



Data processing

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Moderator: Torill Eidhammer Sjøbakk (NTNU)



Learning objectives

After completing this session, you will:

- understand how **ontologies** help **findability** of your research objects (such as data, workflows, etc.)
- be able to **search** for tools and tutorials needed for your **data processing** and **analysis**



Learning activity

Hands-on, or you can follow a demonstration:

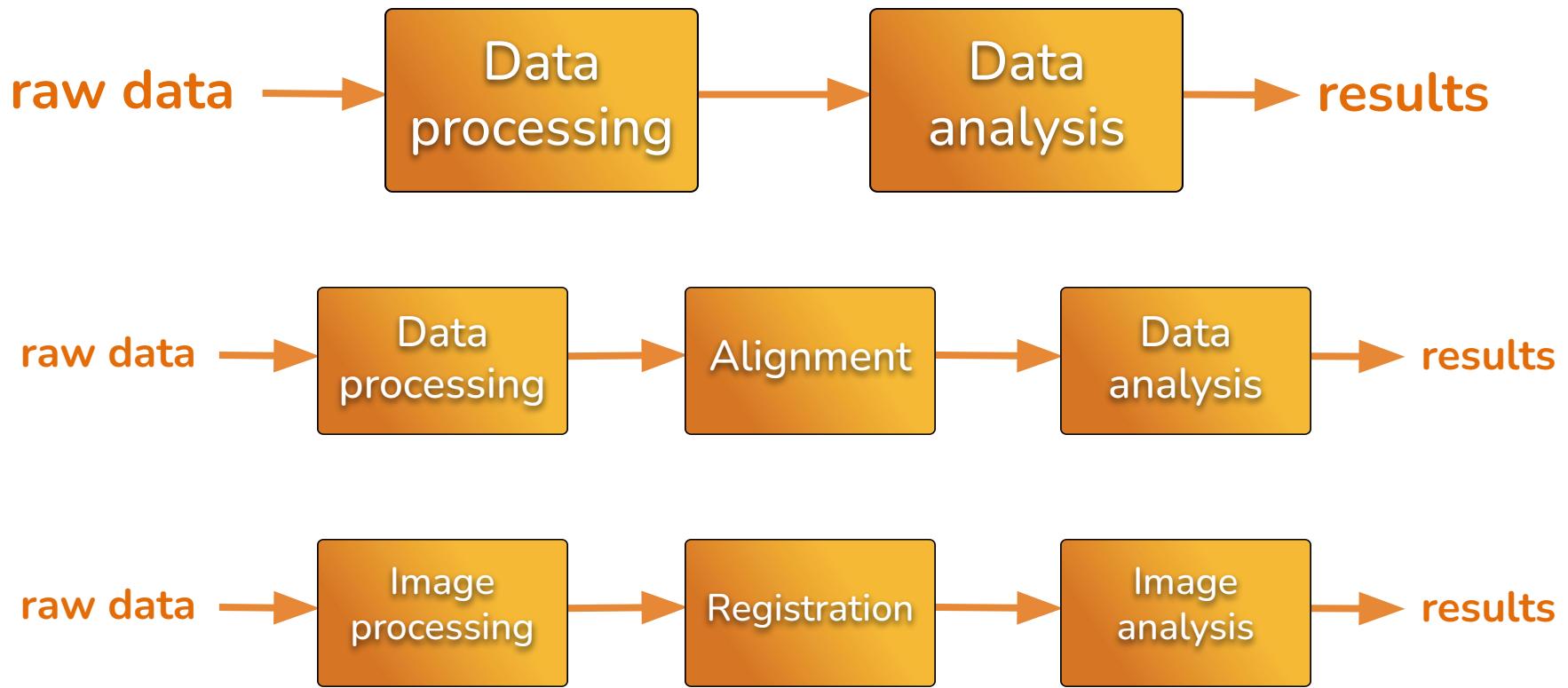
- Finding familiar concepts in the EDAM ontology
- Searching for tools in Bio.tools, Galaxy, ...

What is data processing?

Data processing is ...

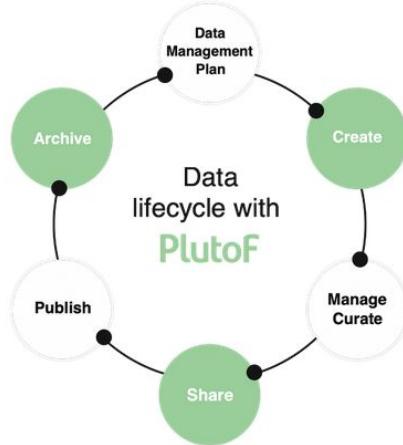


Data processing is ...



Workbenches for data storage, sharing, processing, analysis

NRIS NIRD - National e-Infrastructure for Research Data



What is ontology?

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Ontology is the philosophical study of being.

<https://en.wikipedia.org/wiki/Ontology>

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What's **an** ontology?

... an ontology encompasses ... definition of the categories ... that substantiate ... domains of discourse.

[https://en.wikipedia.org/wiki/Ontology_\(information_science\)](https://en.wikipedia.org/wiki/Ontology_(information_science))

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A **domain ontology** defines concepts important in a given domain.

Motivation

(an example with finding tools)

Search: sequence similarity search protein 

[Home](#)

 [Services](#)

 [Register a Service](#)

 [Service Providers](#)



 [Search by Data](#) |  [Latest](#)

[Home](#) » [Search](#) » All » Results for 'sequence similarity search protein domains'

 [SHARE](#)    ...

 [EMAIL](#)

Search Results

Try our new [Search by Data](#) feature - to search using your input/output data

Search query "sequence similarity search protein domains" returned 0 items

□— Operation

- ⊕ ← □ Annotation
- ⊕ ← □ Comparison and alignment
- ← □ Demonstration
- ⊕ ← □ Design
- ⊕ ← □ Mapping and assembly
- ⊕ ← □ Modelling and simulation
- ← □ Optimisation and refinement
- ⊕ ← □ Plotting and rendering
- ⊕ ← □ Prediction and recognition
- ⊕ ← □ Processing
- ⊕ ← □ Search and retrieval

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- ⊕ ← □ Processing
- ⊖ ← □ Search and retrieval
 - ⊕ ← □ Data and annotation retrieval
 - ← □ Data loading
 - ⊖ ← □ Database search
 - ← □ Literature search
 - ← □ Motif database search
 - ← □ Protein secondary database search
 - ⊖ ← □ Sequence database search
 - ← □ Sequence database search (by amino acid composition)
 - ← □ Sequence database search (by motif or pattern)
 - ⊕ ← □ Sequence database search (by physicochemical property)
 - ⊕ ← □ **Sequence database search (by sequence)**
 - ← □ Sequence profile database search
 - ⊕ ← □ Structure database search



Topic

Classification

Nucleic acid classification

Protein classification

Protein domains

Protein families

Sequence clustering

Structural clustering

Taxonomy

Data handling

Genes

Genomics

Genotype and phenotype

Informatics

Laboratory resources

Literature and documentation

Microarrays

Nucleic acids

Ontologies and nomenclature

Organism

Pathways, networks and models

Phylogenetics

Proteins

Proteomics

Sequence

Sequencing and mapping

Structure

Now we'll look at one concrete ontology ...

EDAM

The ontology of data analysis and data management

github.com/edamontology/edamontology

What is EDAM?

- Phylogeny
- Sequence analysis
- Sequence sites, features and motifs
- Structure analysis
- Computer science
- Experimental design and studies
- Informatics
- Laboratory techniques
- Literature and language
- Mathematics
- Medicine
- Omics
- Genomics
 - Comparative genomics
 - Epigenomics
 - Functional genomics
 - Metagenomics
 - Pharmacogenomics
 - Phylogenomics
 - Population genomics
 - Structural genomics
 - Transcriptomics
- Metabolomics
- Phenomics
- Proteomics
- ...

- Analysis
 - Enrichment analysis
 - Expression analysis
 - Genetic variation analysis
 - Image analysis
 - Pathway or network analysis
 - Phylogenetic tree analysis
 - Protein function prediction
 - Sequence analysis
 - Spectral analysis
 - Structure analysis
 - Text mining
 - Information extraction
 - Information retrieval
- Bioinformatics
 - Transmembrane protein analysis
- Annotation
- Calculation
 - Isotopic distributions calculation
 - Nucleic acid property calculator
 - Protein property calculation
 - Rarefaction
 - Retention time prediction
 - Sequence composition calculator
 - Statistical calculation
- Classification
- Clustering

- URI
 - Image
 - Keyword
 - Map
 - Map data
 - Mathematical model
 - Matrix
 - Molecular property
 - Molecular simulation data
 - Ontology data
 - Over-representation data
 - Pathway or network
 - Phylogenetic data
 - Plot
 - Query script
 - Reaction data
 - Regular expression
 - Report
 - Score
 - Sequence
 - Sequence attribute
 - Sequence coordinates
 - Sequence features
 - Sequence features metadata
 - Sequence signature data
 - Sequence variations
- Format
 - Binary format
 - .nib
 - 2bit
 - AB1
 - ABI
 - ARB
 - BAI
 - BAM
 - BCF
 - bgzip
 - bigBed
 - bigWig
 - BinPos
 - BMP
 - BTrack
 - COMBINE OMEX
 - CRAM
 - DICOM format
 - ebwt
 - ebwtl
 - GIF
 - HDF
 - HDF5
 - ibd
 - IDAT
 - im

~3500 concepts in data analysis and management ...

... with definitions, relations, synonyms, etc.

Scope of EDAM, and example concepts

Topic

Phylogenetics

Electron cryotomography

Operation

Image segmentation

Molecular docking

Data

Gene ID

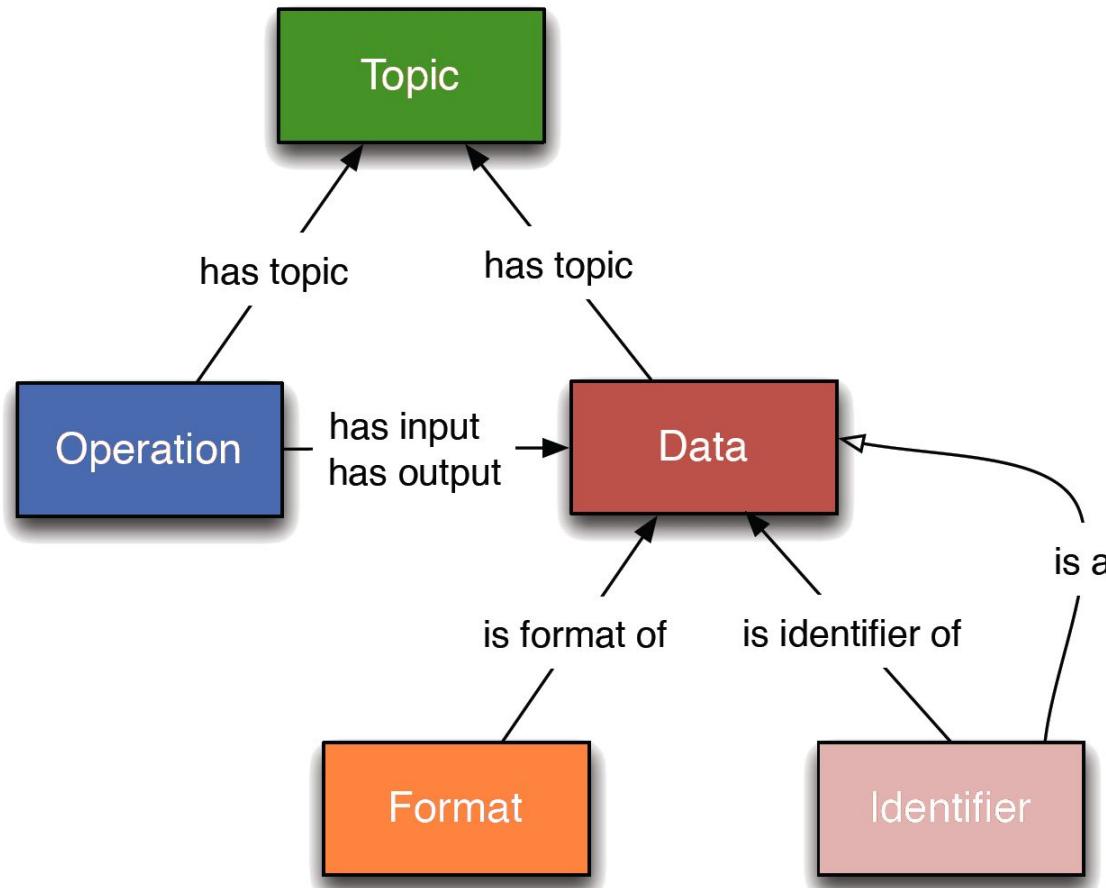
Position-specific scoring matrix

Format

FASTQ

SBML

Relations between concepts in EDAM



Usage areas of EDAM

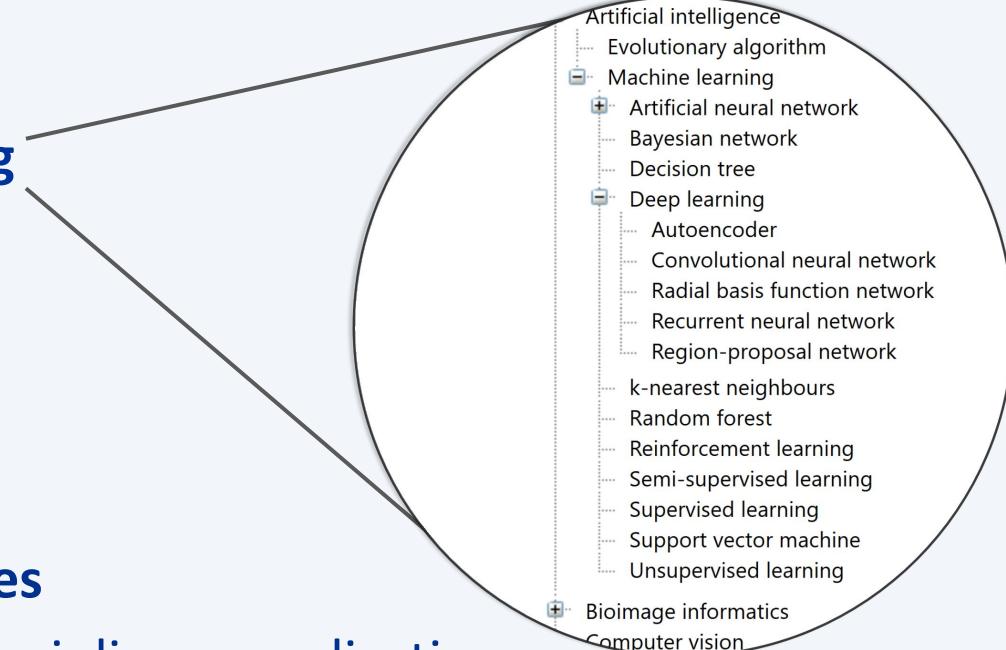
- Searching for tools, workflows, learning materials, ...
- Data provenance (metadata)
- Tools and data integration
- Text mining
- Choosing terminology

EDAM extensions

Enabling specialised communities to develop **EDAM** for their domains

- **Bioimaging**

- **Geosciences**
and interdisciplinary applications



EDAM- -bioimaging

The ontology of bioimage informatics operations, topics, data, and formats

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<https://github.com/edamontology/edam-bioimaging>



[@edamontology](https://twitter.com/edamontology)



[@edamontology/edam-bioimaging](https://github.com/edamontology/edam-bioimaging)



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Topic

- Artificial intelligence
- Big data informatics
- Computer vision
- Data sharing
- High-throughput screening
- Histology
- Imaging
 - Bioluminescence imaging
 - Fixed sample imaging
 - High-content analysis
 - Imaging flow cytometry
 - Live sample imaging
 - Magnetic resonance imaging
 - Medical imaging
 - Microscopy
 - Adaptive microscopy
 - Electron microscopy
 - Force microscopy
 - Light microscopy
 - Array-based detection microscopy
 - Correlative light and electron microscopy**
 - Fluorescence microscopy
 - Interferometric microscopy
 - Light field microscopy
 - Non-linear microscopy
 - Photomanipulation
 - Point-scanning microscopy
 - Stereoscopy
 - Transmission light microscopy
 - X-ray microscopy
 - Multimodal imaging
 - Spectroscopy
 - Tomography
 - Ultrasonography
 - X-ray imaging
 - In silico reconstruction

Operation

- Alignment construction
- Image registration
- Analysis
 - Frequency-domain analysis
 - Image analysis
 - Colocalisation analysis
 - Image classification
 - Image feature detection
 - Image segmentation
 - Cell segmentation
 - Connected-component analysis
 - Filament tracing**
 - Image thresholding
 - Manual segmentation
 - Model-based segmentation
 - Overlap analysis
 - Pixel classification
 - Region growing
 - Object classification
 - Object counting
 - Object detection
 - Object feature extraction
 - Homogeneity extraction
 - Overlap analysis
 - Shape features extraction
 - Stereology
 - Texture extraction
 - Velocity extraction
 - Object tracking
 - Optical flow analysis
 - Annotation
 - Clustering
 - Centroid-based clustering
 - Density-based clustering

Data

- Image
 - 2D image
 - 3D image
 - Image time series
 - Multi-channel image
- Image characteristics
 - Image data properties
 - Image formation characteristics
 - Image sensor characteristics
 - Instrument distortion characteristics
 - Instrument response function
 - Optical transfer function
 - Point spread function
 - Radiometric properties
 - Spatial properties
 - Spatial coordinates
 - Spatial image resolution
 - Volume
 - Spectral properties
 - Colour
 - Greyscale
 - Spectral image resolution
 - Temporal properties
 - Image data
 - Image histogram
 - Object characteristics
 - Region of interest
 - Region properties

~350 concepts in (bio)imaging data analysis ...

... with definitions, relations, synonyms, etc.

Scope of EDAM Bioimaging, with example concepts

Topic

Scanning electron microscopy
Convolutional neural network

Operation

Geometric distortion correction
Deformable registration

Data

3D image
Image time series

Format

MPEG
HDF5

Topic

- Artificial intelligence
- Bioimage informatics
- Computer vision
- Data sharing
- High-throughput screening

Histology

Imaging

- Bioluminescence imaging
- Fixed sample imaging
- High-content analysis
- Imaging flow cytometry
- Live sample imaging
- Magnetic resonance imaging
- Medical imaging

Microscopy

- Adaptive microscopy
- Electron microscopy
- Force microscopy
- Light microscopy
 - Array-based detection microscopy
 - Correlative light and electron microscopy**
 - Fluorescence microscopy
 - Interferometric microscopy
 - Light field microscopy
 - Non-linear microscopy
 - Photomanipulation
 - Point-scanning microscopy
 - Stereoscopy
 - Transmission light microscopy
- X-ray microscopy
- Multimodal imaging
- Spectroscopy
- Tomography
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Operation

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 - Image registration
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 - Image analysis
 - Colocalisation analysis
 - Image classification
 - Image feature detection
 - Image segmentation
 - Cell segmentation
 - Connected-component analysis
 - Filament tracing**
 - Image thresholding
 - Manual segmentation
 - Model-based segmentation
 - Overlap analysis
 - Pixel classification
 - Region growing
 - Semi-automatic segmentation
 - Superpixel extraction
 - Object classification
 - Object counting
 - Object detection
 - Object feature extraction
 - Homogeneity extraction
 - Overlap analysis
 - Shape features extraction
 - Stereology
 - Texture extraction
 - Velocity extraction
 - Object tracking
 - Optical flow analysis
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 - Classification
 - Clustering
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 - Region properties
- Format

Preferred Name	Correlative light and electron microscopy
Definition	Correlative light and electron microscopy is the combination of light microscopy (typically fluorescence microscopy) and electron microscopy of the same sample.
hasExactSynonym	CLEM Correlative light-electron microscopy
hasNarrowSynonym	Integrated light and electron microscopy (ILEM) Integrated light-electron microscopy
seeAlso	https://en.wikipedia.org/wiki/Correlative_light-electron_microscopy
subClassOf	Light microscopy Electron microscopy Multimodal imaging

Preferred Name	Filament tracing
Definition	Filament tracing operations are image analysis operations in which there is an image of a filamentous structure (it may be a tree-like structure, a filament network or a agglomeration of single 'stick-like' filaments) as input and outputs data that represent the filament, most commonly a skeleton representation of the filaments and their diameters or surfaces.
hasExactSynonym	Tubular structure extraction
hasNarrowSynonym	Biofilament tracing
hasRelatedSynonym	Curvilinear structure reconstruction Curvilinear structure detection
Related term	Neuron reconstruction
seeAlso	Neuron image analysis
subClassOf	Image segmentation

Scope of EDAM Geo, with example concepts (EARLY WORK IN PROGRESS)

Topic

Geosciences

Climate research

Operation

Climate simulation

Epidemics tracking

Data

Geographical data

Geographical coordinate

Format

NetCDF-CF

GeoTIFF



Hands-on 1 (a couple of minutes)

Exploring the EDAM ontology

1. Navigate to [EDAM](#) or to [EDAM Bioimaging](#) on the NCBO BioPortal

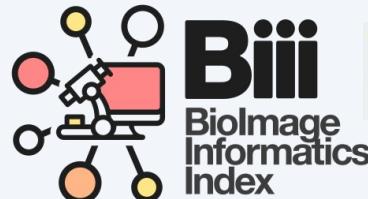
2. Find your favourite topic, operation, or format, using a **full-text search**, or browsing through **the “tree”**

3. **Optional:** Have you found anything needing improvement? See [CONTRIBUTING.md](#)

The screenshot shows the NCBO BioPortal interface with the EDAM ontology loaded. The top navigation bar includes links for BioPortal, Ontologies, Search, Annotator, Recommender, and Mappings. The main content area displays the 'EDAM - Bioscientific data analysis ontology' with a last upload date of February 26, 2021. On the left, there is a tree navigation menu with categories like Data, DeprecatedClass, Format, Operation, Topic, Biosciences, Chemistry, Computer science, Data management, Environmental sciences, Experimental design and studies, Informatics, Laboratory techniques, Literature and language, Mathematics, Open science, and Physics. On the right, the 'Details' tab is selected, showing detailed information for the 'Biosciences' class, including Preferred Name (Biosciences), Synonyms (Life sciences), Definitions (Biosciences, or life sciences, include fields of study related to life), ID (http://edamontology.org/topic_4019), Created in (1.26), hasDefinition (Biosciences, or life sciences, include fields of study related to life), hasExactSynonym (Life sciences), inSubset (<http://purl.obolibrary.org/obo/edam#edam>), and label (Biosciences).

Applications of EDAM

EDAM became a ubiquitous component of numerous resources



Exovsky
Swiss Bioinformatics Resource Portal



= Galaxy
PROJECT

... and many more ...

REMBI is an example of using EDAM for metadata

Box 1 | Archiving use-case: electron microscopy

The electron microscopy (EM) community has agreed to the core principles of how we can organize (and historically relatively tightly knit) community can accomplish archiving of its raw and derived data and metadata, initially

EMDB, which contains extensive metadata about the experiment (for example, specimen preparation, microscopy, image processing and validation). Therefore, the EMPIRI data model was designed to be lightweight and

FOCUS | COMMENT



REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology

Bioimaging data have significant potential for reuse, but unlocking this potential requires systematic archiving of data and metadata in public databases. We propose draft metadata guidelines to begin addressing the needs of diverse communities within light and electron microscopy. We hope this publication and the proposed Recommended Metadata for Biological Images (REMBI) will stimulate discussions about their implementation and future extension.

Ugis Sarkans, Wah Chiu, Lucy Collinson, Michele C. Darrow, Jan Ellenberg, David Grunwald, Jean-Karim Hériché, Andrii Iudin, Gabriel G. Martins, Terry Meehan, Kedar Narayan, Ardan Patwardhan, Matthew Robert Geoffrey Russell, Helen R. Saibil, Caterina Strambio-De-Castillia, Jason R. Swedlow, Christian Tischer, Virginie Uhlmann, Paul Verkade, Mary Barlow, Omer Bayraktar, Ewan Birney, Cesare Catavìtello, Christopher Cawthoner, Stephan Wagner-Conrad, Elizabeth Duke, Perrine Paul-Gilloteaux, Emmanuel Gustin, Maria Harkiolaki, Pasi Kankaanpää, Thomas Lemberger, Jo McEntyre, Josh Moore, Andrew W. Nicholls, Shuichi Onami, Helen Parkinson, Maddy Parsons, Marina Romanchikova, Nicholas Sofroniew, Jim Swoger, Nadine Utz, Lenard M. Voortman, Frances Wong, Peijun Zhang, Gerard J. Kleywegt and Alvis Brazma

Spectacular advances in light and electron microscopy^{1,2} are rapidly transforming the life sciences. For instance, scientists are now able to image molecular complexes at atomic resolution^{3–5}, follow the fates of individual molecules in a living cell, and image the development of an organism starting from a single fertilized cell⁶. These imaging technologies are generating large amounts of complex data, the interpretation of which often requires sophisticated analyses, as

called Euro-BioImaging has recently been established and is developing imaging data management and publishing solutions such as Cell-IDR and Tissue IDR⁷. In Japan, RIKEN launched the Systems Science of Biological Dynamics database (SSBD) in 2013, with the goal of sharing quantitative biological dynamics data including time-lapse microscopy images¹⁰. In 2016, the database expanded its remit to all bioimage data from the Japanese community. In the United States, the National Institutes of

in particular, in reporting the metadata we need to give information describing the experiments and the samples—for instance, what instrument was used to generate the images and how the sample were prepared. To achieve this, ‘appropriate minimal’ or recommended information guidelines or standards have been adopted by various life-science communities. One of the first such initiatives was MIAME (Minimum Information About a Microscopy Experiment), which was published¹¹ in

Module	Attribute	Comments	Data entry method	Relevant existing standards and ontologies
Study (contains 1 or more Study components)	Study type	Type of the overall study, which may include other imaging and/or non-imaging data	text, ontology	EDAM-BIOIMAGING, FBbi, EFO, IDR
	Study description	Study description, e.g., title of published paper	text	IDR
	General dataset info	Authors, publications, licenses etc	misc	Dublin Core, DataCite Metadata schema.org, IDR
Study component (contains Image data and Analysed data)	Imaging method	Technique used to acquire image data	ontology	EDAM-BIOIMAGING, FBbi, OME
	Study component description	Description specific to this image dataset component	text	IDR
Biosample	Identity	Internal unique ID		
	Biological entity	What is being imaged	text and/or ontology entry (multiple possible)	EFO
	Organism	Species (multiple possible)	taxonomy	NCBI Taxonomy
	Intrinsic variable	Intrinsic (e.g. genetic) alteration if applicable	text and/or ontology entry (multiple possible)	EFO
	Extrinsic variable	External biosample treatment (e.g. reagent) if applicable	text and/or ontology entry (multiple possible) or associated file	EFO, IDR
Specimen (linked to Biosample)	Experimental variables	What is intentionally varied (e.g. time) between multiple entries in this study component	text and/or ontology entry (multiple possible)	EFO
	Experimental status	Test/ control		
	Location within Biosample	Plate/dish coordinate or tissue location	text or associated file	OME
	Preparation method	Sample preparation protocol	text, file, ontology, or widget for specific method types	EDAM-BIOIMAGING, FBbi
	Signal/contrast mechanism	How is the signal generated by this sample	text, ontology	EDAM-BIOIMAGING, FBbi
Image acquisition (linked to Specimen)	Channel - content	Specific specimen staining (e.g. IEM, DAB)	text	
	Channel - biological entity	What molecule is stained	text, ontology entries	EFO
Image data (result of image acquisition, or processing of image data)	Instrument attributes	Details about instruments used	text, file, ontology, or widget for specific instrument types	EDAM-BIOIMAGING, FBbi, OME, 4DN-BINA-OME
	Image acquisition parameters	Image acquisition details	text, file, ontology, or widget for specific acquisition method types	EDAM-BIOIMAGING, OME, 4DN-BINA-OME
	Type	Primary image/processed image/segmentation	pull-down	EDAM-BIOIMAGING
	Format & compression	File type	extract from data if possible	EDAM-BIOIMAGING, OME
	Dimension extents	Volume in pixels: x, y, z, tils	extract from data if possible	OME
	Size description	Physical size of image volume in x,y,z & units (pull-down), OR magnification	extract from data if possible	
	Pixel/Voxel size description	Physical size of pixels in x, y, z & units (pull-down)	extract from data if possible	OME
	Channel information	How are individual channels represented in the image	extract from data if possible	OME
	Image processing method	Image registration, other processing applied to this dataset	text, file, ontology, or widget for specific method types	EDAM-BIOIMAGING, FBbi
	Contrast inversion to TEM	Y/N: If stained features result in brighter (whiter) signal; Y if it looks like a TEM image	pull-down	
Image Correlation (linked to 1 or more Image data)	QC info	QC score for uploaded image quality if applicable	text or controlled vocabulary	
	Spatial and temporal alignment	Method used to correlate images from different modalities (e.g. manual overlay, alignment algorithm etc)	text, ontology	EDAM-BIOIMAGING
	Fiducials used	Features from correlated datasets used for colocalization	text	
	Transformation matrix/ other info	Correlation transformations	text, or related project files (e.g. h5 Amira files)	
Analysed data	Related images and relationship	Correlated dataset or images	link	
	Analysis result type	Numerical analysis, segmentation (non-image), categorical features/phenotypes	text, ontology	EDAM-BIOIMAGING, OME
	Data used for analysis	Specific feature set used for analysis (e.g. volume measurements, locations of features)	text or file(s)	
Referenced existing standards and ontologies	Analysis method and details	Analysis method	text, file, ontology, or pointer to Methods section	EDAM-BIOIMAGING

EDAM-BIOIMAGING, an extension to the EDAM ontology (edamontology.org) for bioimage analysis, bioimage informatics, and bioimaging. <https://bioimaging.bioimageontology.org/ontologies/EDAM-BIOIMAGING>

Search Standards

Search

Search

Reset

Advanced

FAIRsharing is in read-only mode until September while we migrate our data to our new, improved system. In the meantime, please read our blog post or get in touch with us if you need to edit or add records, or have any questions.

Showing records 1 - 50 of 1541.

View as Table

View as Grid

Sort by

Name

«	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	
	28	29	30	31	»																							

Recommended Records

Recommended

Associated Publication?

No Publication

Has Publication

Claimed?

No Maintainer

Has Maintainer

Record Status

Registry	Name	Abbreviation	Type	Subject	Domain	Taxonomy	Related Database	Related Standard
	ABA Adult Mouse Brain	ABA	Standard	Neuroscience	Gene Expression	<i>Mus musculus</i>	NeuroMorpho.Org	None
	Access to Biological Collection Data	ABCD	Standard	Life Science	None	All	GBIF ALA IPT - GBIF Australia Repository GBIF Spain IPT - GBIF Spain Repository Canadensys IPT - GBIF	ABCDDNA OWL XSD ABCDEFG GBBN

https://bio.tools



Topic: "Proteomics" x

Search bio.tools

1482 tools

About

Menu ▾

matus.kalas@uib.no 1 ▾

Sort by

Score

Updated

Added

Name

Citation Count

Publication Date

↓^z

Display as

Compact

Detailed

PeptideShaker | 🐧 🍏

PeptideShaker is a search engine independent platform for interpretation of proteomics identification results from multiple search engines, currently supporting X!Tandem, MS-GF+, MS Amanda, OMSSA, MyriMatch, Comet, Tide, Mascot, Andromeda and mzIdentML. By combining the results from multiple search engines, while re-calculating PTM localization scores and redoing the protein inference, PeptideShaker attempts to give you the best possible understanding of your proteomics data

Proteomics Proteomics experiment Proteome

PTM localisation Protein identification Structure visualisation Validation Peptide identification Mass spectrum visualisation Enrichment analysis

Command-line tool Desktop application Apache-2.0 de.NBI Proteomics BioInfra.Prot

j mzReader

A Java parser library to process and visualize multiple text and XML-based mass spectrometry data formats.

Proteomics

Loading

Library

Proteomics

MSqRob | 🐧 🍏 🍓

<https://expasy.org>



Swiss Institute of
Bioinformatics

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Expasy

Swiss Bioinformatics Resource Portal



e.g. BLAST, UniProt, MSH6, Albumin...

Genes & Genomes

- Genomics
- Metagenomics
- Transcriptomics

Proteins & Proteomes

- Evolution biology
- Population genetics

Structural Biology

- Drug design
- Medicinal chemistry
- Structural analysis

Systems Biology

- Glycomics
- Lipidomics
- Metabolomics

SIB Resources

SwissRegulon Portal
Tools and data for regulatory genomics

SWISS-MODEL
Protein structure homology-modelling

V-pipe
Viral genomics pipeline

SwissDrugDesign
Widening access to computer-aided drug design

EPD
Eukaryotic Promoter Database

Bgee
Gene expression expertise

UniProtKB/Swiss-Prot
Protein knowledgebase

STRING
Protein-protein interaction networks and enrichment analysis

<https://biii.eu>



Advanced search (under construction)



All Content

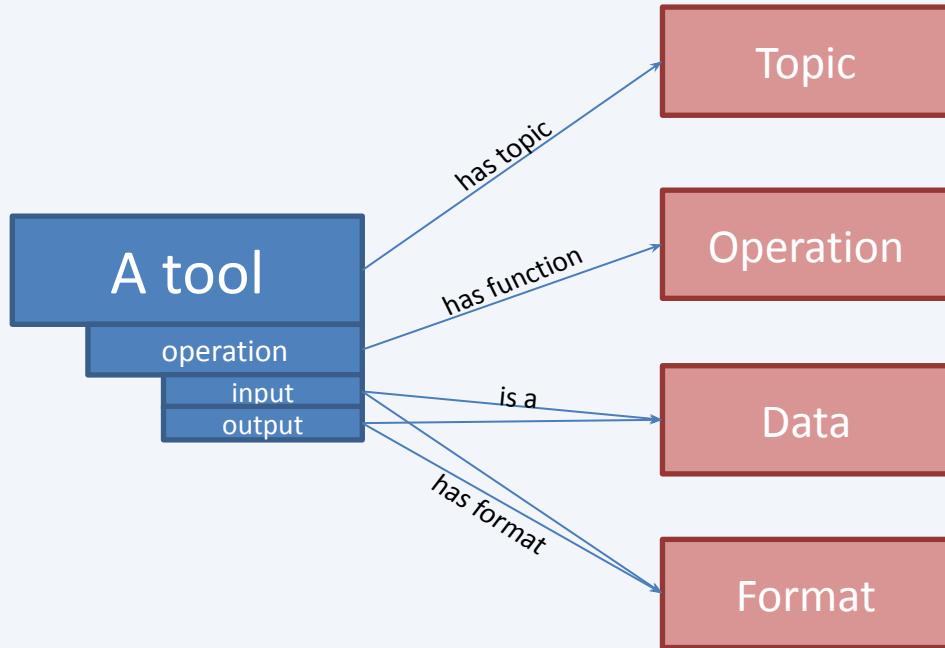
Displaying 1 - 20 of 41. Total number of pages: 3

Content type	Software	For which operation?	—Filament tracing <input type="button" value="X"/>
for which topic?	Choose some values (one or more)	Supported image dimension	Choose some values (one or more) <input type="button" value="Type -Any-"/>
Interaction level	Choose some values (one or more) <input type="button" value="License/Openness"/>	Choose some values (one or more) <input type="button" value="Programming language"/>	Choose some values (one or more)
specific biological term	Choose some values (one or more)	<input type="button" value="Apply"/>	

listing content

Name	Category	Image	requires	Type	interaction level	License/Openness	has function	has topic
Alvia - Alvia Cloud - Alvia Web	Software			Collection, Workflow	Automated, Manual, Semi-automated	Commercial	Analysis, Frequency analysis, Image analysis, Colocalisation analysis, Object-based colocalisation, Pixel-based colocalisation, Filament tracing, Image feature detection, Image segmentation, Cell segmentation, Pixel classification, Neuron image analysis, Object classification, Object tracking, Texture extraction, Object tracking, Cell tracking, Particle tracking, Annotation, Classification, Editing, Image deconvolution, Visualisation, Image visualisation, Volume rendering, Plotting	Machine learning
AnalyzeSkeleton	Software		ImageJ, Analyze 12.0	Component	Automated, Semi-automated		Filament tracing, Object detection, Pixel classification	
AnaMorf	Software		ImageJ	Component	Automated	Free and open source	Filament tracing	
Angiogenesis / Sprout Analyzer (ImageJ)	Software		ImageJ	Component	Semi-automated	Free and open source	Filament tracing, Neuron image analysis	Bioimage informatics, Fluorescence microscopy
APP (All-path pruning)	Software		Vaa3D	Component	Automated	Free and open source	Filament tracing, Image thresholding, Neuron image analysis	Confocal microscopy

Annotation of computational tools with EDAM



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Date Added

Scientific topic

RNA-Seq	53
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Data management	42
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Rare diseases	36
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Statistics and probability	20
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Bioinformatics	17
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Genomics	16
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Proteomics	16
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Phylogenetics	13
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Pathway or network	11
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Analysis of RNA-Seq Data

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, 1560 software packages, and an...

Scientific topics: RNA-Seq

eQTL / molecular-QTL analyses

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, 1560 software packages, and an...

Hands-on 2 (a couple of minutes)

- Search for tools relevant to your research topic, using the [Bio.tools](#) registry

or

- Search for educational materials in [TeSS](#)

Optional / Note: You can also sort tools in [Galaxy](#), using EDAM



Useful resources

Data processing

- rdmkit.elixir-europe.org/processing



EDAM ontology

EDAM

- github.com/edamontology/edamontology
- If you want to contribute, please find guide in [CONTRIBUTING.md](#) and join the community chat at gitter.im/edamontology/edamontology

Bio.tools bio.tools

BIII (Biolimage Informatics Index) biii.eu

TeSS (ELIXIR training portal) tess.elixir-europe.org

Thank you!



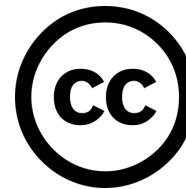
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