ome-ngff: scalable format strategies for interoperable bioimaging data

https://j.mp/ome-ngff-biorxiv (10.1101/2021.03.31.437929)





exchange and re-use of bioimaging data.





Bioimaging Domain

Imaging Modalities

5D Image Data Model





3D, multi-color, movies, or any combination thereof



150+ Proprietary File Formats (PFFs)





Search for a format

	Maturity	Dimensionality	Scalability
TIFF	Ubiquitous	2D tiles	Linear slowdown



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HDF5	Well-supported	3D+ chunks	Serial writes *









Search for a format

	Maturity	Dimensionality	Scalability
TIFF	Ubiquitous	2D tiles	Linear slowdown
HDF5	Well-supported	3D+ chunks	Serial writes *
Zarr/N5	Next- generation	3D+ chunks	Parallel writes / cloud-native











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Serverless access from S3



30 GB from EBI's S3 to your browser https://bit.ly/ngff-covid-zarr (http://bit.ly/ngff-covid-source)

Highest resolution image of SARS-CoV-2 in May 2020

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Viv





More advanced vis.gl layers



http://bit.ly/idr0002-vizarr

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Viv

Gehlenborg Lab (HMS)





Cross-platform





MoBIE Plugin Christian Tischer, EMBL Heidelberg





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http://j.mp/ome-ngff-biorxiv (Fig 4.)

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By Conversion

Imaris H5 Format

\$ bioformats2raw retina_large.ims retina_large.ome.zarr

\$ find retina_large.ome.zarr -name ".z*" -o -name 0.0.0.0.0

retina_large.ome.zarr/.zattrs
retina_large.ome.zarr/.zgroup

```
retina_large.ome.zarr/0/.zarray
retina_large.ome.zarr/0/0.0.0.0
```

retina_large.ome.zarr/1/.zarray
retina_large.ome.zarr/1/0.0.0.0

retina_large.ome.zarr/2/.zarray
retina_large.ome.zarr/2/0.0.0.0.0

retina_large.ome.zarr/3/.zarray
retina_large.ome.zarr/3/0.0.0.0.0



Levels of a pyramid



•••





By Reference

intake/fsspec-reference-maker



with fsspec.open(INPUT,) as i: with fsspec.open(OUTPUT, mode="w") as o: h5 = SingleHdf5ToZarr(i, INPUT) o.write(json.dumps(h5.translate()))



By Reference

intake/fsspec-reference-maker

	intake/fsspec-reference-maker × +	•
	C 🗎 github.com/intake/fsspec-reference-maker @ 🖈 🏟	
	README.md	
V M "ç ol w	Version 1 letadata structure in JSON. We note, for future possible binary storage, that "version", gen" and "templates" should be considered attributes, and "refs" as the data that ught to dominate the storage size. The previous definition, Version 0, is compatible ith the "refs" entry, but here we add features. It will also be possible to <i>expand</i> this ew enhanced spec into Version 0 format.	,
	<pre>{ "version": (required, must be equal to) 1, "templates": (optional, zero or more arbitary keys) { "template_name": jinja-str }, "gen": (optional, zero or more items) ["key": (required) jinja-str, "url": (required) jinja-str, "offset": (optional, required with "length") jinja-str, "length": (optional, required with "offset") jinja-str, "dimensions": (required, one or more arbitrary keys) { "variable_name": (required) {"start": (optional) int, "stop": (required) int, "step": (optional) int OR [int,] }], "refs": (optional, zero or more arbitriary keys) { "key_name": (required) str OR [url(jinja-str)] OR [url(jinja-str), offset(ir } } } </pre>	nt





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Simone Leo 👩

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Blazej Pindelski 🕥

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Development Teams

Other teams are also working on developing or integrating OME tools.

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Faas et al. (idr0053, CC BY-NC-SA 3.0) J Cell Biol (2012)

KLB

(Janelia)



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Blin et al. (idr0062, CC BY 4.0) PLOS Biology (2019)



Lamers et al. (idr0083, CC BY 4.0) **Science (2020)**







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Specifications:

- Multiscales
- Labels
- HCS Plates



Process:

- Discussions: <u>https://image.sc/tag/ome-ngff</u>
- Publication: <u>https://ngff.openmicroscopy.org</u>
- Samples: https://s3.embassy.ebi.ac.uk/idr/zarr





