Importing data with rich metadata @scale

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@openmicroscopy #OME2016

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EMBL-EBI

UNIVERSITY OF CAMBRIDGE

Talk Outline

- Our metadata pipeline for the Image Data Repository (IDR)
- What kinds of metadata are we adding?
- How do we record the metadata?
- How we load it into OMERO?
- What are we thinking about next?

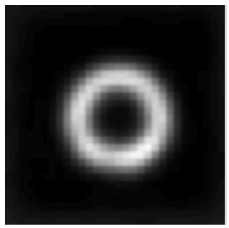
Our metadata pipeline

- Typical publication workflow
- Single processes which take more than an hour
- Groups of processes more than a dozen
- Batched imports, i.e. not real-time
- Nor automated (background) imports

Example datasets

Nuclear pore Complex

- Super resolution microscopy and particle averaging
- 7 proteins in the Nup107-160 complex, 524 image stacks
- Immunolabelling and nanobody labeling of GFP fusion proteins to determine average radial positions

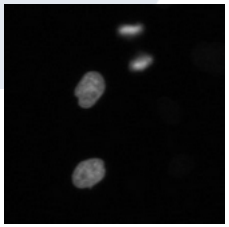


idr0023-szymborska-nucleopore

Szymborska et al. Science 2013

Mitocheck

- High Content Screen
- siRNA knockdown of ~22,000 human genes, over 500 plates, ~200,000 wells
- time-lapse imaging of fluorescently labelled chromosomes.
- Computational analysis of phenotypes

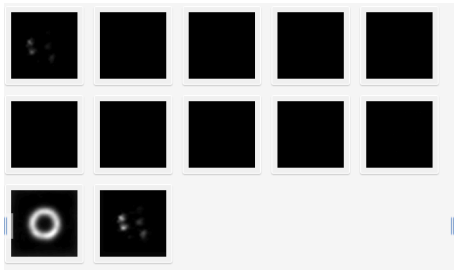


idr0013-neumann-mitocheck

Neumann et al. Nature 2010

What kinds of metadata?

Nuclear pore Complex



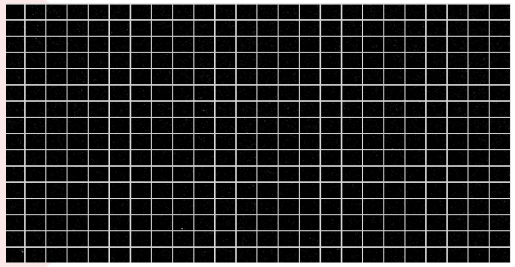
Experimental Metadata

- Study and experiment descriptors
- Organism, cell line
- Targeted protein, gene identifier, symbol
- Antibody
- File type

Analytic Metadata

- Phenotype and Ontology annotation
- NumberOfImages, NumberOfParticles
- RadialDistance, SEMerror

Mitocheck



Experimental Metadata

- Study and screen descriptors
- siRNA identifiers and sequences
- Gene identifier and symbol
- Controls, quality control at well level
- What is labeled in each channel

Analytic Metadata

- Manual and automatic scores
- Phenotype reproducibility at siRNA level
- Phenotypes and Ontology annotations

What kinds of metadata?

Adding Gene Identifiers

Image Name	Targeted Protein	Gene Identifier	Gene Symbol	Gene Symbol Synonyms
nup96_corr2_low500_6.tif	Nup96	ENSG00000110713	NUP98	NUP96, ADAR2, NUP196, ADIR2

Adding Phenotype Mappings

Phenotype 1	Phenotype 1 Term Name	Phenotype 1 Term Accession
nuclei stay close together (manual)	binuclear cell phenotype	CMPO_0000213

Recording the metadata

study file

study type
imaging method
study description
phenotype ontology
mappings

library or assay file

reagent identifiers
gene identifiers
controls
quality control

results file

measurements
scores
phenotypes

MAGE-TAB, ISA-TAB style

Recording the metadata

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reagent identifiers
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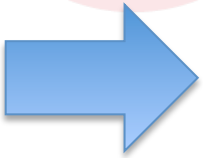
controls
quality control



annotation csv file

results file

measurements
scores
phenotypes

Recording the metadata

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phenotypes

annotation csv file

OMERO

https://github.com/IDR/idr-metadata

Recording the metadata

annotation csv file

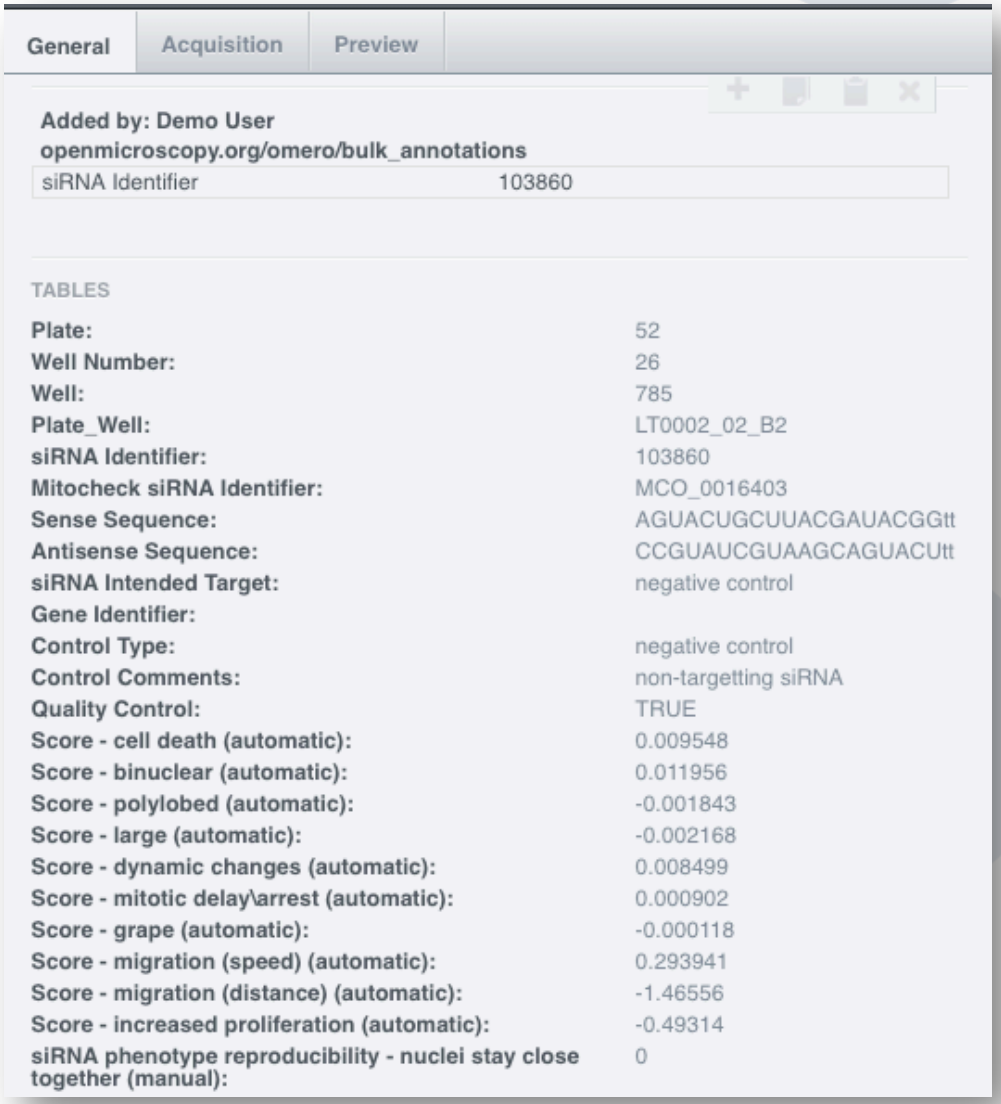
Plate	Well	siRNA	Gene Identifier	Gene Symbol	Control	Score	Phenotype	Phenotype Term Name	Phenotype Term Accession
HT1	A1				empty				
HT1	A2	s5673	ENSG023	ARP1		32	small cells	decreased cell size phenotype	CMPO_003
HT1	A3	s4562	ENSG023	ARP1		45	small cells	decreased cell size phenotype	CMPO_003
HT1	A4	s4567	ENSG055	KAT2		6			

library file

results file

study file

What it looks like in OMERO

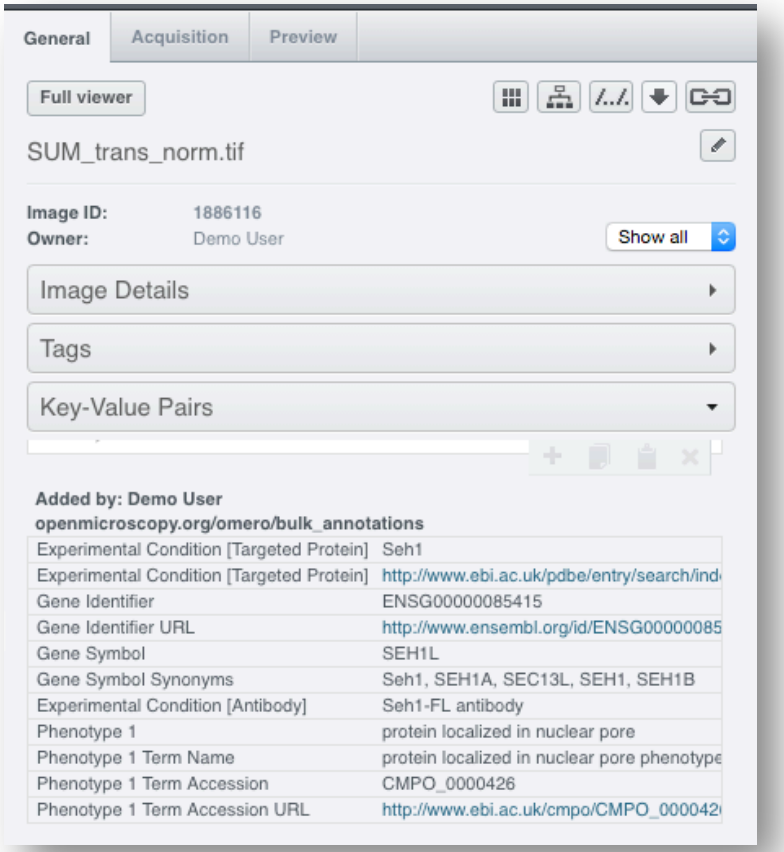


Mitocheck

http://idr-demo.openmicroscopy.org/

Annotations in OMERO

- Convert chosen columns to Map Annotations (yml)
  - Makes them searchable
  - Highlights key information (not all results details)
  - Some can be made into links



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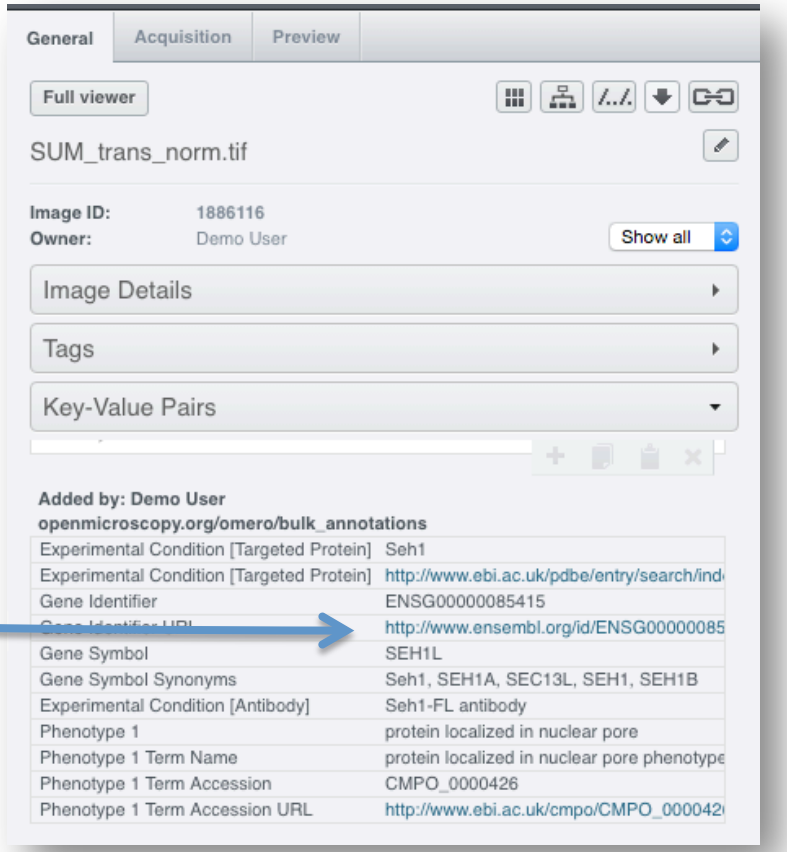
Annotations in OMERO

- name: Gene Identifier

  clientname: Gene Identifier URL

  clientvalue: http://…/result/{{value}}

  include: yes



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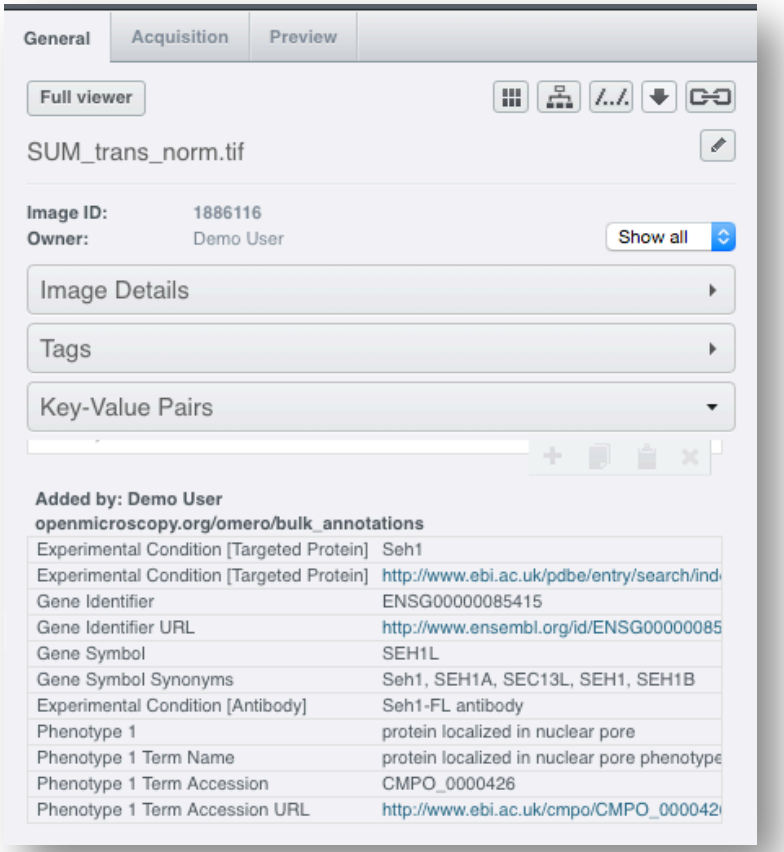
Annotations in OMERO

- bin/omero metadata populate
  - Screens, Plates
  - Projects, Datasets



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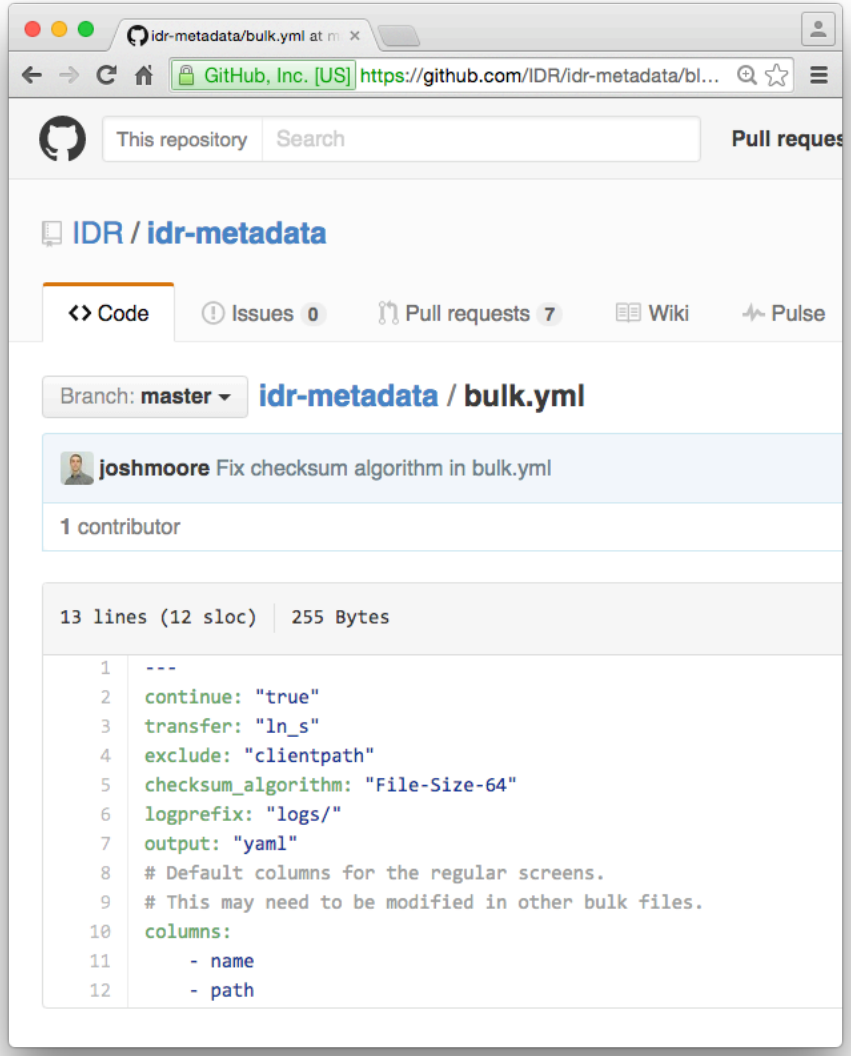
Other types of metadata

- Bulk import (yml + tsv)
  - Config:

    ```
    exclude: “clientpath”
    transfer: “ln_s”
    ```

  - Run:

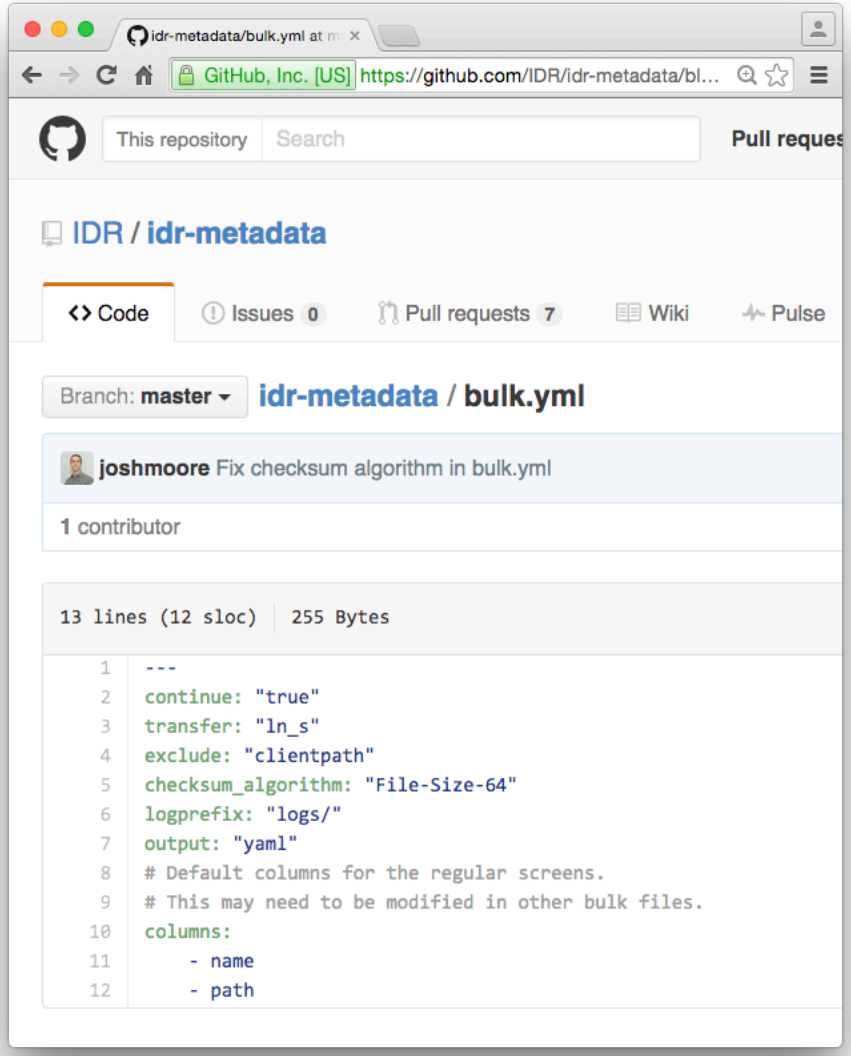
    ```
    bin/omero import
    --bulk config.yml
    ```



Other types of metadata

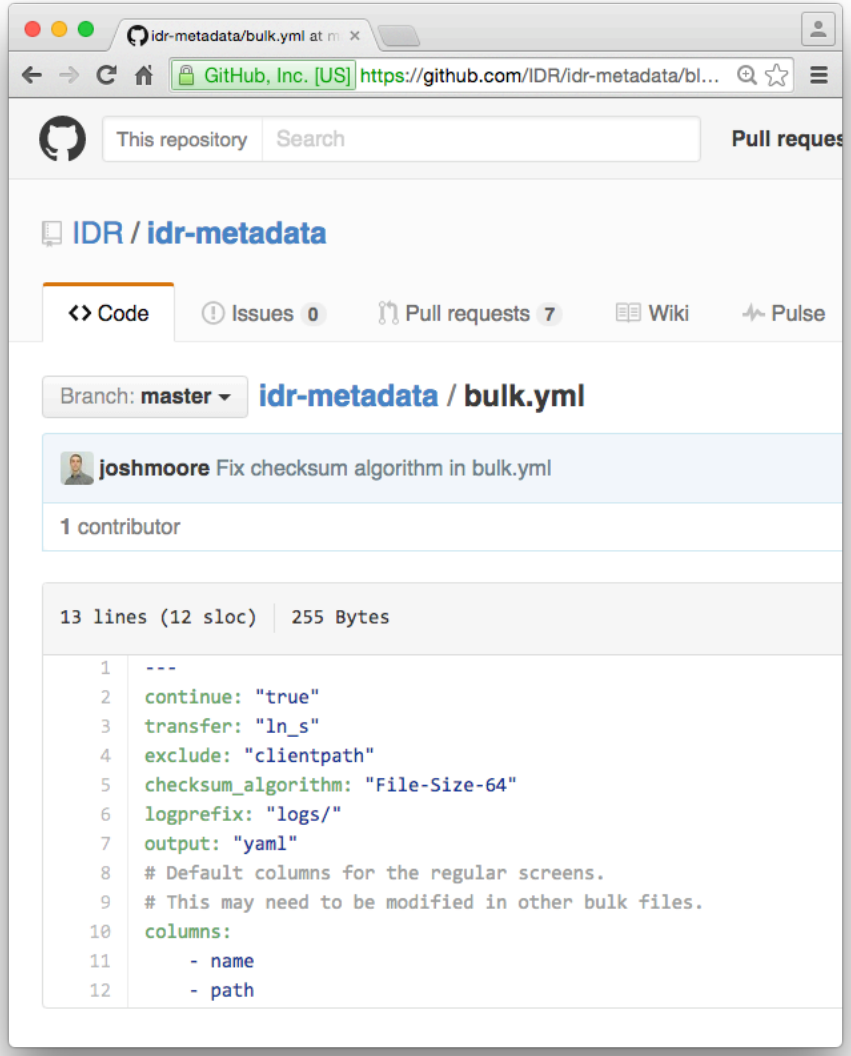
- Bulk import (yml + tsv)
- Rendering settings (yml)
  - channels:

```
1:
  label: “DAPI”
  min: 0
  max: 750
  color: “0000FF”
```



Other types of metadata

- Bulk import (yml + tsv)
- Rendering settings (yml)
- TBD: Regions-of-interest



What next?

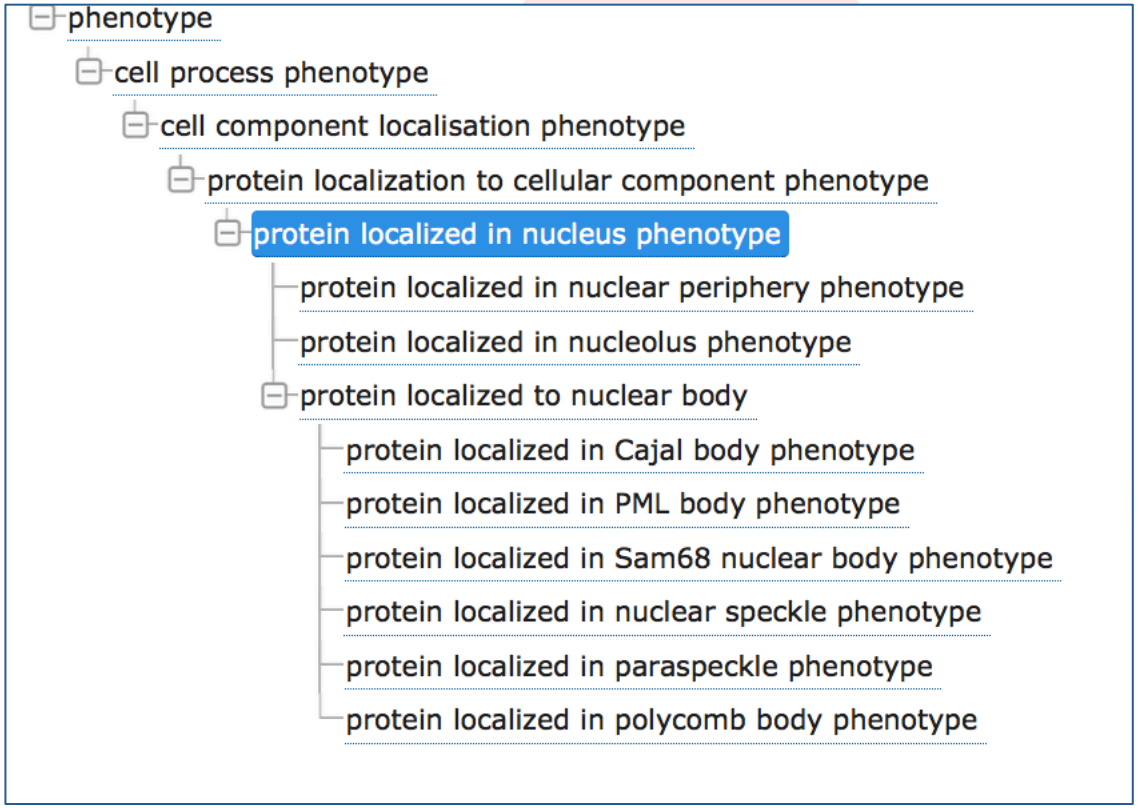
- Better display of search results

	0108-05--2006-03-10 [Well 85, Field 1 (Spot 85)]	2015-09-25 06:21:59	2015-09-25 06:21:59	demo	Browse
	0108-05--2006-03-10 [Well 55, Field 1 (Spot 55)]	2015-09-25 06:21:59	2015-09-25 06:21:59	demo	Browse
	0108-32--2006-03-06 [Well 85, Field 1 (Spot 85)]	2015-09-25 06:36:51	2015-09-25 06:36:51	demo	Browse
	0108-32--2006-03-06 [Well 55, Field 1 (Spot 55)]	2015-09-25 06:36:51	2015-09-25 06:36:51	demo	Browse
	11059 [Well H06 Field #1]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well H06 Field #2]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well H06 Field #3]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well H06 Field #4]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well H06 Field #5]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well H06 Field #6]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse
	11059 [Well G11 Field #1]	2011-12-13 17:18:26	2015-10-01 00:31:08	demo	Browse

Search for “Pipox”

What next?

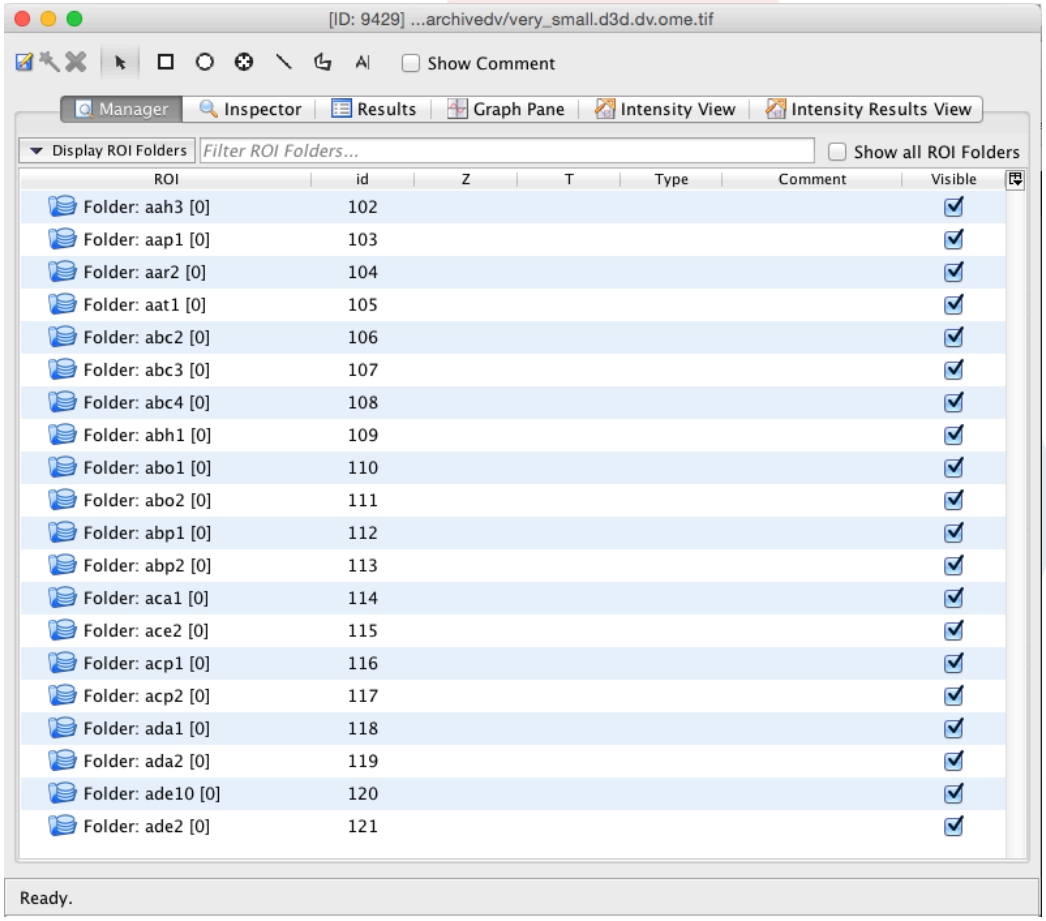
- Make more use of ontologies – integrate OLS



Ontology Look Up Service, www.ebi.ac.uk/ols

What next?

- Look at bulk annotation of ROIs – folders



What next?

- Providing a “standardized” template

study file

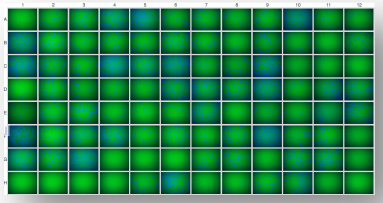
library or assay file

results file

- Incorporate other types of imaging study e.g. light sheet microscopy, plant studies, medical imaging
- Alignment with other efforts at standardization e.g. Multimot

What next?

- Handling annotation server-side
- Error-detection and feedback on background steps



images

bulk.yml

renderdef.yml

annotation csv file

bulk-map.yml

1 load images

2 apply rendering settings

3 add annotations to tables

4 create map annotations

Image Data Repository URL

http://idr-demo.openmicroscopy.org/

Thank you

- OME group - Dundee – Colin Blackburn, Jean-Marie Burel, Mark Carroll, Gus Ferguson, Helen Flynn, David Gault, Kenny Gillen, Roger Leigh, Simone Leo, Simon Li, Dominik Lindner, June Matthew, Josh Moore, Will Moore, Balaji Ramalingam, Gabriella Rustici, Aleksandra Tarkowska, Petr Walczysko, Harald Waxenegger, Eleanor Williams

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