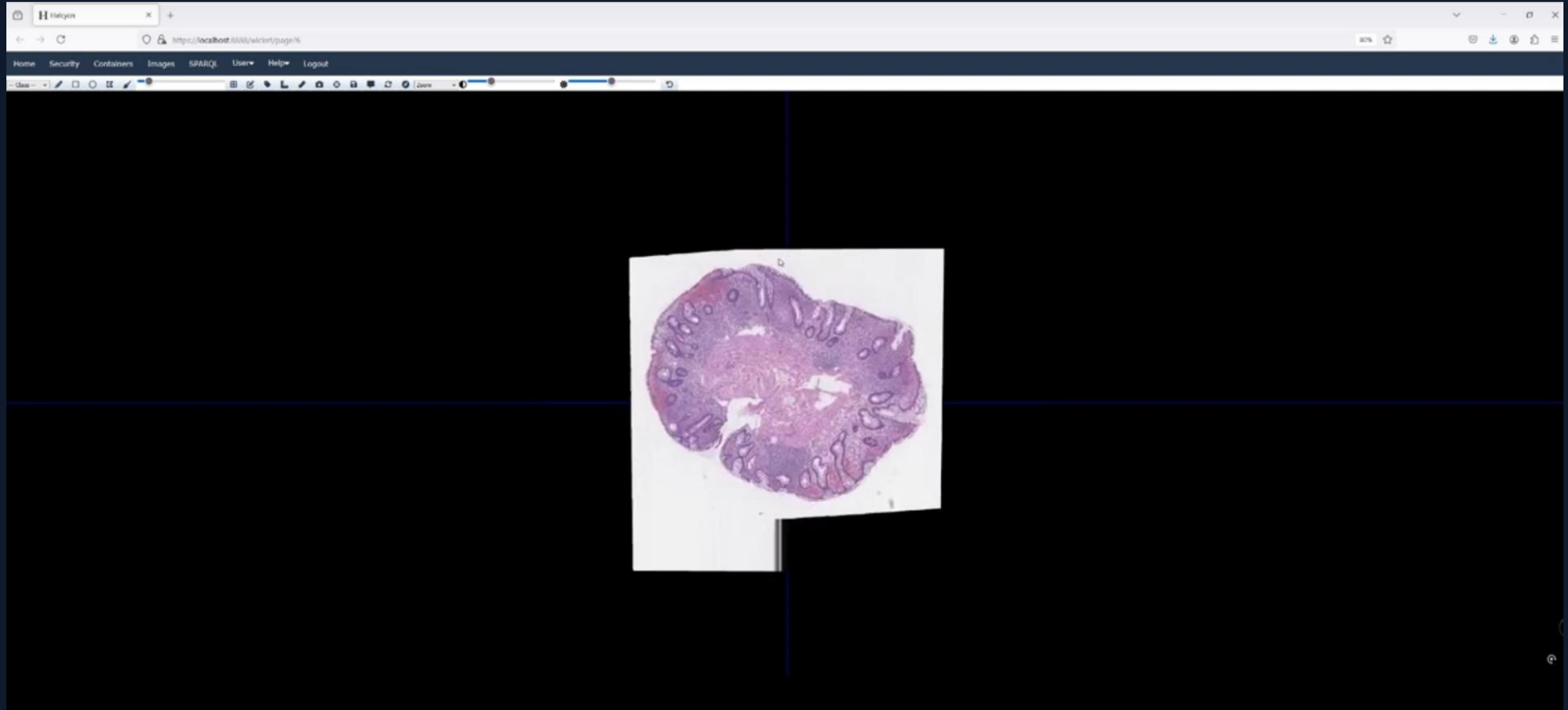
Showing 6 to 10 of 10
 << < 1 2 > >>

Class	Color
Mitochondrion (cell structure) <http://snomed.info/id/75056005>	<input type="color" value="#6666ff"/> delete
Name Unknown	<input type="color" value="#ffffff"/> delete
<input type="text" value="heart"/> <small>Name Unknown</small>	<input type="color" value="#008080"/> delete
Heart structure (body structure) <http://snomed.info/id/80891009>	<input type="color" value="#ffff00"/> delete
Heartburn (finding) <http://snomed.info/id/16331000>	<input type="color" value="#0000ff"/> delete
Heart beat (observable entity) <http://snomed.info/id/248646004>	
Heart failure (disorder) <http://snomed.info/id/84114007>	
Heart part (body structure) <http://snomed.info/id/119202000>	
Heart rate (observable entity) <http://snomed.info/id/364075005>	
Computed tomography of heart (procedure) <http://snomed.info/id/241547009>	

localhost:8888/user/colorclasses78-2-sform-form-priv-2-childRepeatingView-1-table-topToolbars-toolbars-1-span-navigator-navigation-1-pageLink

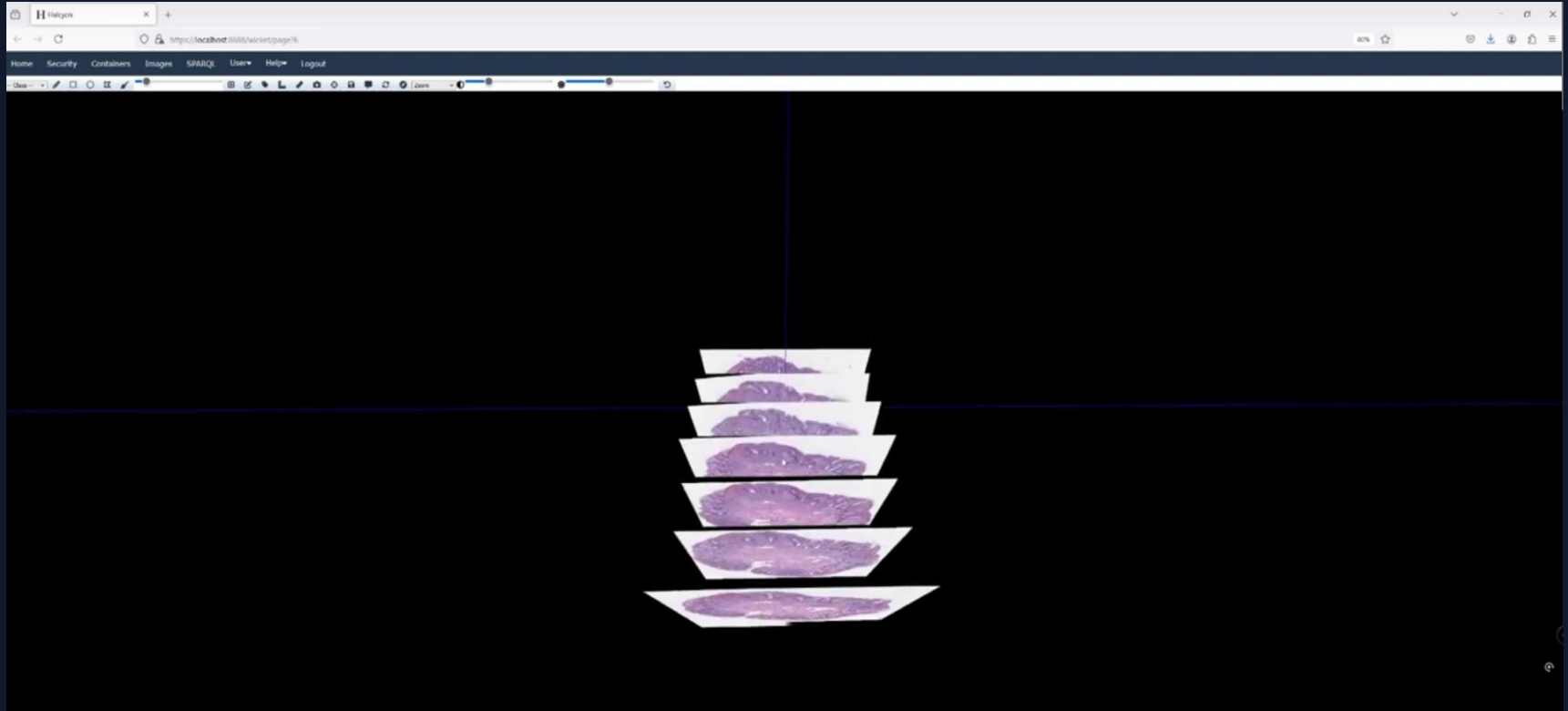
Each class is bound to a SNOMED CT concept — annotations become semantic.

Slide stack — single tissue level



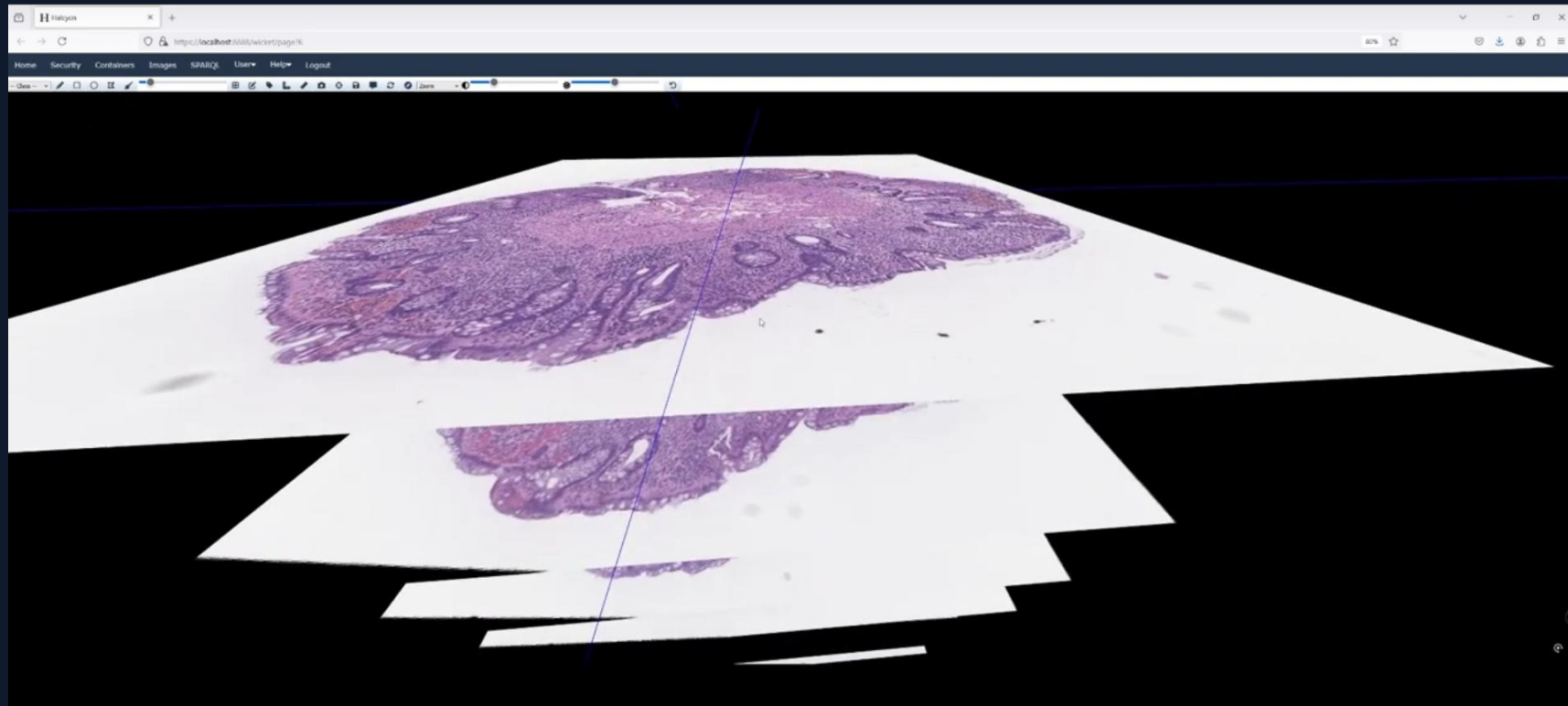
Each slide is a 2-D surface in a 3-D scene — enabling serial-section alignment.

Multi-level stack



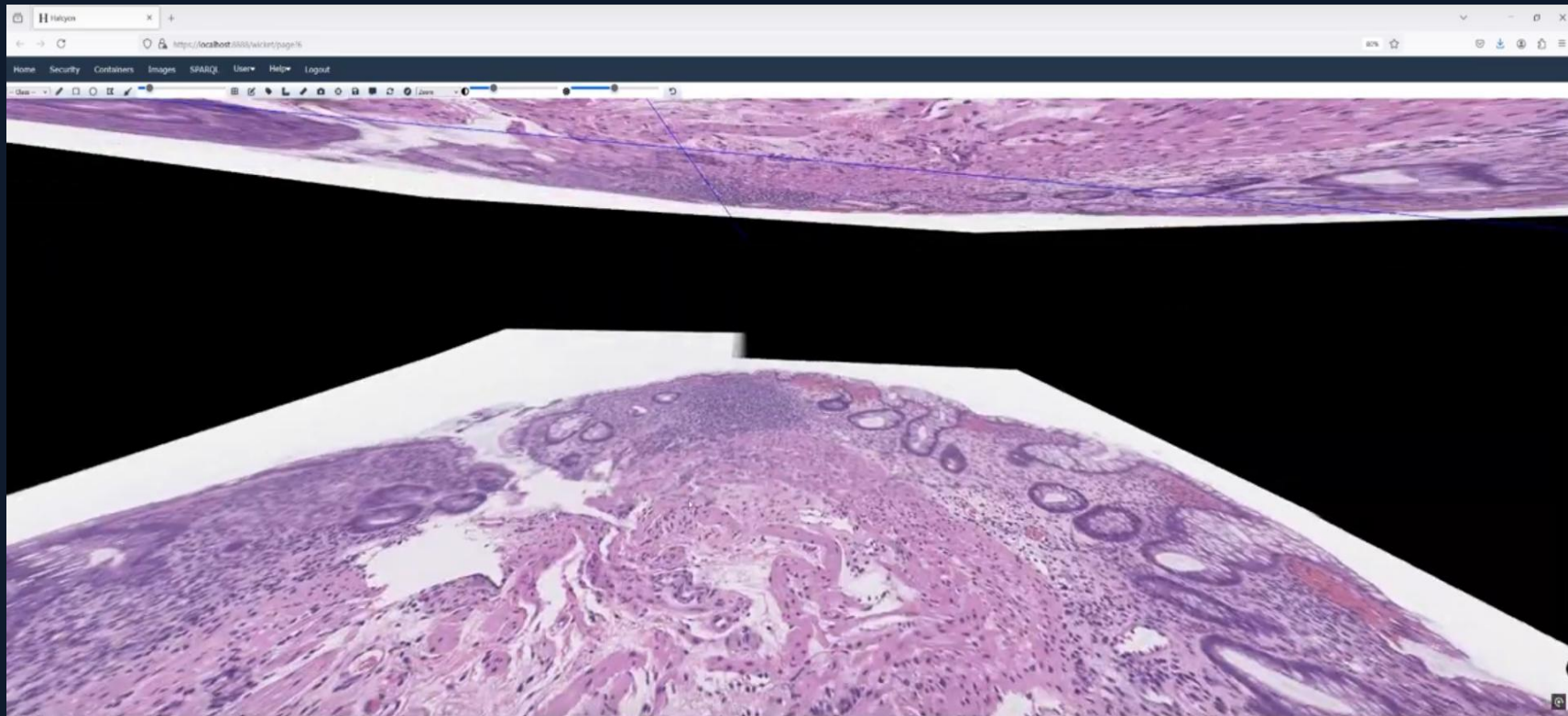
Browse up and down through the stack — correlate features across sections.

Angled view of the stack



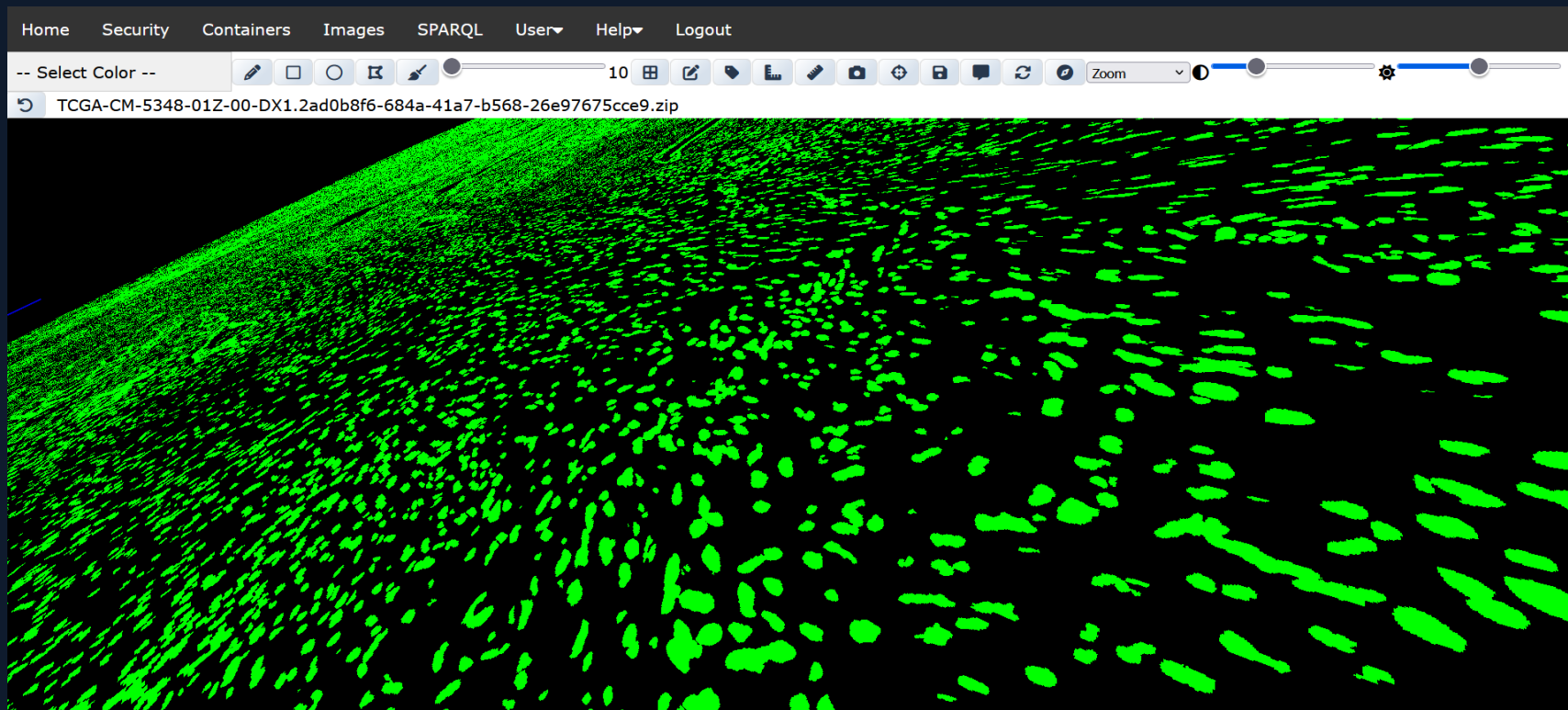
All native WebGL — no plugins, no downloads.

Annotations rendered over the stack



Every drawn shape is written back to the graph — queryable by SPARQL.

1.5M nuclei rendered as an overlay



Each green shape is one polygon.

dcm2rdf

Convert DICOM metadata to RDF — losslessly.

- **LOSSLESS** Every DICOM tag becomes an RDF property — nothing is discarded.
- **ROUND-TRIPPABLE** The RDF is being designed faithfully to DICOM spec to promote round-tripping
- **QUERYABLE** SPARQL across thousands of studies without opening a single DCM file.
- **OPEN SOURCE** Apache 2.0 licensed, community-developed, runs on any JVM.

G I T H U B github.com/ebremer/dcm2rdf

DICOM tags become first-class RDF.

DICOM TAG

```
(0008,0018)  
SOPInstanceUID  
1.3.6.1.4.1.5962.99...
```

RDF TRIPLE

```
<urn:oid:...>  
  dcm:00080018  
  <urn:oid:...> .
```

QUERY

```
SELECT ?s WHERE {  
  ?s dcm:00080060  
    "CT" .  
}
```

Full worked examples and the source code at github.com/ebremer/dcm2rdf

The Cancer Imaging Archive

TCIA

A public, open-access repository of de-identified cancer imaging freely available to researchers worldwide.
Principal Investigator: Fred Prior

30.9M+

de-identified images

37,500+

subjects across collections

2011

launched by the NCI

cancerimagingarchive.net

Funded by NCI · NIH

What TCIA does, and who runs it

WHO THEY ARE

A public service of the NCI

Funded by the National Cancer Institute (Cancer Imaging Program, DCTD).

Operated by the University of Arkansas for Medical Sciences since 2015.

Managed day-to-day by the Cancer Imaging Informatics Lab at FNLCR.

DE-IDENTIFY & CURATE

Rigorously strip PHI from incoming DICOM data to meet HIPAA and NIH sharing policies.

HOST & ORGANIZE

Maintain collections of CT, MRI, PET, and digital pathology - grouped by cancer type.

ENABLE OPEN ACCESS

Free web and API downloads, with persistent DOIs for exact dataset citation.

SUPPORT NIH PROGRAMS

Power QIN, CPTAC, APOLLO, and public imaging-analysis challenges.

A pod-native research layer

W3C Linked Web Storage / SOLID separates where data lives from who controls it — exactly the split TCIA researchers need.

CANONICAL SOURCE

TCIA Archive

Stays the authoritative host of curated images, DOIs, and collection metadata. One place, one truth.

OPEN PROTOCOL

Linked Web Storage

Standardized identity, access control, and URIs — so images, annotations, and models cite each other by ID.

RESEARCHER OWNS

Your Pod

Annotations, segmentations, notes, and model outputs live in the researcher's own storage — revocable, portable, theirs.

Annotate in place — No download-edit-reupload. Link to exact DICOM URIs.

Share on your terms — Grant a lab, a collaborator, or the public — revoke anytime.

Submit from your pod — Draft collections privately, let TCIA pull when ready.

Agents that work for researchers

MCP servers + reusable Skills give AI agents a standard way to reach TCIA and a researcher's pod — without either side giving up control.

AI Agent

Acts on behalf of the researcher

Research workflows, one prompt away

"Fetch the LIDC collection, run my segmentation, save masks to my pod." The agent resolves URIs across both systems.

Skills + MCP

Bundles the know-how, wires it in

Access stays with the owner

The pod enforces permissions. Grant, scope, or revoke any tool's reach at any time.

TCIA MCP · Pod MCP

Read from archive, write to pod

Curation-assisted submissions

Agents pre-scan DICOM headers for PHI, suggest labels, and draft metadata before TCIA intake.

TCIA stays the trusted archive. · Researchers keep the keys. · Agents do the legwork.

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THANK YOU

Questions?

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