bio.tools and **EDAM** - making it easier to find, understand, and cite bioscientific software tools

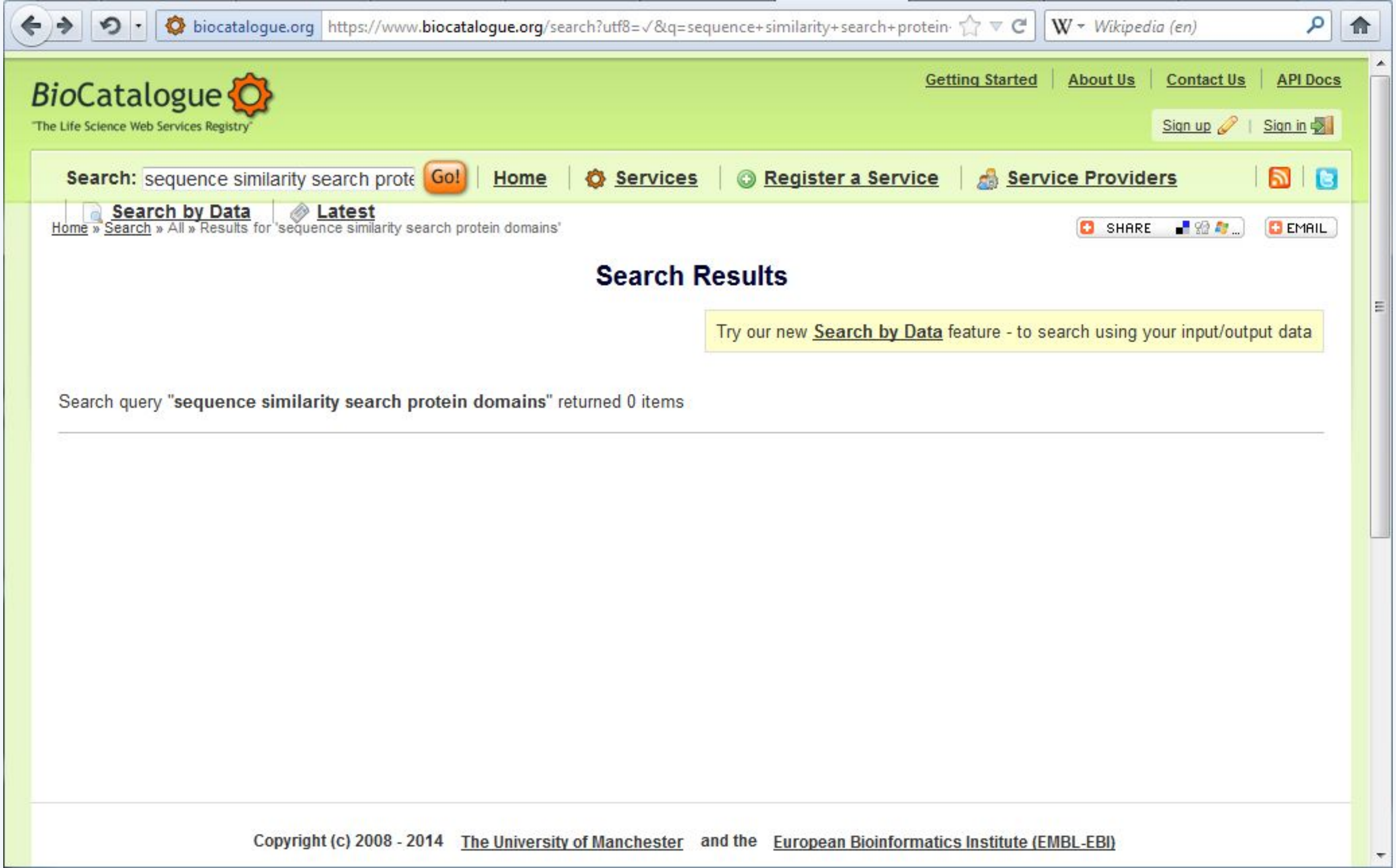
Hans Ienasescu, Technical University of Denmark, ELIXIR Denmark
Matúš Kalaš, University of Bergen, ELIXIR Norway

Australian BioCommons Webinar, 21 June 2022

www.elixir-europe.org

Motivation

(an example)



Home » Search » All » Results for 'sequence similarity search protein domains'

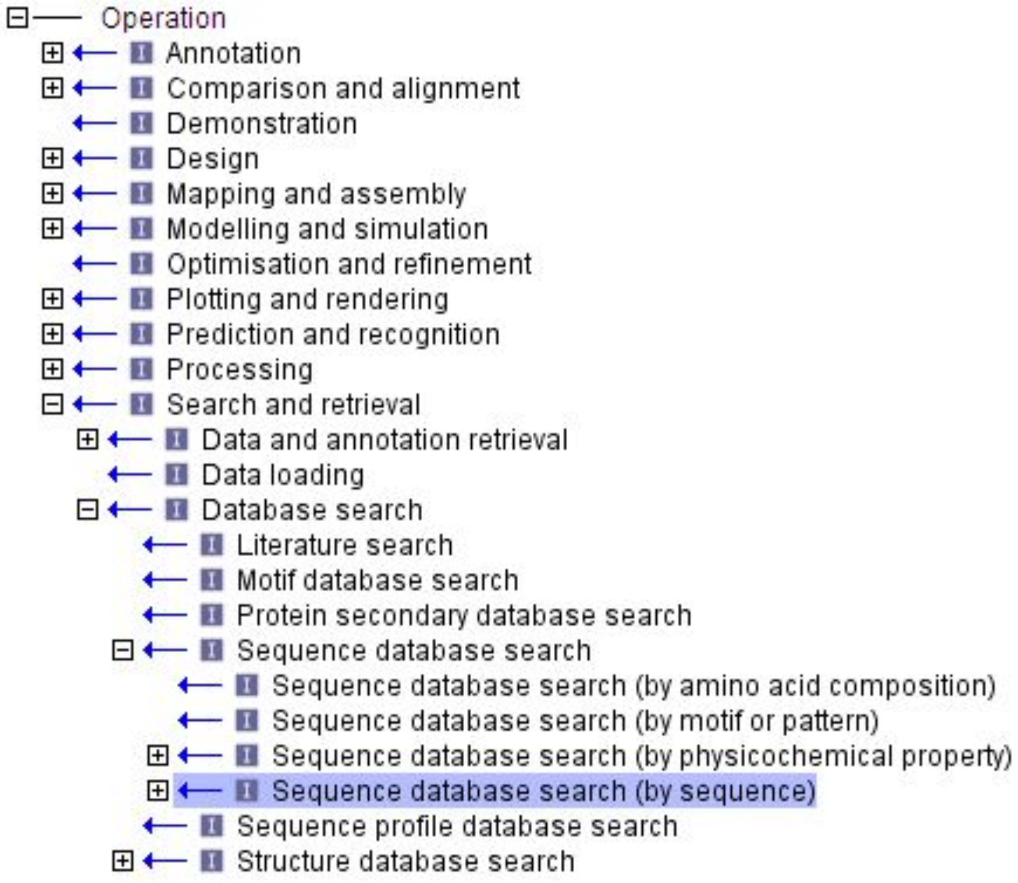
Search Results

Try our new **Search by Data** feature - to search using your input/output data

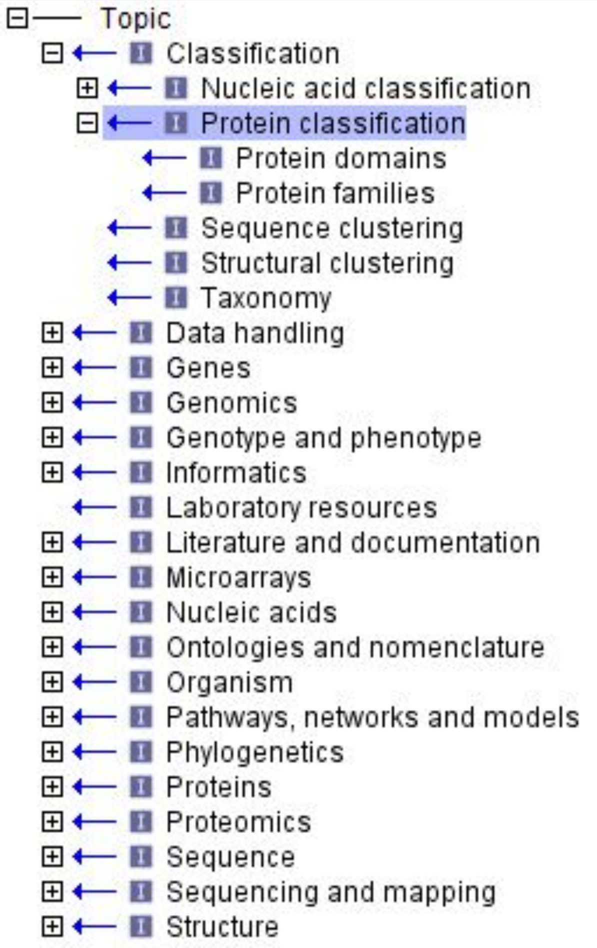
Search query "**sequence similarity search protein domains**" returned 0 items

Copyright (c) 2008 - 2014 The University of Manchester and the European Bioinformatics Institute (EMBL-EBI)

- 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



- 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
    - 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

1. **We need an ontology to describe what the tools do**

2. **We need a comprehensive registry of tools**

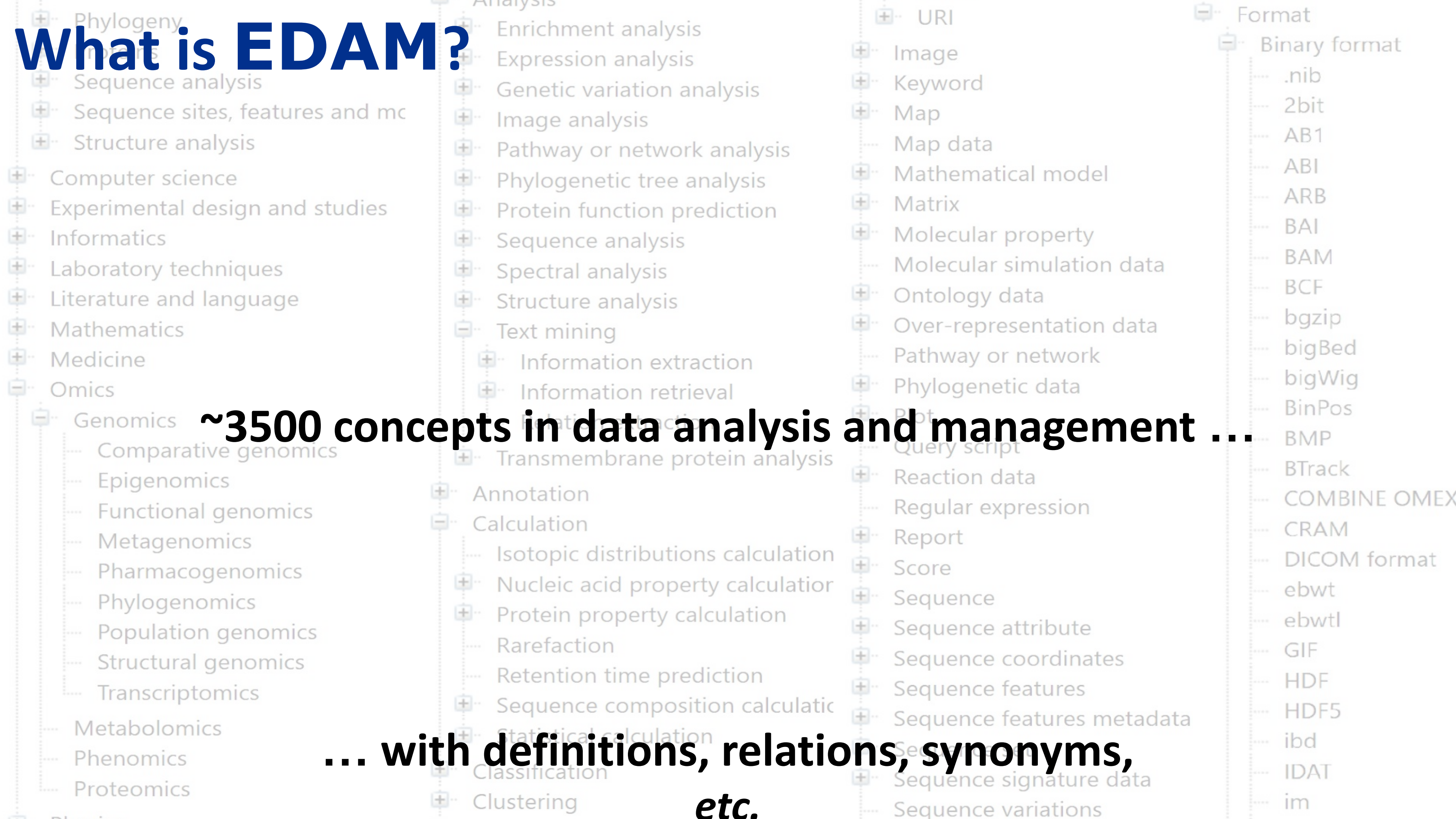
1. We need an ontology …

EDAM

The ontology of data analysis and data management

github.com/edamontology/edamontology

What is EDAM?



- Phylogeny
- Proteins
- Sequence analysis
- Sequence sites, features and mc
- 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
    - Relation extraction
  - Transmembrane protein analysis
- Annotation
- Calculation
  - Isotopic distributions calculation
  - Nucleic acid property calculatior
  - Protein property calculation
  - Rarefaction
  - Retention time prediction
  - Sequence composition calculatic
  - 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

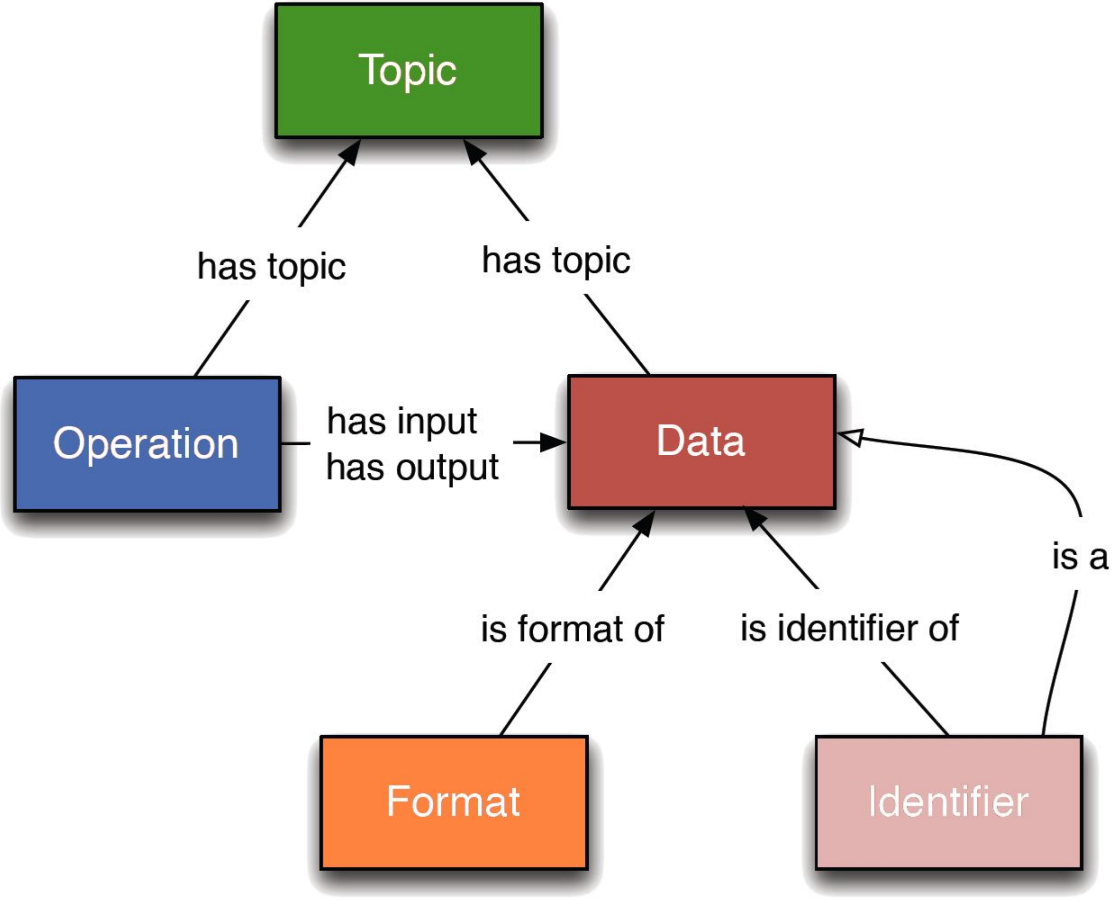
Position-specific scoring matrix

Format

FASTQ

SBML

Relations between concepts in EDAM



Usage areas of EDAM

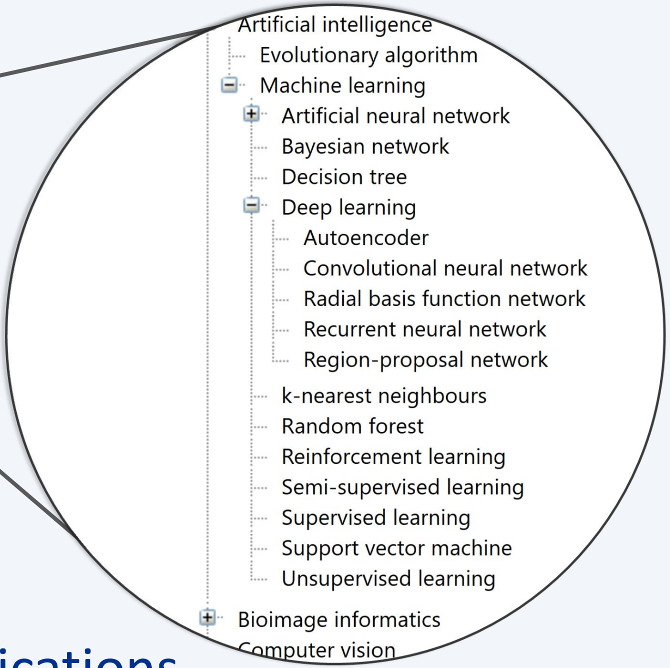
- Searching for tools, workflows, learning materials, ...
- Data provenance (metadata)
- Tools and data integration
- Text mining
- Choosing terminology

EDAM extensions

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

- **Bioimaging**

- **Geosciences**
  and interdisciplinary applications



- Artificial intelligence
  - Evolutionary algorithm
  - Machine learning
    - Artificial neural network
    - Bayesian network
    - Decision tree
    - Deep learning
      - Autoencoder
      - Convolutional neural network
      - Radial basis function network
      - Recurrent neural network
      - Region-proposal network
    - k-nearest neighbours
    - Random forest
    - Reinforcement learning
    - Semi-supervised learning
    - Supervised learning
    - Support vector machine
    - Unsupervised learning
- Bioimage informatics
- Computer vision

EDAM-
-bioimaging

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

---

Matúš Kalaš[1]✉, Laure Plantard[2], Joakim Lindblad[3], Martin Jones[4], Nataša Sladoje[3], Moritz A. Kirschmann[5], Anatole Chessel[6], Leandro Scholz[7], Fabienne Rössler[5], Laura Nicolás Sáenz[8], Estibaliz Gómez de Mariscal[8], John Bogovic[9], Alexandre Dufour[10], Xavier Heiligenstein[11], Dominic Waithe[12], Marie-Charlotte Domart[4], Matthia Karreman[13], Raf Van de Plas[14], Robert Haase[2], David Hörl[15], Lassi Paavolainen[16], Ivana Vrhovac Madunić[17], Dean Karaica[17], Arrate Muñoz-Barrutia[8], Paula Sampaio[18], Daniel Sage[19], Sebastian Munck[20], Ofra Golani[21], Josh Moore[22], Florian Levet[23], Jon Ison[24], Alban Gaignard[25], Hervé Ménager[10], Chong Zhang[26], Kota Miura[27], Julien Colombelli[28], and Perrine Paul-Gilloteaux[25]. ***We are welcoming new contributors!***

*[1]Computational Biology Unit, Department of Informatics, University of **Bergen, Norway**; [2]Max Planck Institute of Molecular Cell Biology and Genetics, **Dresden, Germany**; [3]Centre for Image Analysis, **Uppsala** University, **Sweden**; [4]Francis Crick Institute, **London, UK**; [5]Center for Microscopy and Image Analysis, University of **Zürich, Switzerland** (M.A.K. at the time of contribution); [6]École Polytechnique, **Palaiseau, France**; [7]Federal University of Paraná, **Curitiba, Brazil**; [8]Universidad Carlos III de **Madrid, Spain**; [9]Janelia Research Campus, **Ashburn, VA, USA**; [10]Institut Pasteur, **Paris, France** (A.D. at the time of contribution); [11]Institut Curie, **Paris, France**; [12]University of **Oxford, UK**; [13]Deutsches Krebsforschungszentrum, **Heidelberg, Germany**; [14]**Delft** University of Technology, **Netherlands**; [15]Ludwig-Maximilians-University of **Munich, Germany**; [16]FIMM, University of **Helsinki, Finland**; [17]Institute for Medical Research and Occupational Health, **Zagreb, Croatia**; [18]University of **Porto, Portugal**; [19]École Polytechnique Fédérale de **Lausanne, Switzerland**; [20]VIB & Dept. of Neuroscience, KU **Leuven, Belgium**; [21]Weizmann Institute, **Rehovot, Israel**; [22]Glencoe Software & University of **Dundee, UK**; [23]University of **Bordeaux, France**; [24]French Institute of Bioinformatics (IFB), **ELIXIR France**; [25]University of **Nantes, France**; [26]University Pompeu Fabra, **Barcelona, Spain**; [27]Nikon Imaging Center, University of **Heidelberg, Germany**; [28]Advanced Digital Microscopy core facility, Institute for Research in Biomedicine, **Barcelona, Spain**.*

https://github.com/edamontology/edam-bioimaging ***@edamontology*** ***/edamontology/edam-bioimaging*** ***wg4-edam_ontology@irbbarcelona.org.glip.com***

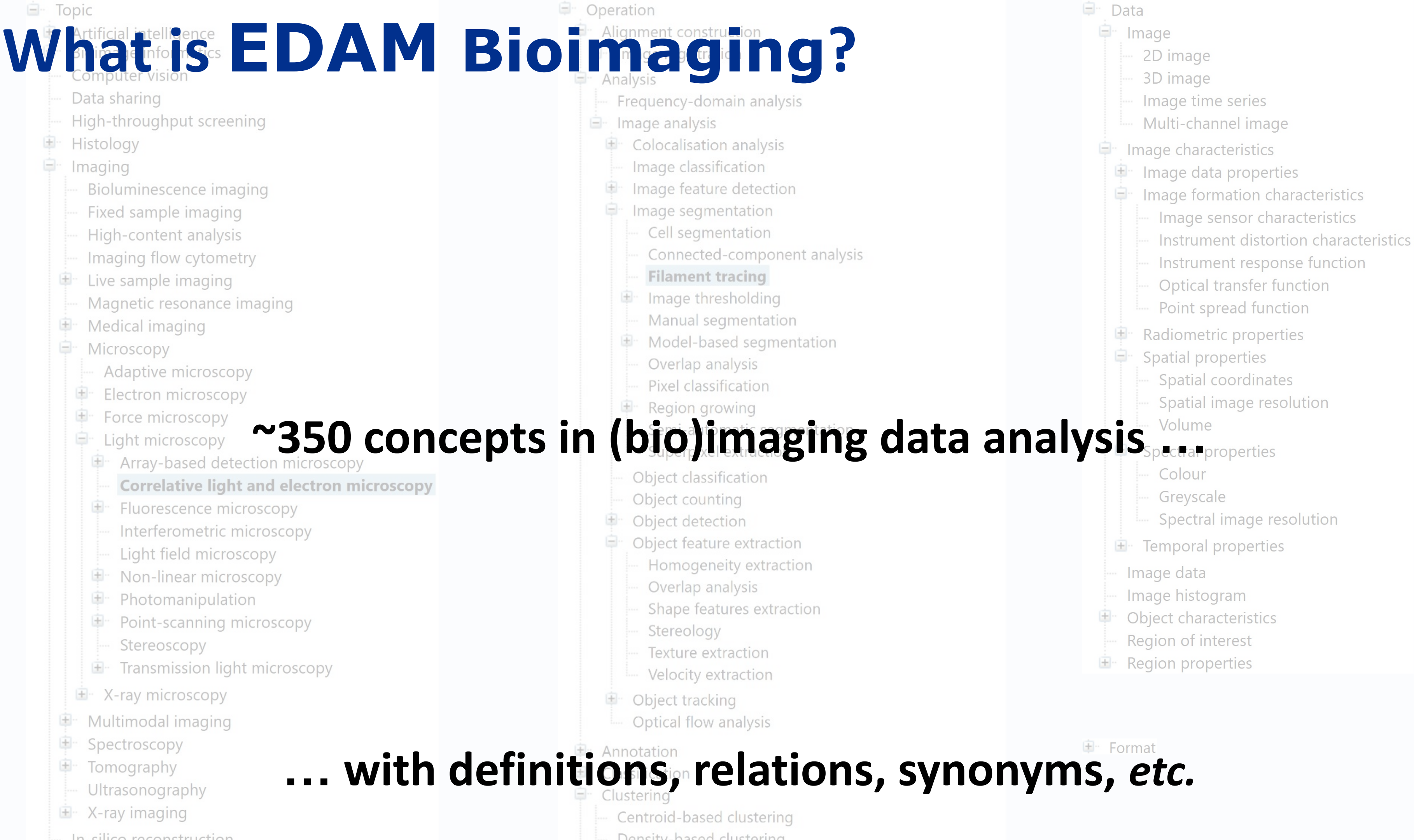
✉ *matus.kalas@uib.no* *@matuskalas*

2020 DOI 10.7490/f1000research.1117826.1

What is EDAM Bioimaging?

~350 concepts in (bio)imaging data analysis …

… with definitions, relations, synonyms, *etc.*



- 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
    - 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
        - 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
  - Annotation
  - Classification
  - 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

- Format

The scope of EDAM Bioimaging, with example concepts

Topic

Scanning electron microscopy

Convolutional neural network

Operation

Geometric distortion correction

Deformable registration

Data

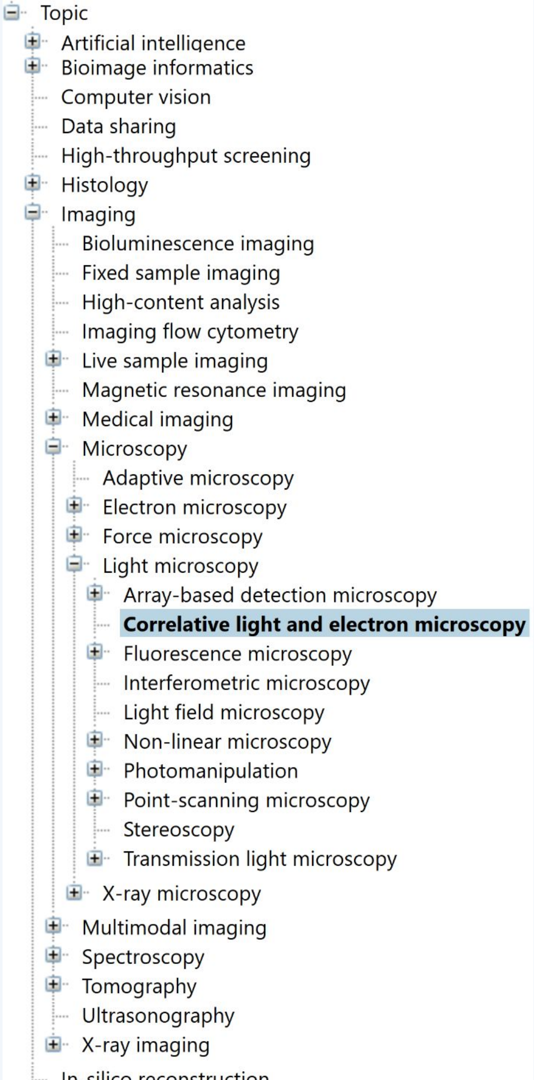
3D image

Image time series

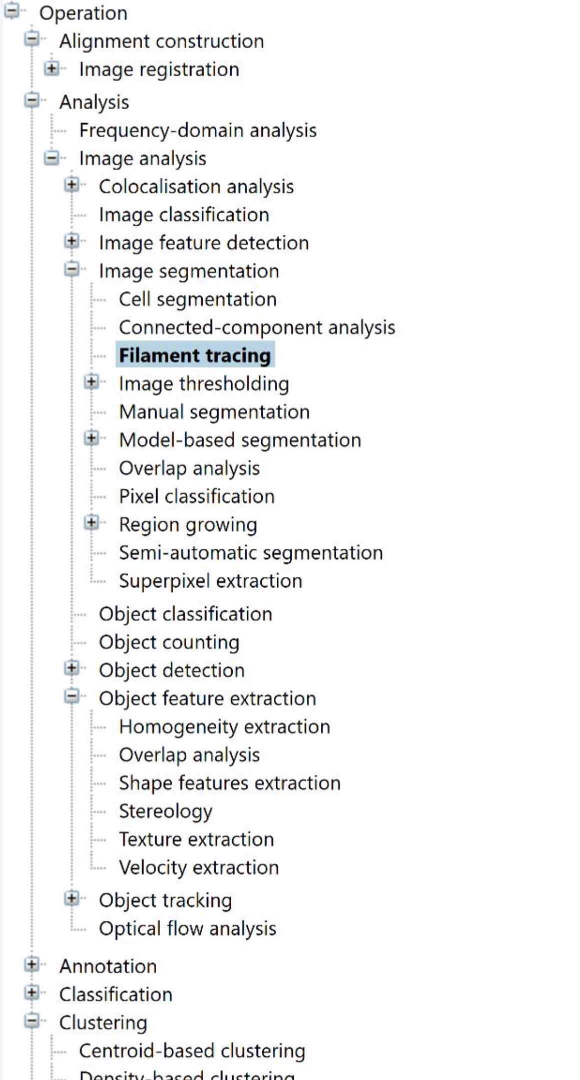
Format

MPEG

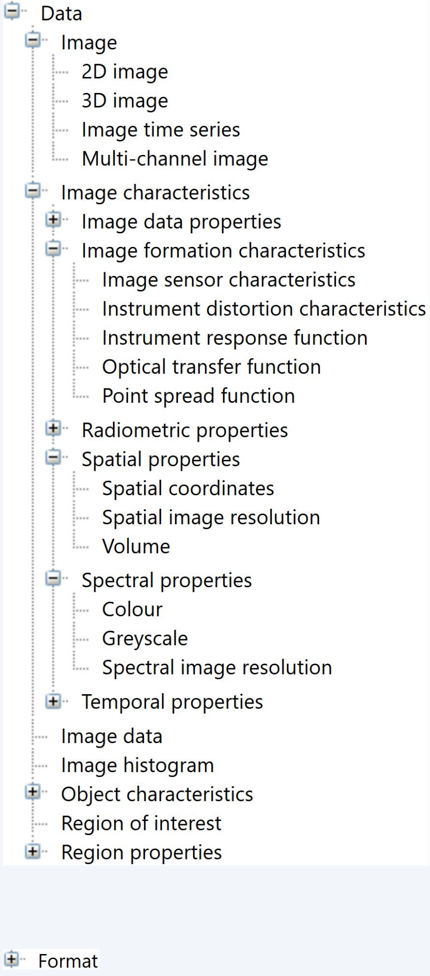
HDF5



- 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
    - Ultrasonography
    - X-ray imaging
  - In-silico reconstruction

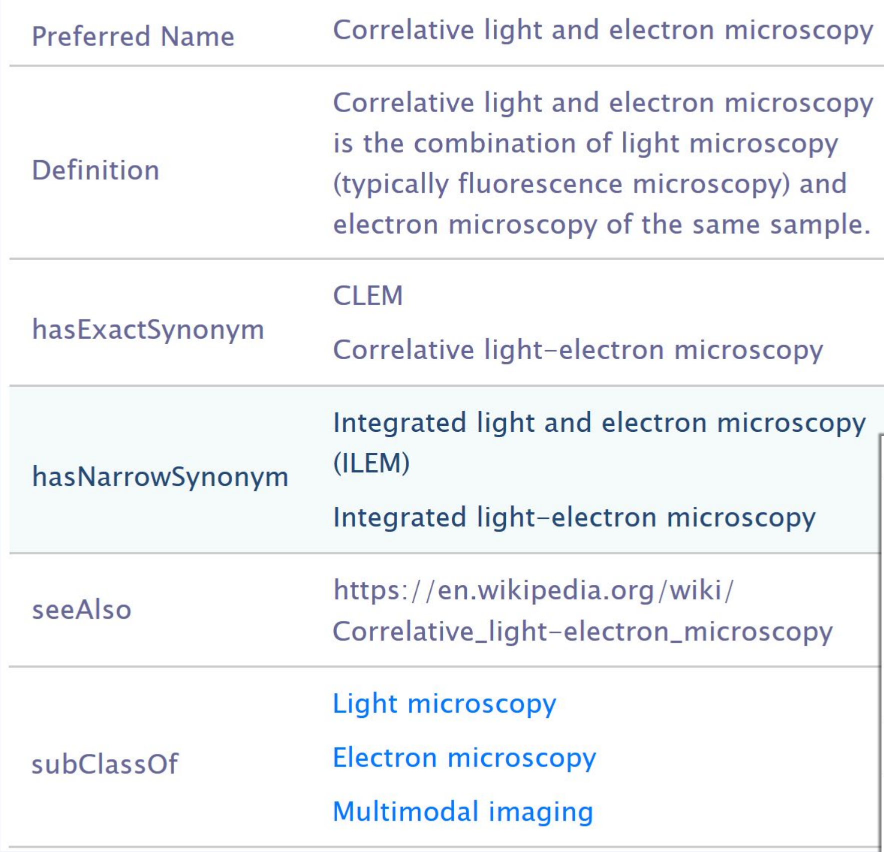


- Operation
  - Alignment construction
    - Image registration
  - Analysis
    - Frequency-domain analysis
    - Image analysis
      - Colocalisation analysis
      - Image classification
      - Image feature detection
      - Image segmentation
        - Cell segmentation
        - Connected-component analysis
        - **Filament tracing**
        - Image thresholding
        - Manual segmentation
        - Model-based segmentation
        - Overlap analysis
        - Pixel classification
        - Region growing
        - 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
  - Annotation
  - Classification
  - Clustering
    - Centroid-based clustering
    - Density-based clustering

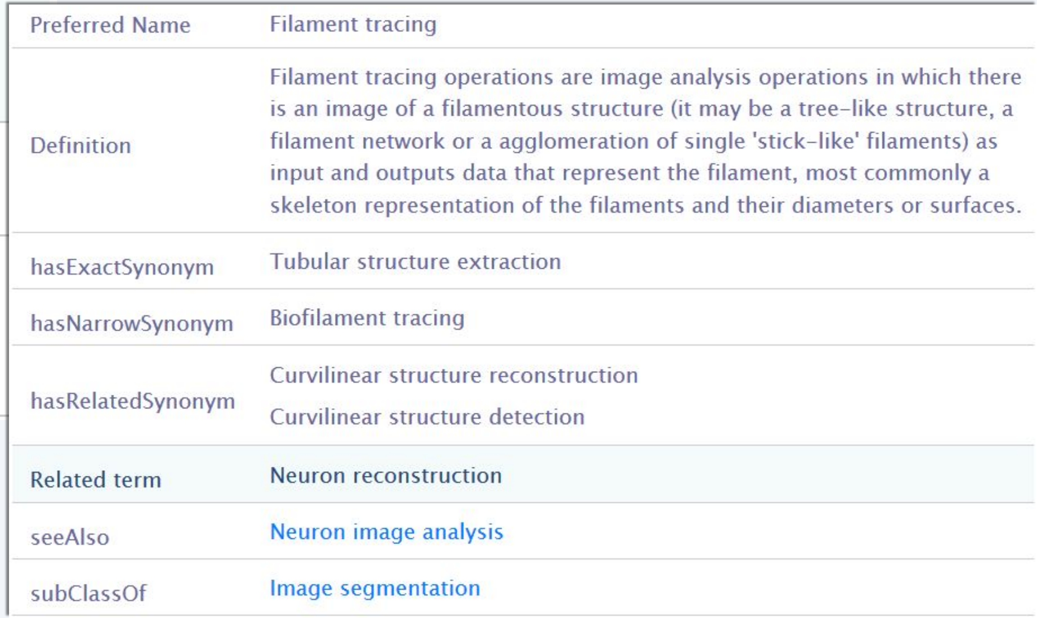


- Data
  - Image
    - 2D image
    - 3D image
    - Image time series
    - Multi-channel image
  - Image characteristics
    - Image data properties
    - Image formation characteristics
      - Image sensor characteristics
      - Instrument distortion characteristics
      - Instrument response function
      - 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

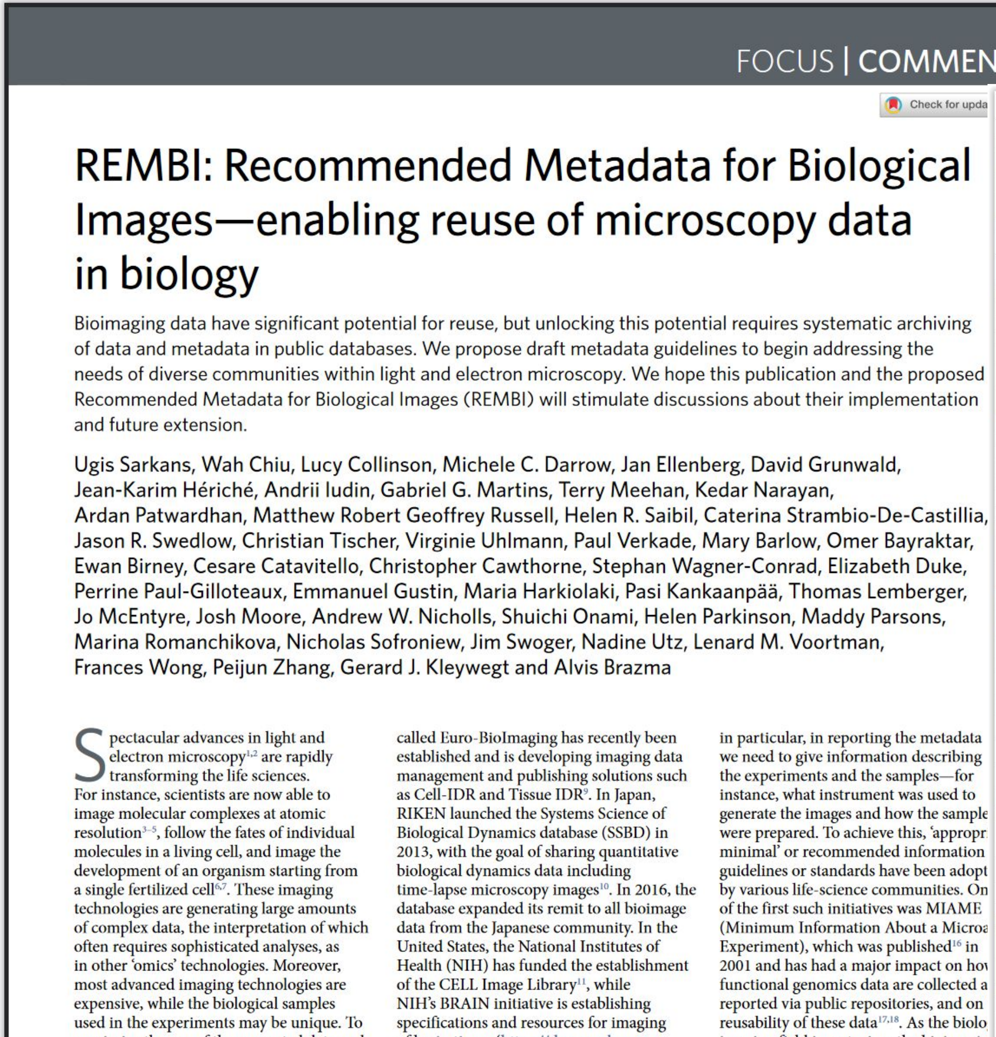
- Format



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



FOCUS | COMMENT

Check for upda

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

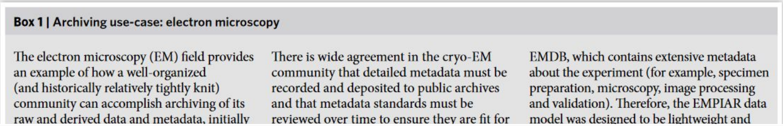
Bioimaging data have significant potential for reuse, but unlocking this potential requires systematic archiving of data and metadata in public databases. We propose draft metadata guidelines to begin addressing the needs of diverse communities within light and electron microscopy. We hope this publication 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 Catavitello, Christopher Cawthorne, 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 cell[6,7]. These imaging technologies are generating large amounts of complex data, the interpretation of which often requires sophisticated analyses, as in other 'omics' technologies. Moreover, most advanced imaging technologies are expensive, while the biological samples used in the experiments may be unique. To

called Euro-BioImaging has recently been established and is developing imaging data management and publishing solutions such as Cell-IDR and Tissue IDR[9]. 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 images[10]. In 2016, the database expanded its remit to all bioimage data from the Japanese community. In the United States, the National Institutes of Health (NIH) has funded the establishment of the CELL Image Library[11], while NIH's BRAIN initiative is establishing specifications and resources for imaging

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, 'appropr minimal' or recommended information guidelines or standards have been adopt by various life-science communities. On of the first such initiatives was MIAME (Minimum Information About a Microa Experiment), which was published[16] in 2001 and has had a major impact on ho functional genomics data are collected a reported via public repositories, and on reusability of these data[17,18]. As the biolo



Box 1 | Archiving use-case: electron microscopy

The electron microscopy (EM) field provides an example of how a well-organized (and historically relatively tightly knit) community can accomplish archiving of its raw and derived data and metadata, initially

There is wide agreement in the cryo-EM community that detailed metadata must be recorded and deposited to public archives and that metadata standards must be reviewed over time to ensure they are fit for

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

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
	Experimental variables	What is intentionally varied (e.g. time) between multiple entries in this study component	text and/or ontology entry (multiple possible)	EFO
Specimen				
(linked to Biosample)	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
	Channel - content	Specific specimen staining (e.g. IEM, DAB)	text	
	Channel - biological entity	What molecule is stained	text, ontology entries	EFO
Image acquisition				
(linked to Specimen)	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
Image data				
(result of Image acquisition, or processing of Image data)	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, tilts	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	OME
	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; N if stained features result in brighter (whiter) signal; Y if it looks like a TEM image	pull-down	
	QC info	QC score for uploaded image quality if applicable	text or controlled vocabulary	
Image Correlation				
(linked to 1 or more Image data)	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. .hx Amira files)	
	Related images and relationship	Correlated dataset or images	link	
Analysed data				
	Analysis result type	Numerical analyses, segmention (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)	
	Analysis method and details	Analysis method	text, file, ontology, or pointer to Methods section	EDAM-BIOIMAGING

Referenced existing standards and ontologies

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

The scope of EDAM Geo, with example concepts (WORK IN PROGRESS🦑)

Topic

Geosciences

Climate research

Operation

Climate simulation

Epidemics tracking

👾

Data

Geographical data

Geographical coordinate

Format

NetCDF-CF

GeoTIFF

EDAM became a ubiquitous component of numerous resources

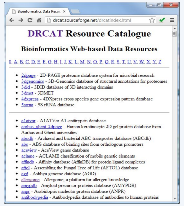
elixir bio.tools

elixir TeSS

Bioschemas

COMMON WORKFLOW LANGUAGE

FAIRsharing.org standards, databases, policies



Bioinformatics Data Reso… ×

drcat.sourceforge.net/drcatindex.html

DRCAT Resource Catalogue

Bioinformatics Web-based Data Resources

0, A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, Z

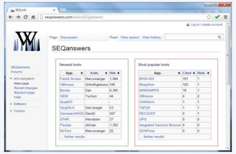
- 2dpage - 2D-PAGE proteome database system for microbial research
- 3dgenomics - 3D-Genomics database of structural annotations for proteomes
- 3did - 3DID database of 3D interacting domains
- 3dmet - 3DMET
- 4dxpress - 4DXpress cross species gene expression pattern database
- 5srrna - 5S rRNA database

- a1atvar - A1ATVar A1-antitrypsin database
- aarhus_ghent-2dpage - Human keratinocyte 2D gel protein database from Aarhus and Ghent universities
- abcdb - Archaeal and bacterial ABC transporter database (ABCdb)
- abs - ABS database of binding sites from orthologous promoters
- aceview - AceView genes database
- aclame - ACLAME classification of mobile genetic elements
- affindb - Affinity database (AffinDB) for protein ligand complexes
- aftol - Assembling the Fungal Tree of Life (AFTOL) database
- agd - Ashbya genome database (AGD)
- allergome - Allergome; a platform for allergen knowledge
- amypdb - Amyloid precursor proteins database (AMYPDB)
- anpr - Arabidopsis nucleolar protein database (ANPR)
- antibodypedia - Antibodypedia database of antibodies to human proteins

BioSimulators REPRODUCING & REUSING BIOMODELS & SIMULATIONS

EMBL-EBI

Workflow RO-Crate



SEQwiki ×

seqanswers.com/wiki/SEQanswers

Log in / create account

Page Discussion Read View source View history

SEQanswers

SEQanswers Forums
- wiki navigation
  - Main page
  - Recent changes
  - Random page
  - Help
- Software
- Toolbox

Newest tools:

App.	Auth.	Hits
FastQ Screen	Marcowanger	1,084
GBrowse	Girlwithglasses	595
Bowtie	Dan	6,365
GEM	Yuchun	44
QuadGT		
Seq2HLA	Seb.boegel	53
GensearchNGS	David2	567
STAR	Alexdobin	37
Flexbar	Jtbiman	1,305
MuTect	Marcowanger	25
… further results		

Most popular tools:

App.	Cited	Refs.
BWA-SW	191	1
Biopython	103	1
MARGARITA	18	1
GBrowse	4	2
CNANorm	1	1
TAPyR	1	1
RECOUNT	0	1
GPS	0	0
Integrated Genome Browser	0	0
SOAPsnp	0	0
… further results		

Australian BioCommons

HUMAN CELL ATLAS

Institut Pasteur

SIB

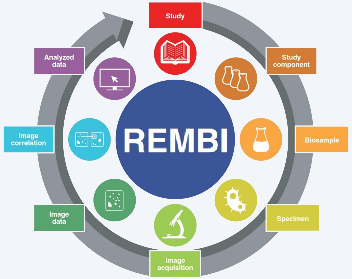
Expasy Swiss Bioinformatics Resource Portal

emboss *The European Molecular Biology Open Software Suite*

debian med

Biii BioImage Informatics Index

BioImage.IO



Galaxy PROJECT

… and many more …

2. We need a comprehensive registry of tools

The registry’s motivation

- Large number of tools and databases created to support (life-science) research
- Fragmented documentation and access to resources:
  - Hard to find, understand, compare and use
  - Lack formalised descriptions of scientific and technical functions
  - Persistence of identifiers not ensured
  - Reproducibility made hard

- **Need for a registry / portal / database of bioscientific software tools**
- Examples of tools registries / portals
  - Galaxy ToolShed
  - EMBOSS
  - EMBRACE Tools Registry
  - BioCatalogue
  - SEQanswers
  - OMICtools
  - Debian Med
  - Bioconductor

What is bio.tools?

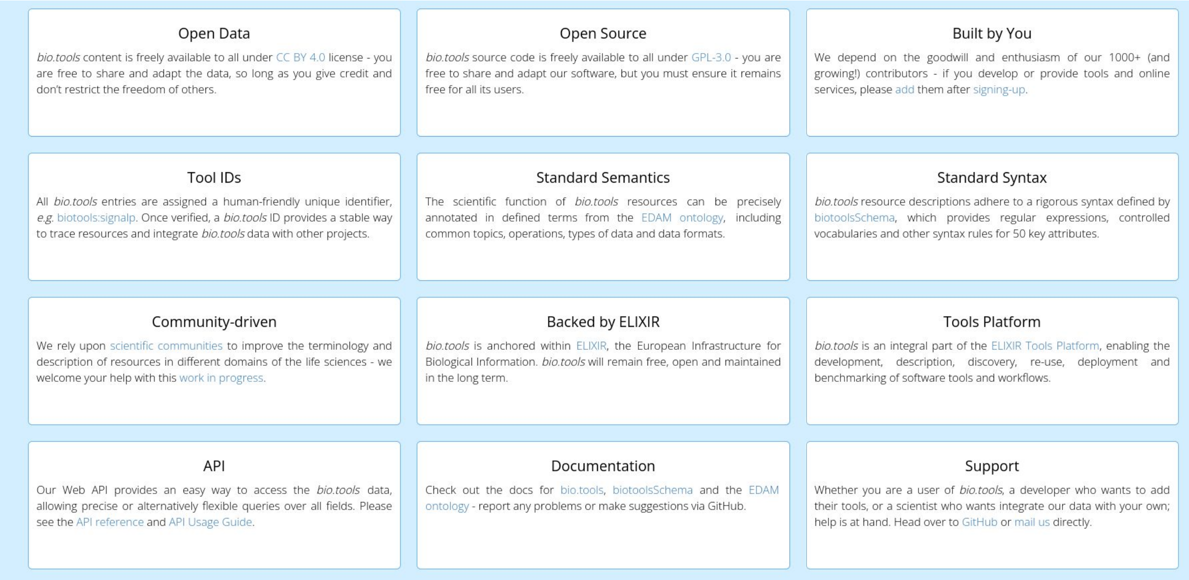
- **bio.tools** strives to provide a comprehensive registry of software and data services facilitating researchers from across the spectrum of biological and biomedical science to find, understand, utilise and cite the resources they need in their day-to-day work

Created in the context of the ELIXIR Europe life science infrastructure project

From simple command-line tools and online services, through to databases and complex, multi-functional analysis workflows

Contains tool descriptions (information, annotations about tools), not the actual tools themselves

https://bio.tools



Open Data

bio.tools content is freely available to all under CC BY 4.0 license - you are free to share and adapt the data, so long as you give credit and don't restrict the freedom of others.

Open Source

bio.tools source code is freely available to all under GPL-3.0 - you are free to share and adapt our software, but you must ensure it remains free for all its users.

Built by You

We depend on the goodwill and enthusiasm of our 1000+ (and growing!) contributors - if you develop or provide tools and online services, please add them after signing-up.

Tool IDs

All *bio.tools* entries are assigned a human-friendly unique identifier, *e.g.* biotools:signalp. Once verified, a *bio.tools* ID provides a stable way to trace resources and integrate *bio.tools* data with other projects.

Standard Semantics

The scientific function of *bio.tools* resources can be precisely annotated in defined terms from the EDAM ontology, including common topics, operations, types of data and data formats.

Standard Syntax

bio.tools resource descriptions adhere to a rigorous syntax defined by biotoolsSchema, which provides regular expressions, controlled vocabularies and other syntax rules for 50 key attributes.

Community-driven

We rely upon scientific communities to improve the terminology and description of resources in different domains of the life sciences - we welcome your help with this work in progress.

Backed by ELIXIR

bio.tools is anchored within ELIXIR, the European Infrastructure for Biological Information. *bio.tools* will remain free, open and maintained in the long term.

Tools Platform

bio.tools is an integral part of the ELIXIR Tools Platform, enabling the development, description, discovery, re-use, deployment and benchmarking of software tools and workflows.

API

Our Web API provides an easy way to access the *bio.tools* data, allowing precise or alternatively flexible queries over all fields. Please see the API reference and API Usage Guide.

Documentation

Check out the docs for bio.tools, biotoolsSchema and the EDAM ontology - report any problems or make suggestions via GitHub.

Support

Whether you are a user of *bio.tools*, a developer who wants to add their tools, or a scientist who wants integrate our data with your own; help is at hand. Head over to GitHub or mail us directly.

bio.tools principles

- Open data
  - Content is freely available for everyone, under the CC BY 4.0 licence
- Open source
  - Source code is freely available under GPL-3.0
- Built by the community
  - 5000+ (and growing!) contributors
- Persistent IDs
  - Unique, persistent, human-readable resource identifiers
- Standard semantics
  - Scientific function of bio.tools resources can be precisely annotated with defined concepts from the EDAM ontology, including common topics, operations, types of data, and data formats
- Standard syntax
  - Resources adhere to a rigorous syntax
  - ~50 key scientific, technical and administrative attributes (4 required)
- Community-driven
- Backed by ELIXIR
  - bio.tools will remain free, open, and maintained in the long-term

bio.tools stats

- 25,200+ tool entries
- 439,000+ total annotations
- 157,000+ EDAM annotations
- 5,100+ users
- 55,000+ average monthly visits in 2022 (Jan-May)

Data model behind: biotoolsSchema

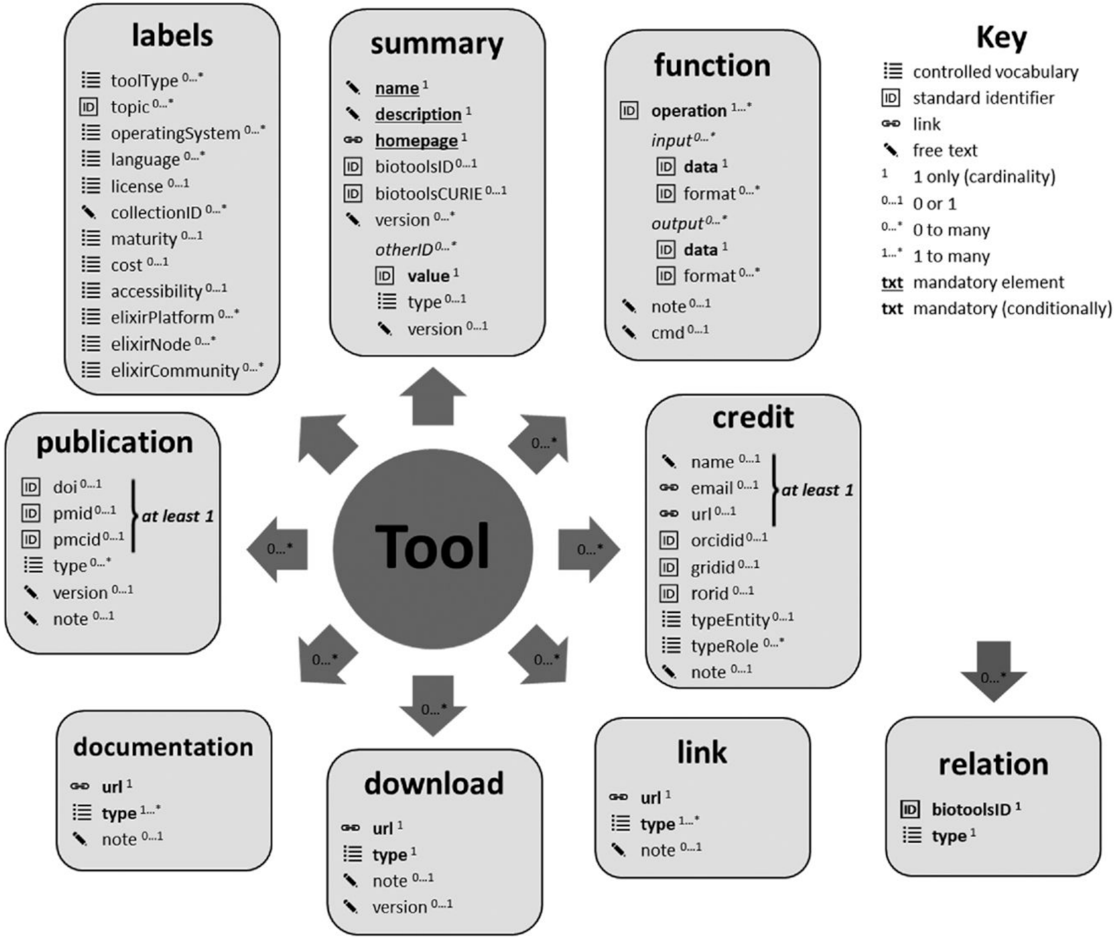
A simplified model which defined the attributes, information and scope provided to best describe software tools. A formal machine readable (and human understandable) schema to allow for data interoperability

- XML Schema (JSON Schema coming soon)
    - ~50 key scientific, technical and administrative attributes, uniform & rigorous syntax and semantics
- Controlled vocabularies (18 in total)
    - *e.g.* tool type, software licence, software maturity
- Community-defined standard (v3.3.0, mature)
    - from multiple workshops / iterations
- Compatible with related initiatives
    - Schema.org/Bioschemas, CodeMeta
- https://doi.org/10.1093/gigascience/giaa157

Data model: examples

- Required *
  - Name
  - biotoolsID
  - Description
  - Homepage
- Labels:
  - Topics
  - Tool Type
  - OS
  - Licence
  - Language
  - Cost
- Publication
- Download links
- Documentation links
- Other links
- Credits
- Function

bio.tools provides curation guidelines for each attribute to help curators and regular users describe tools in a standard manner

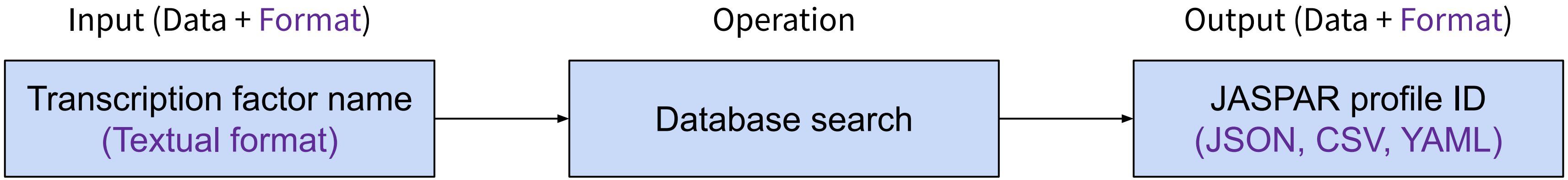


EDAM ontology in bio.tools

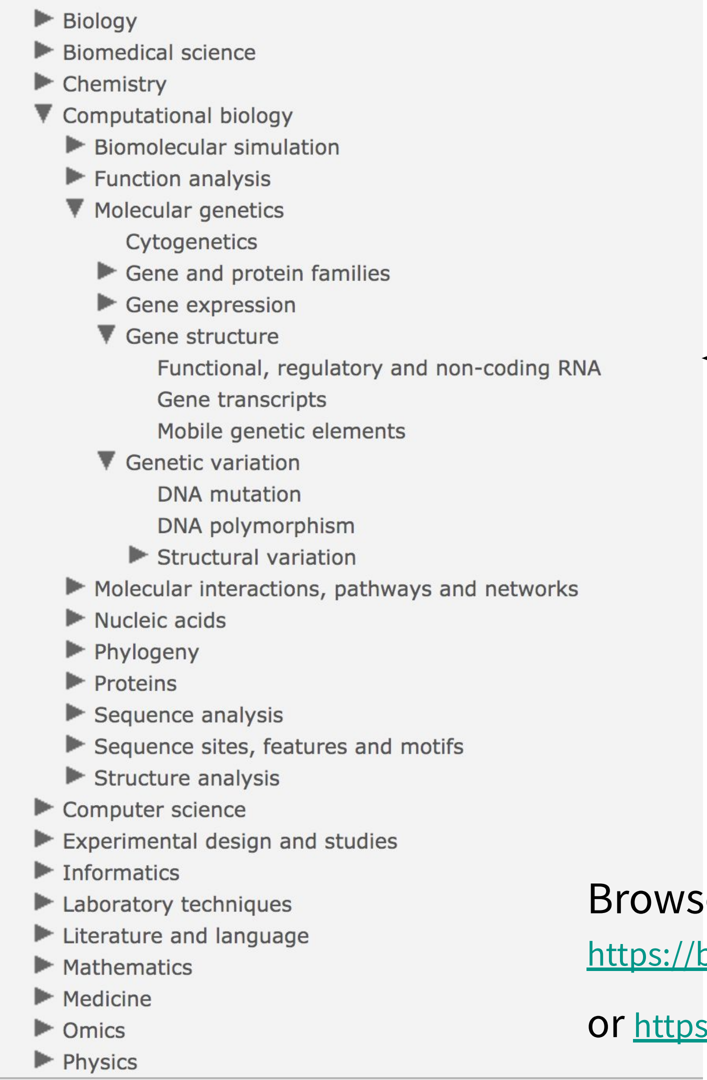
- Topics in *bio.tools* define the scientific or technical domains the tool is developed for

  e.g. Transcription factors and regulatory sites, Genomics, Gene regulation

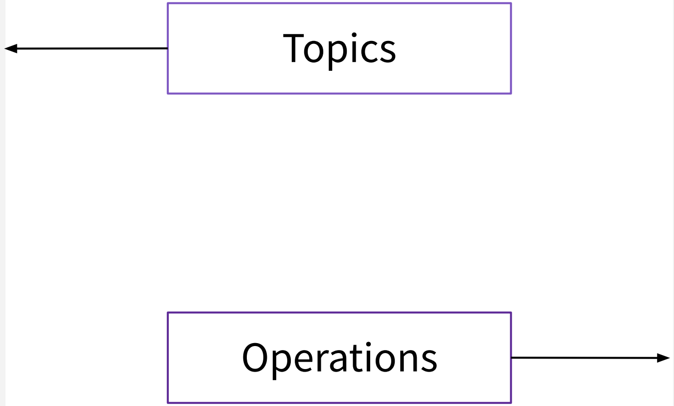
- EDAM Operations, Data, and Formats are used in the context of functional units
- Functional units in *bio.tools* are represented as “Input - Operation - Output” triplets
  - Input (EDAM Data + EDAM Format)
  - Operation (EDAM Operation)
  - Output (EDAM Data + EDAM Format)



EDAM has
a hierarchical structure

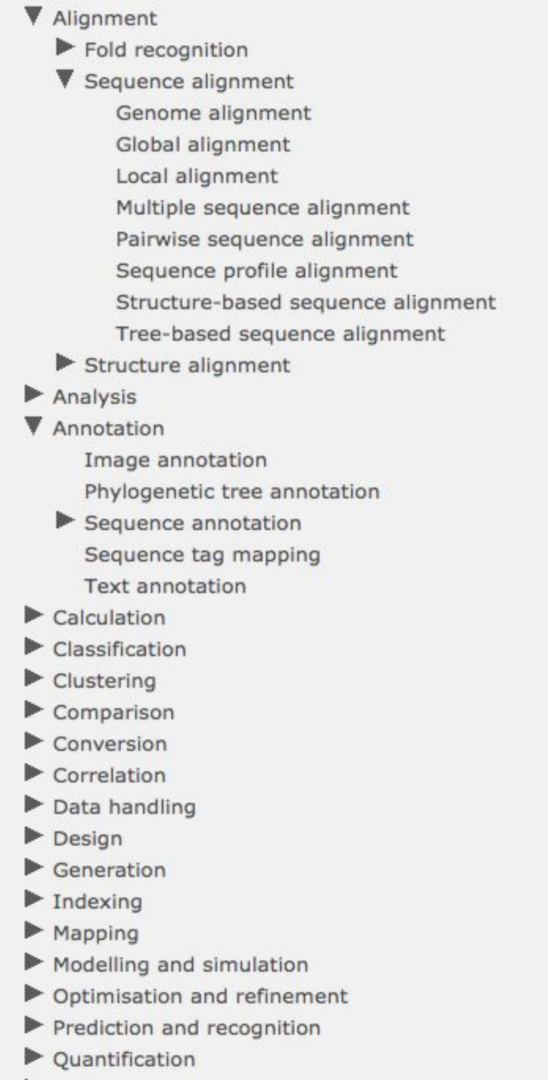


- ▶ Biology
- ▶ Biomedical science
- ▶ Chemistry
- ▼ Computational biology
  - ▶ Biomolecular simulation
  - ▶ Function analysis
  - ▼ Molecular genetics
    - Cytogenetics
    - ▶ Gene and protein families
    - ▶ Gene expression
    - ▼ Gene structure
      - Functional, regulatory and non-coding RNA
      - Gene transcripts
      - Mobile genetic elements
    - ▼ Genetic variation
      - DNA mutation
      - DNA polymorphism
      - ▶ Structural variation
  - ▶ Molecular interactions, pathways and networks
  - ▶ Nucleic acids
  - ▶ Phylogeny
  - ▶ Proteins
  - ▶ Sequence analysis
  - ▶ Sequence sites, features and motifs
  - ▶ Structure analysis
- ▶ Computer science
- ▶ Experimental design and studies
- ▶ Informatics
- ▶ Laboratory techniques
- ▶ Literature and language
- ▶ Mathematics
- ▶ Medicine
- ▶ Omics
- ▶ Physics



Topics

Operations



- ▼ Alignment
  - ▶ Fold recognition
  - ▼ Sequence alignment
    - Genome alignment
    - Global alignment
    - Local alignment
    - Multiple sequence alignment
    - Pairwise sequence alignment
    - Sequence profile alignment
    - Structure-based sequence alignment
    - Tree-based sequence alignment
  - ▶ Structure alignment
- ▶ Analysis
- ▼ Annotation
  - Image annotation
  - Phylogenetic tree annotation
  - ▶ Sequence annotation
  - Sequence tag mapping
  - Text annotation
- ▶ Calculation
- ▶ Classification
- ▶ Clustering
- ▶ Comparison
- ▶ Conversion
- ▶ Correlation
- ▶ Data handling
- ▶ Design
- ▶ Generation
- ▶ Indexing
- ▶ Mapping
- ▶ Modelling and simulation
- ▶ Optimisation and refinement
- ▶ Prediction and recognition
- ▶ Quantification

Browse EDAM visually at

https://bioportal.bioontology.org/ontologies/EDAM

or https://edamontology.github.io/edam-browser

Collaboration with diverse projects & communities

- Australian BioCommons: https://www.biocommons.org.au
- EDAM ontology: https://edamontology.org
- Debian Med: https://www.debian.org/devel/debian-med
- Galaxy: https://usegalaxy.eu
- BioContainers: https://biocontainers.pro
- Bioconda: https://bioconda.github.io
- SciCrunch: https://scicrunch.org
- ELIXIR TeSS: https://tess.elixir-europe.org
- FAIRsharing: https://fairsharing.org
- EuropePMC: https://europepmc.org
- ELIXIR Scientific Communities: https://elixir-europe.org/communities
- MathWorks: https://www.mathworks.com
- OpenEBench: https://openebench.bsc.es
- and others

Find tools in bio.tools

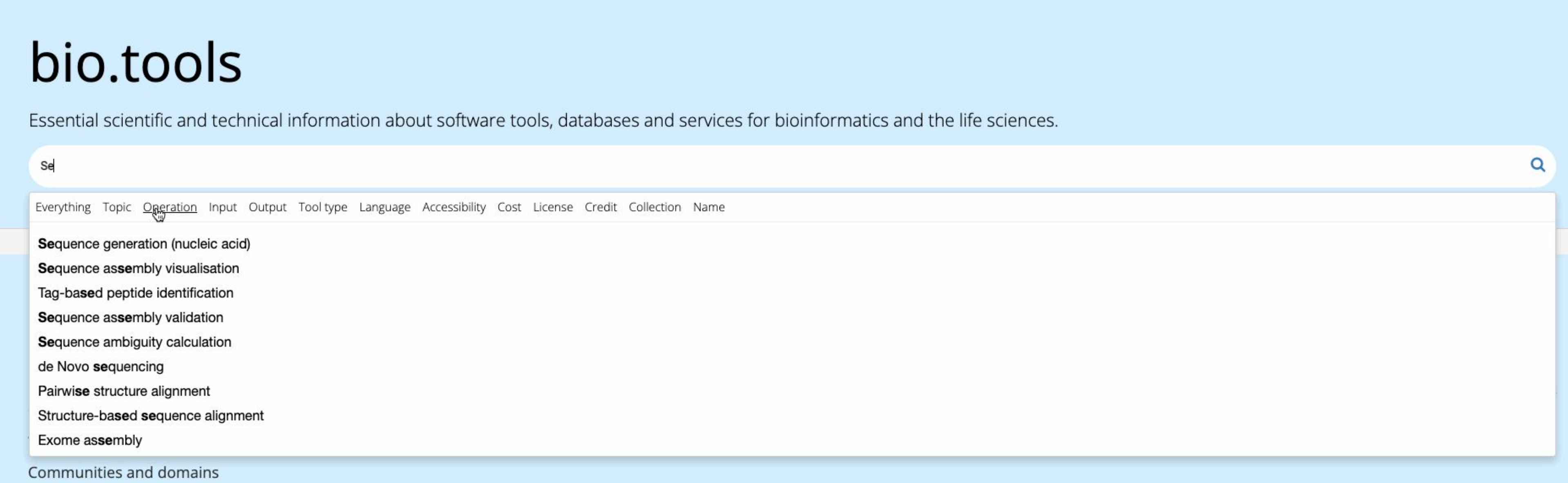
- Find tools by searching the registry
- Find tools by browsing by popular scientific concepts
- Find tools via *bio.tools* domains
- Find tools via *bio.tools* communities

Find tools in bio.tools: searching

- Find tools by searching the registry
    - Start typing what you’re looking for
- Find tools by browsing by popular scientific concepts
- Find tools via *bio.tools* domains
- Find tools via *bio.tools* communities

Searching bio.tools

- Faceted searching based on tool properties
- As-you-type query suggestion based on tool properties



bio.tools

Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.

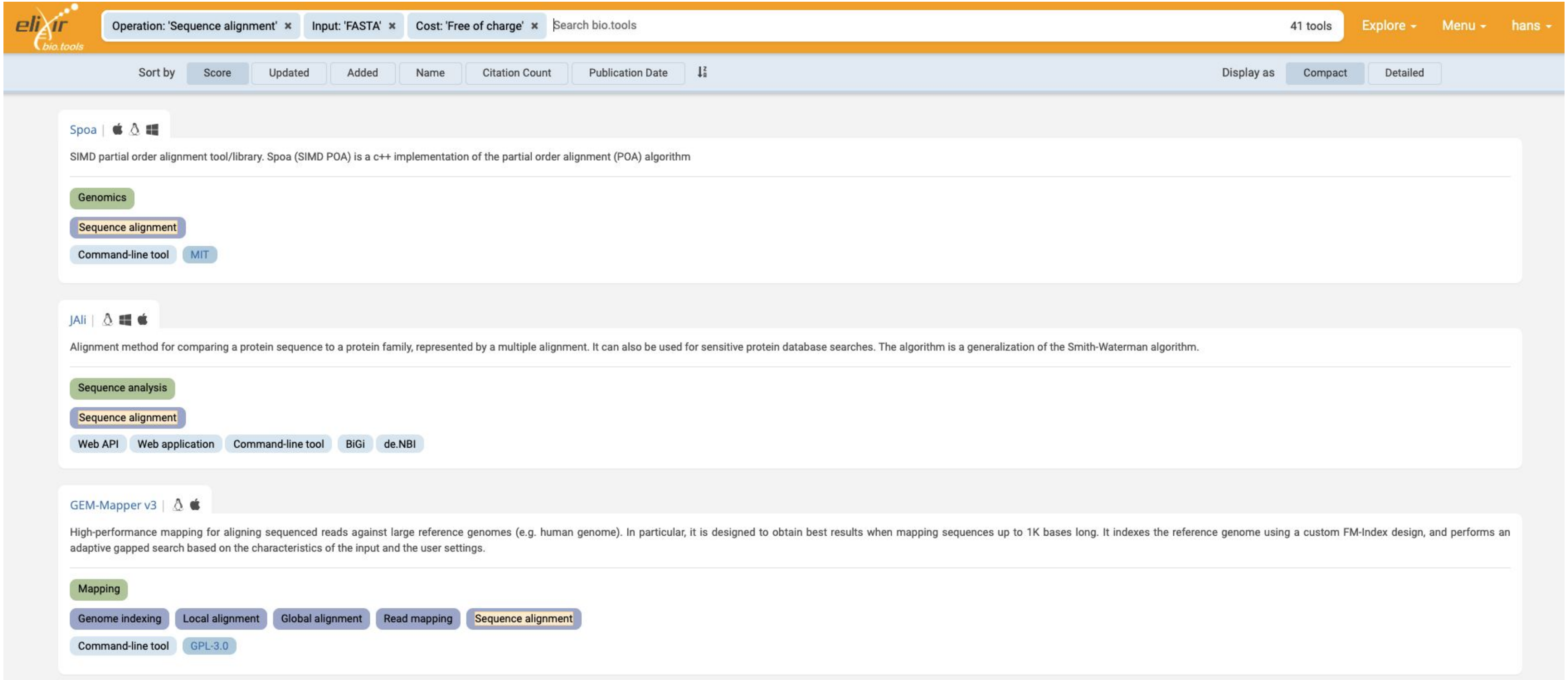
Se

Sequence generation (nucleic acid)
Sequence as**se**mbly visualisation
Tag-ba**se**d peptide identification
Sequence as**se**mbly validation
Sequence ambiguity calculation
de Novo **se**quencing
Pairwi**se** structure alignment
Structure-ba**se**d **se**quence alignment
Exome as**se**mbly

Communities and domains

Search results

- Preview tool information
- Sort search results



Spoa |

SIMD partial order alignment tool/library. Spoa (SIMD POA) is a c++ implementation of the partial order alignment (POA) algorithm

Genomics

Sequence alignment

Command-line tool MIT

JAli |

Alignment method for comparing a protein sequence to a protein family, represented by a multiple alignment. It can also be used for sensitive protein database searches. The algorithm is a generalization of the Smith-Waterman algorithm.

Sequence analysis

Sequence alignment

Web API Web application Command-line tool BiGi de.NBI

GEM-Mapper v3 |

High-performance mapping for aligning sequenced reads against large reference genomes (e.g. human genome). In particular, it is designed to obtain best results when mapping sequences up to 1K bases long. It indexes the reference genome using a custom FM-Index design, and performs an adaptive gapped search based on the characteristics of the input and the user settings.

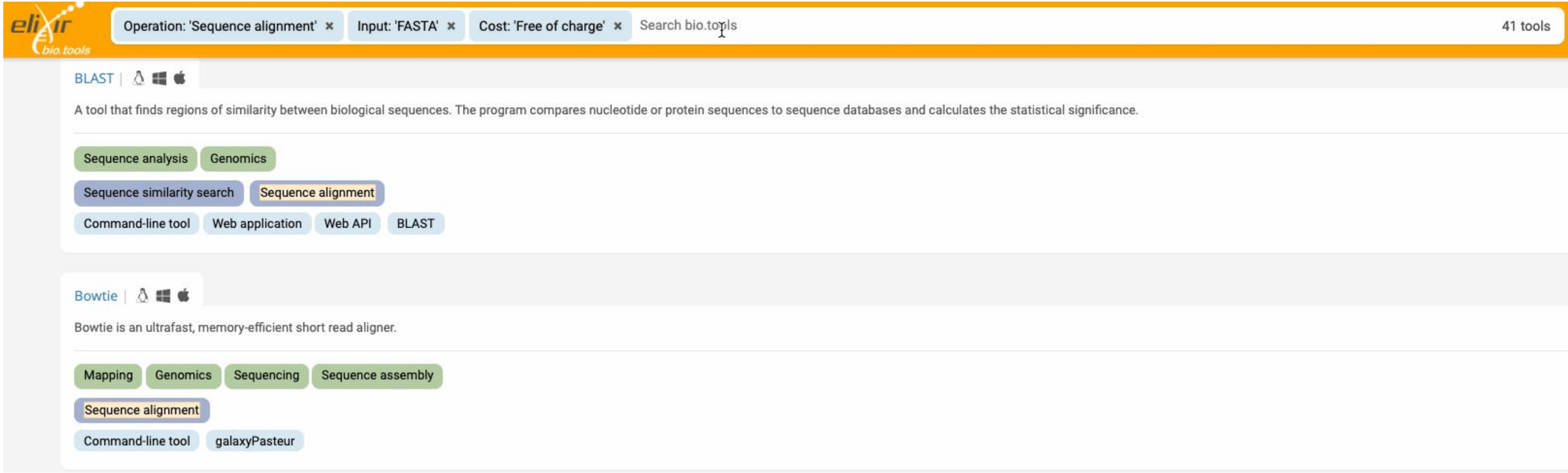
Mapping

Genome indexing Local alignment Global alignment Read mapping Sequence alignment

Command-line tool GPL-3.0

Search results and more search

- Refine your search as you view results
- Add / change / remove search query parameters



BLAST |

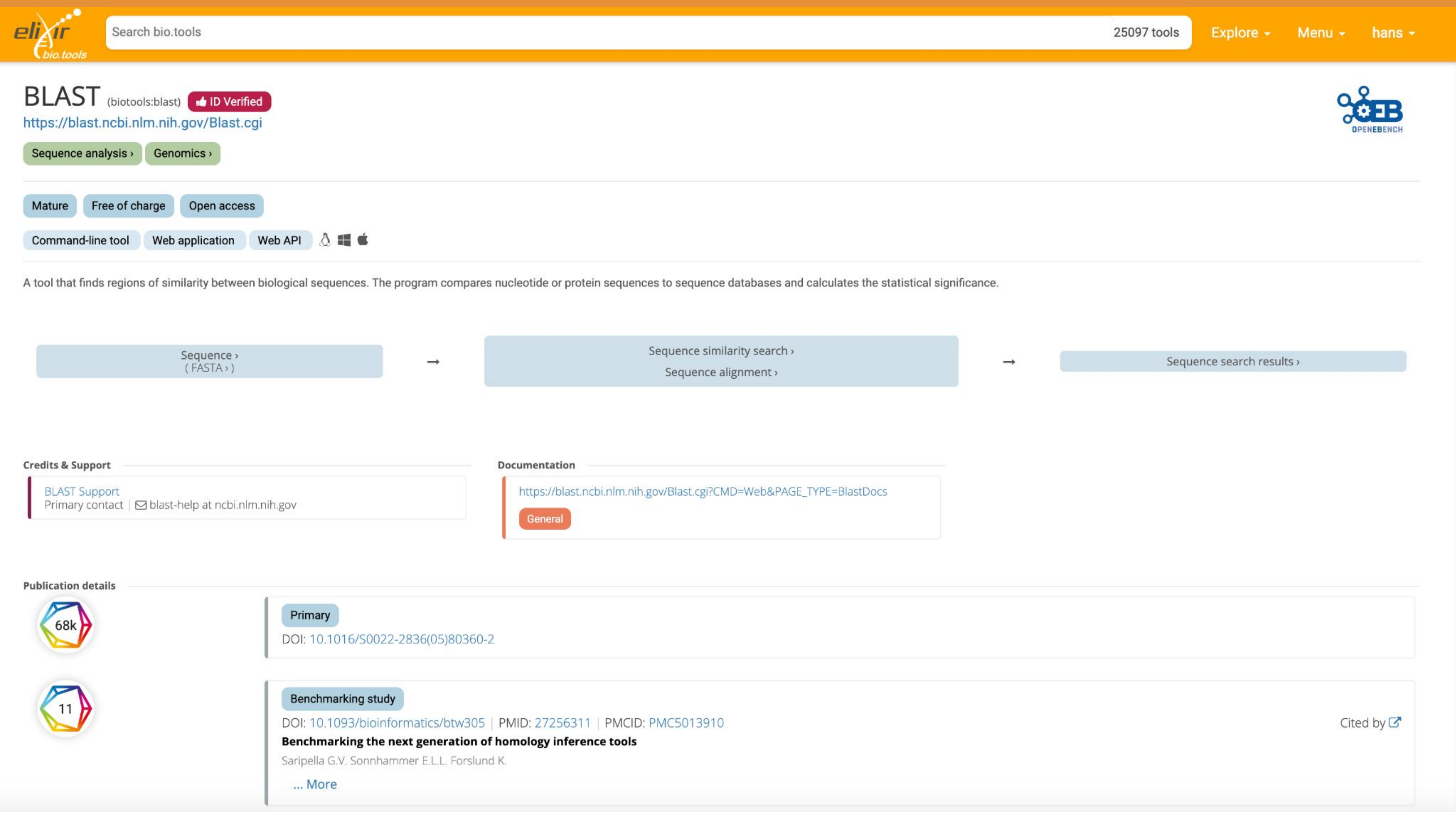
A tool that finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

Bowtie |

Bowtie is an ultrafast, memory-efficient short read aligner.

Even more searching options

- Search dropdown provides only *some* of the available searching options
- There are over 50 properties that can be used
- See all available properties at:
    - https://biotools.readthedocs.io/en/latest/api_reference.html#list-tools
    - https://biotools.readthedocs.io/en/latest/api_reference.html#attributes-1
- Any search via the interface can also be done via the API
- Example interface *vs.* API search URLs:
    - https://bio.tools/t?page=1&operation="Sequence alignment"&input="FASTA"&sort=score
    - https://bio.tools/**api**/t?page=1&operation="Sequence alignment"&input="FASTA"&sort=score
- bio.tools offers regular and quoted search; quoted search is more restrictive
    - https://bio.tools/t?page=1&q=proteomics&sort=score
    - https://bio.tools/t?page=1&q="proteomics"&sort=score
    - Both single and double quotes work (as long as they match)



BLAST (biotools:blast)

https://blast.ncbi.nlm.nih.gov/Blast.cgi

A tool that finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

Sequence › (FASTA ›) → Sequence similarity search › Sequence alignment › → Sequence search results ›

Credits & Support

BLAST Support
Primary contact | blast-help at ncbi.nlm.nih.gov

Documentation

https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastDocs

Publication details

Primary
DOI: 10.1016/S0022-2836(05)80360-2

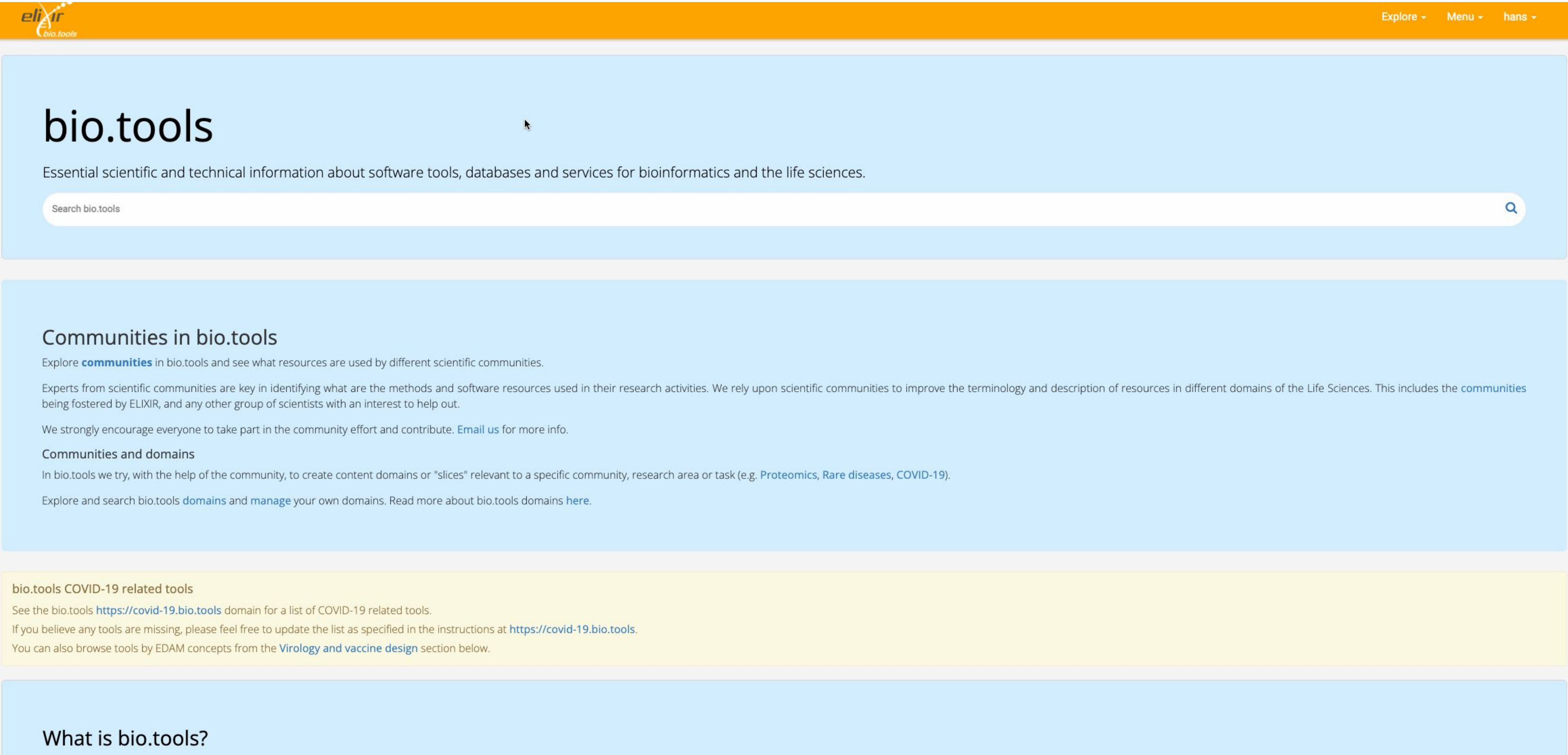
Benchmarking study
DOI: 10.1093/bioinformatics/btw305 | PMID: 27256311 | PMCID: PMC5013910

Benchmarking the next generation of homology inference tools
Saripella G.V. Sonnhammer E.L.L. Forslund K.

Find tools in bio.tools: browse concepts

- Find tools by searching the registry
- Find tools by browsing by popular scientific concepts
  - Scroll down on the homepage and click on the concepts
- Find tools via *bio.tools* domains
- Find tools via *bio.tools* communities

Browse by popular EDAM concepts



bio.tools

Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences.

Communities in bio.tools

Explore **communities** in bio.tools and see what resources are used by different scientific communities.

Experts from scientific communities are key in identifying what are the methods and software resources used in their research activities. We rely upon scientific communities to improve the terminology and description of resources in different domains of the Life Sciences. This includes the communities being fostered by ELIXIR, and any other group of scientists with an interest to help out.

We strongly encourage everyone to take part in the community effort and contribute. Email us for more info.

Communities and domains

In bio.tools we try, with the help of the community, to create content domains or "slices" relevant to a specific community, research area or task (e.g. Proteomics, Rare diseases, COVID-19).

Explore and search bio.tools domains and manage your own domains. Read more about bio.tools domains here.

bio.tools COVID-19 related tools

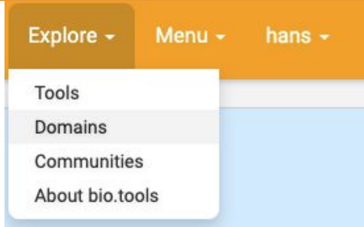
See the bio.tools https://covid-19.bio.tools domain for a list of COVID-19 related tools.

If you believe any tools are missing, please feel free to update the list as specified in the instructions at https://covid-19.bio.tools.

You can also browse tools by EDAM concepts from the Virology and vaccine design section below.

What is bio.tools?

Find tools in bio.tools: domains

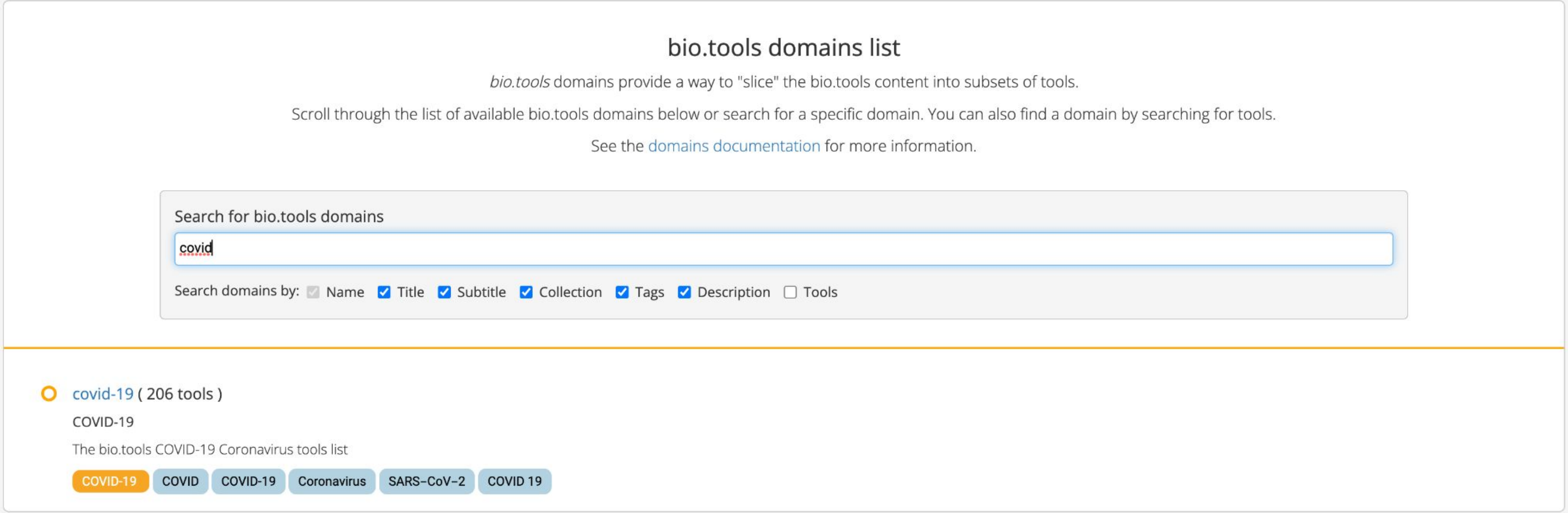


- Find tools by searching the registry
- Find tools by browsing by popular scientific concepts
- Find tools via *bio.tools* domains
  - Explore ➡ Domains
- Find tools via *bio.tools* communities

bio.tools domains

- Sets of tools related to each other in some way (“slices” of bio.tools content)
  - *e.g.* tools from a research institution, tools related to COVID, rare diseases, *etc.*; your favorite tools
  - Start with a smaller number of tools
  - Perform the same type of searches
  - https://bio.tools/domains

Create or manage your domains at https://bio.tools/domain-manager



bio.tools domains list

bio.tools domains provide a way to "slice" the bio.tools content into subsets of tools.

Scroll through the list of available bio.tools domains below or search for a specific domain. You can also find a domain by searching for tools.

See the domains documentation for more information.

Search for bio.tools domains

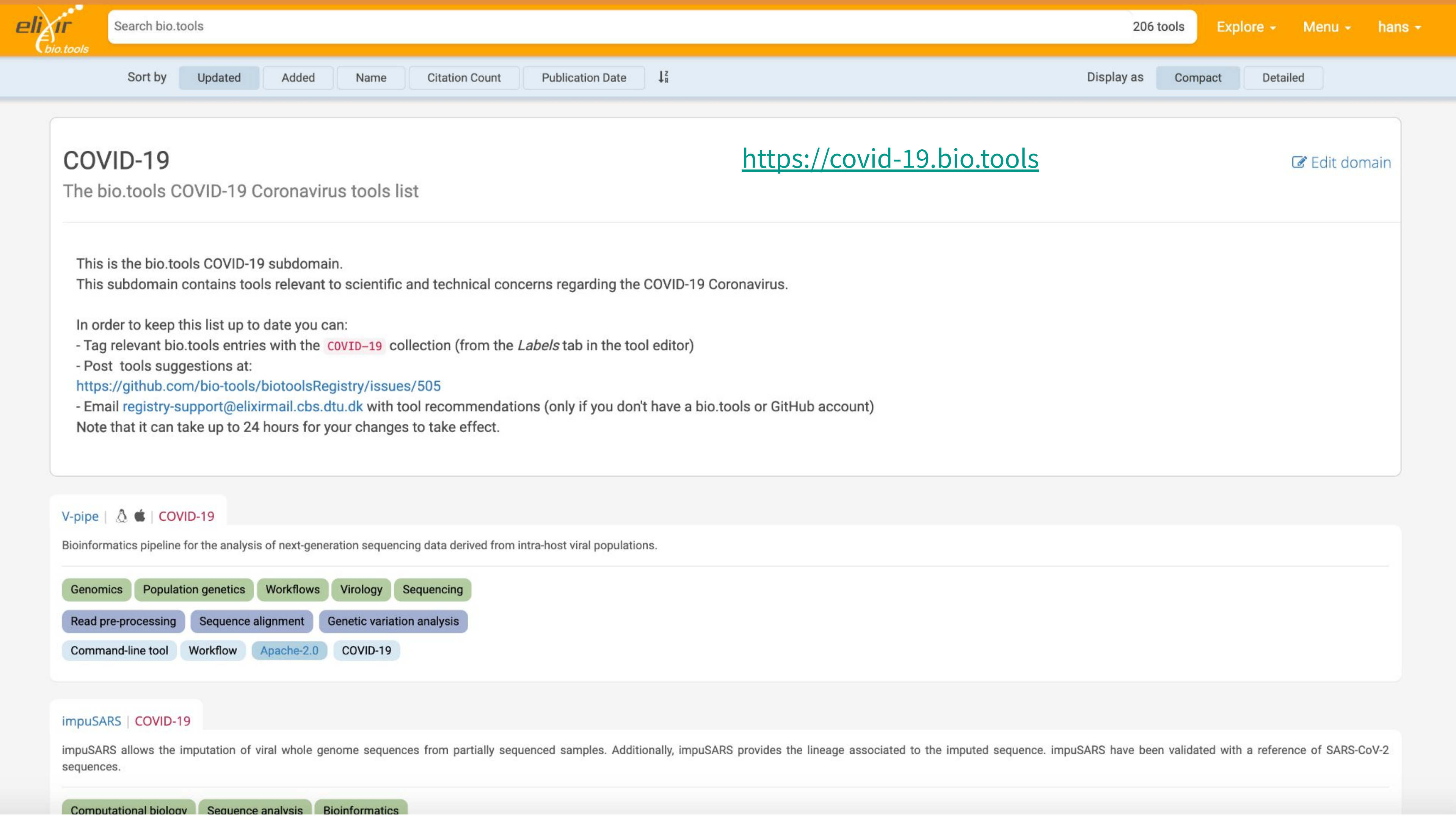
covid

Search domains by: ☑ Name ☑ Title ☑ Subtitle ☑ Collection ☑ Tags ☑ Description ☐ Tools

○ covid-19 (206 tools)

COVID-19

The bio.tools COVID-19 Coronavirus tools list



https://covid-19.bio.tools

COVID-19

The bio.tools COVID-19 Coronavirus tools list

This is the bio.tools COVID-19 subdomain.
This subdomain contains tools relevant to scientific and technical concerns regarding the COVID-19 Coronavirus.

In order to keep this list up to date you can:
- Tag relevant bio.tools entries with the `COVID-19` collection (from the *Labels* tab in the tool editor)
- Post tools suggestions at: https://github.com/bio-tools/biotoolsRegistry/issues/505
- Email registry-support@elixirmail.cbs.dtu.dk with tool recommendations (only if you don't have a bio.tools or GitHub account)

Note that it can take up to 24 hours for your changes to take effect.

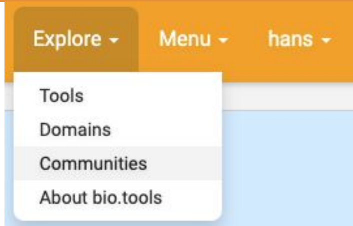
V-pipe | COVID-19

Bioinformatics pipeline for the analysis of next-generation sequencing data derived from intra-host viral populations.

impuSARS | COVID-19

impuSARS allows the imputation of viral whole genome sequences from partially sequenced samples. Additionally, impuSARS provides the lineage associated to the imputed sequence. impuSARS have been validated with a reference of SARS-CoV-2 sequences.

Find tools in bio.tools: communities

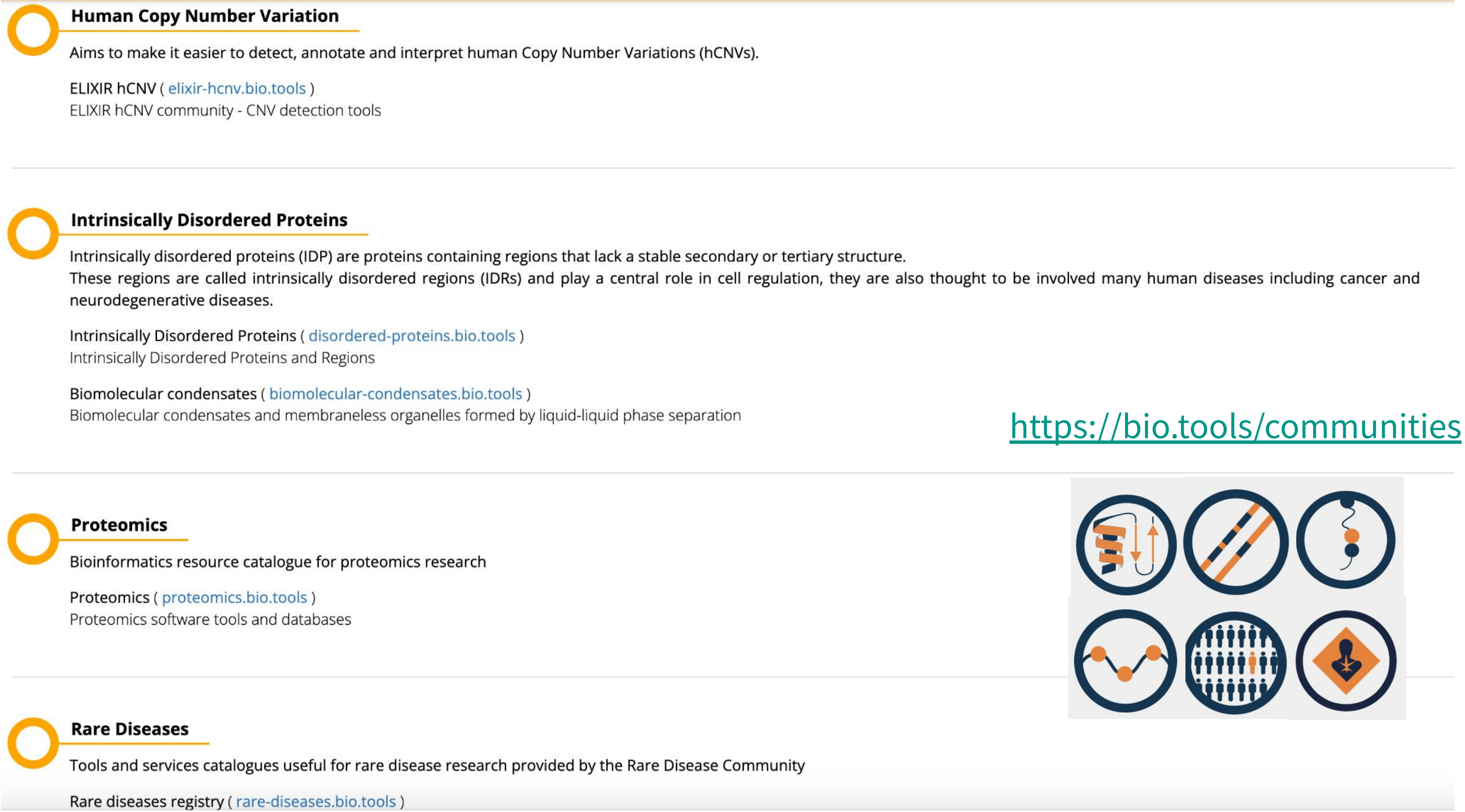


- Find tools by searching the registry
- Find tools by browsing by popular scientific concepts
- Find tools via *bio.tools* domains
- Find tools via *bio.tools* communities
  - Explore ➡ Communities

bio.tools and communities

- (Tool) Experts come from various specialised scientific communities
- Communities drive the state-of-the-art research
- What are the tools used by the scientific communities?
- Are those tools in *bio.tools*?
- Do *bio.tools* / EDAM offer the necessary context for communities to annotate their tools?
- Are there new tools that can become part of the “state of the art” for a community?

bio.tools communities



Human Copy Number Variation

Aims to make it easier to detect, annotate and interpret human Copy Number Variations (hCNVs).

ELIXIR hCNV (elixir-hcnv.bio.tools)
ELIXIR hCNV community - CNV detection tools

Intrinsically Disordered Proteins

Intrinsically disordered proteins (IDP) are proteins containing regions that lack a stable secondary or tertiary structure.
These regions are called intrinsically disordered regions (IDRs) and play a central role in cell regulation, they are also thought to be involved many human diseases including cancer and neurodegenerative diseases.

Intrinsically Disordered Proteins (disordered-proteins.bio.tools)
Intrinsically Disordered Proteins and Regions

Biomolecular condensates (biomolecular-condensates.bio.tools)
Biomolecular condensates and membraneless organelles formed by liquid-liquid phase separation

Proteomics

Bioinformatics resource catalogue for proteomics research

Proteomics (proteomics.bio.tools)
Proteomics software tools and databases

Rare Diseases

Tools and services catalogues useful for rare disease research provided by the Rare Disease Community

Rare diseases registry (rare-diseases.bio.tools)

https://bio.tools/communities

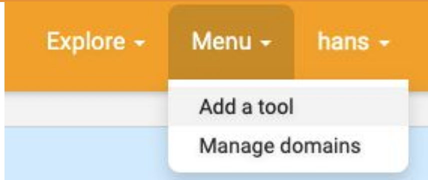
Contributing to bio.tools

- Add new tools
- Claim ownership of tools
- Request edit rights
- Update existing tools
- Create domains
- Create a community
- Contribute to code
  - https://github.com/bio-tools/biotoolsRegistry
  - https://github.com/bio-tools/content
- Contribute to documentation
  - https://biotools.readthedocs.io

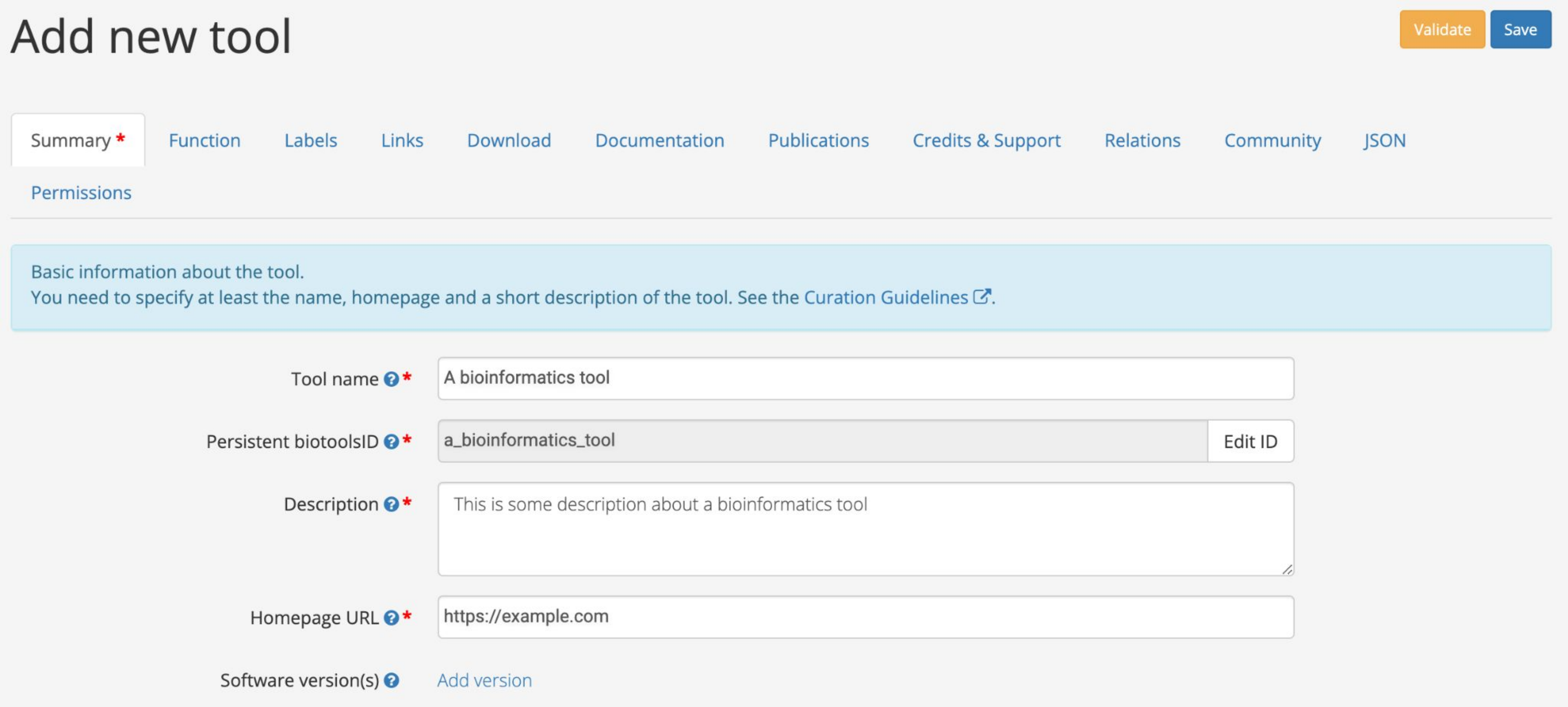
- help@bio.tools

Add a new tool

- Requires an account and login
  - Username
  - Email address
  - https://bio.tools/signup
- Menu ➡ Add a tool
- Can add any tool you think belongs to bio.tools
  - You don't have to be the creator of the tool
  - Just make sure the tool isn't already added
- Only 4 required fields



New tool: required* fields



Add new tool

Basic information about the tool.
You need to specify at least the name, homepage and a short description of the tool. See the Curation Guidelines.

Tool name *: A bioinformatics tool

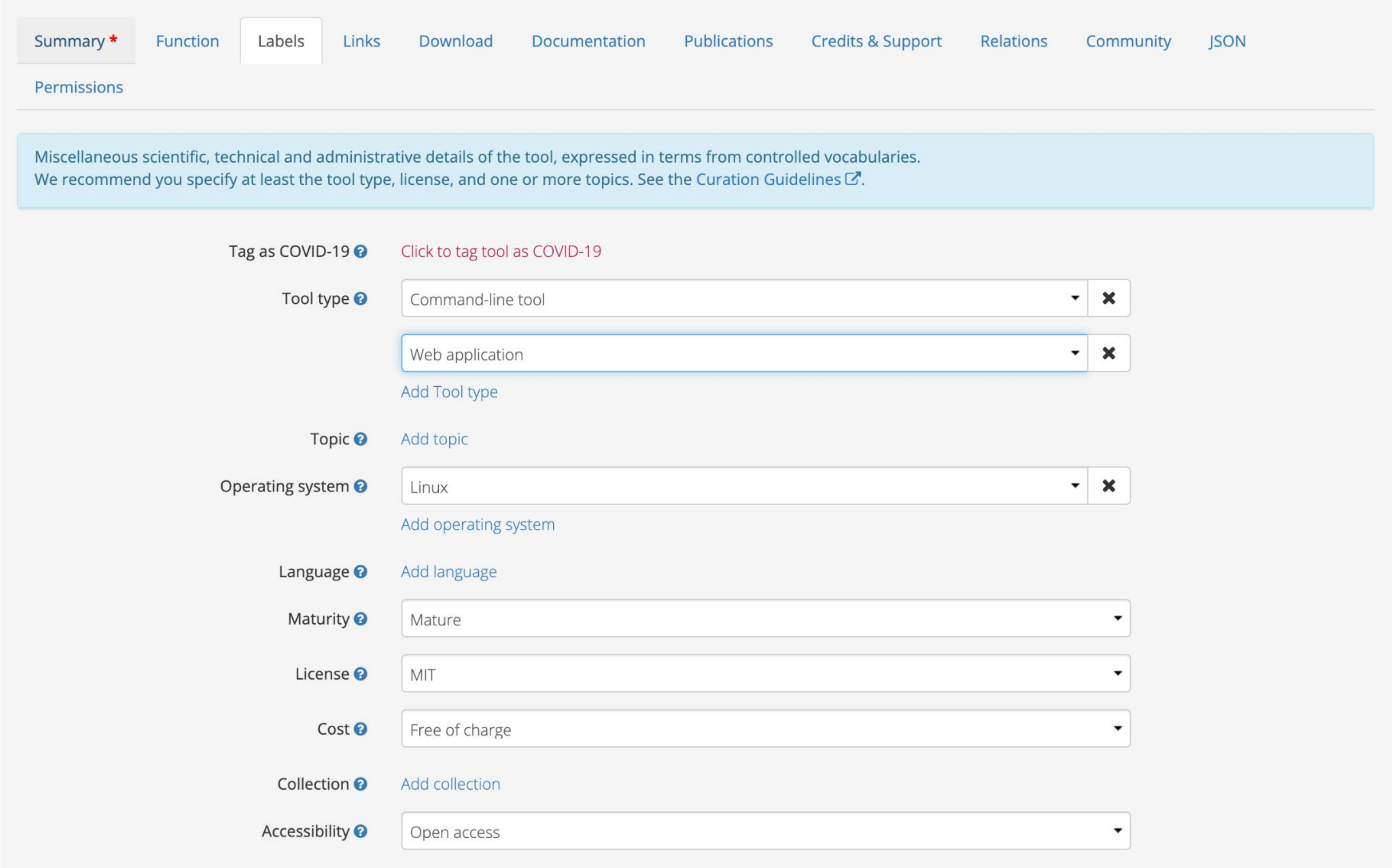
Persistent biotoolsID *: a_bioinformatics_tool

Description *: This is some description about a bioinformatics tool

Homepage URL *: https://example.com

Software version(s)

New tool: Labels



Miscellaneous scientific, technical and administrative details of the tool, expressed in terms from controlled vocabularies.
We recommend you specify at least the tool type, license, and one or more topics. See the Curation Guidelines.

Tag as COVID-19: Click to tag tool as COVID-19

Tool type: Command-line tool

Web application

Add Tool type

Topic: Add topic

Operating system: Linux

Add operating system

Language: Add language

Maturity: Mature

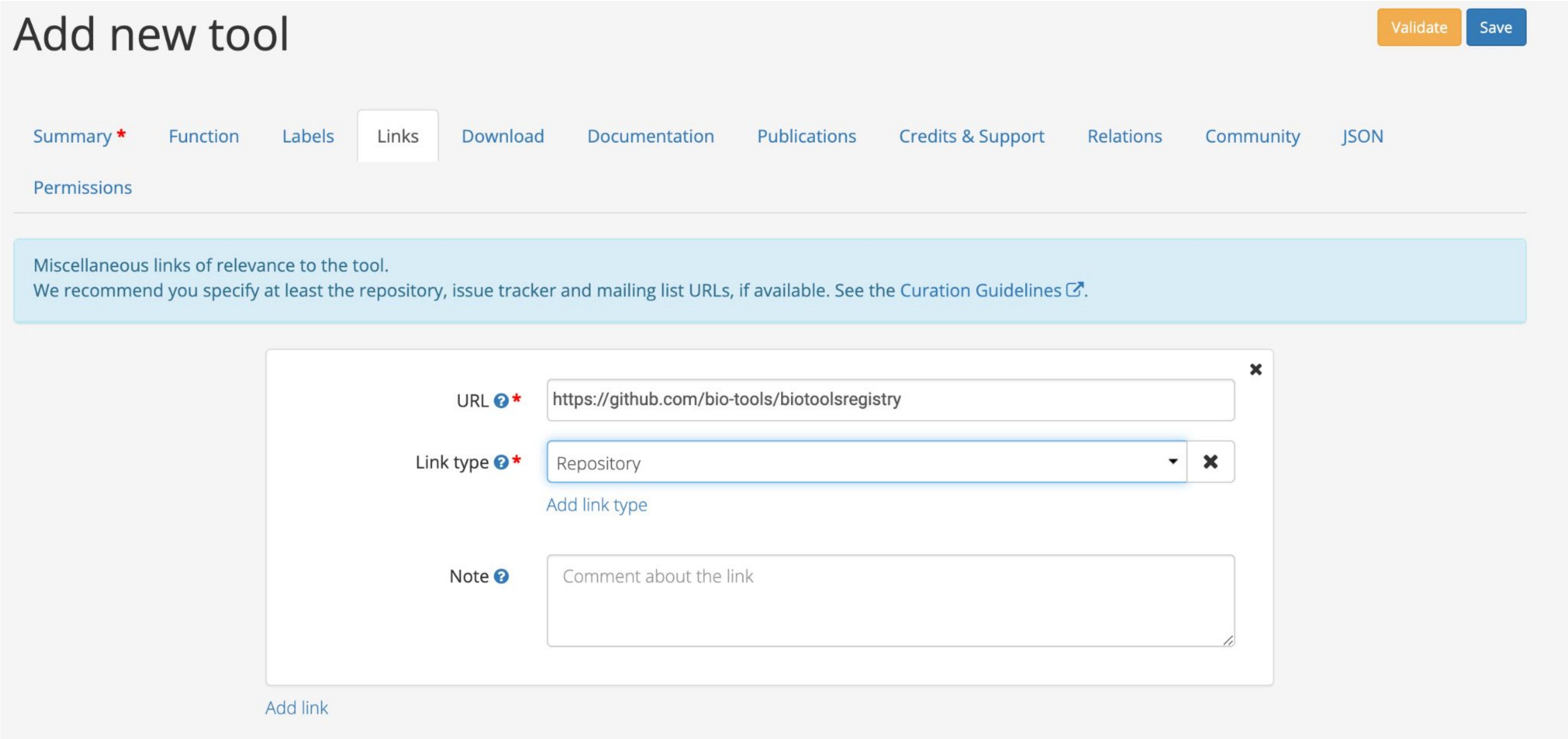
License: MIT

Cost: Free of charge

Collection: Add collection

Accessibility: Open access

New tool: Links



Add new tool

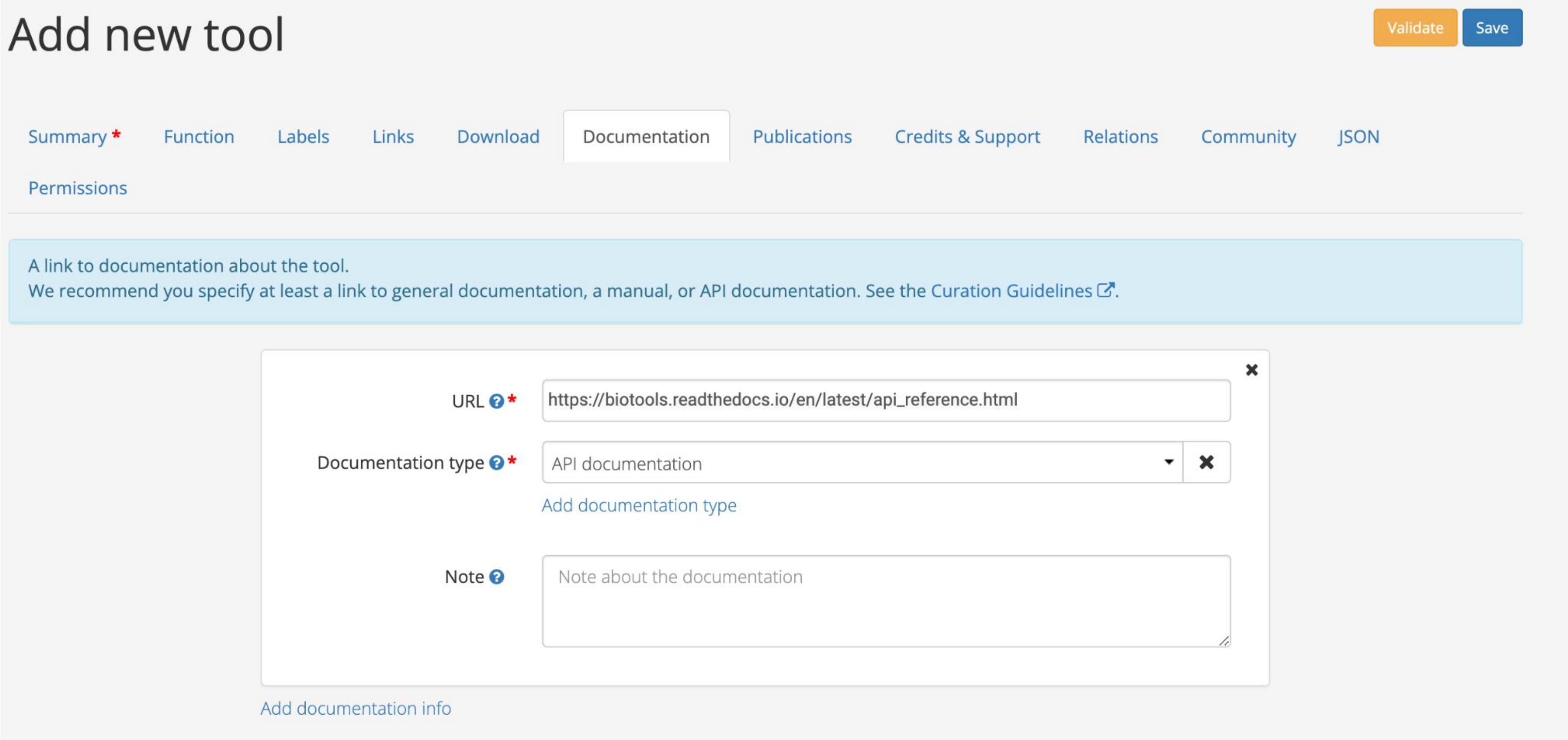
Miscellaneous links of relevance to the tool.
We recommend you specify at least the repository, issue tracker and mailing list URLs, if available. See the Curation Guidelines.

URL *: https://github.com/bio-tools/biotoolsregistry

Link type *: Repository

Note: Comment about the link

New tool: Documentation

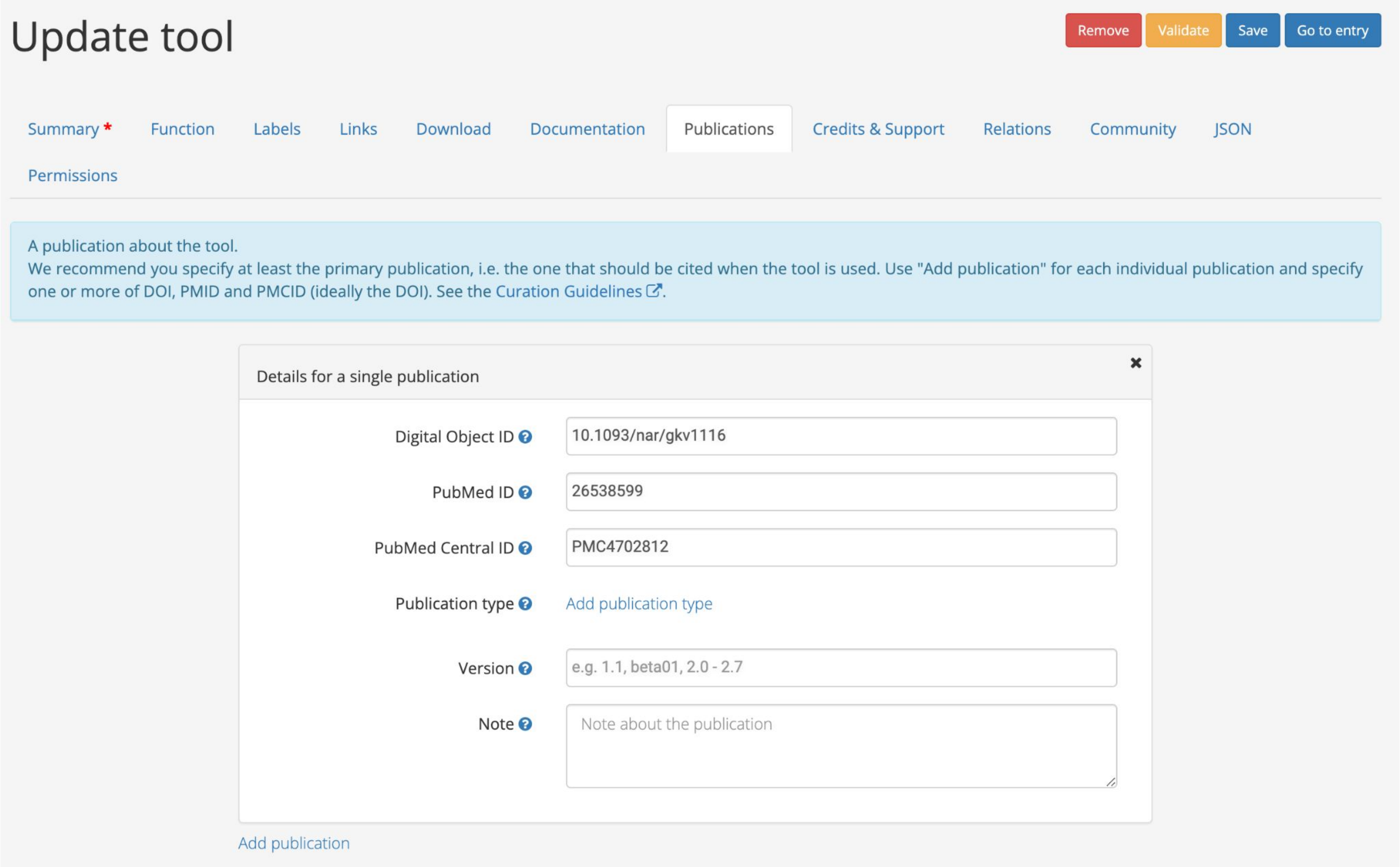


A link to documentation about the tool.
We recommend you specify at least a link to general documentation, a manual, or API documentation. See the Curation Guidelines.

URL *: https://biotools.readthedocs.io/en/latest/api_reference.html

Documentation type *: API documentation

New tool: Publication

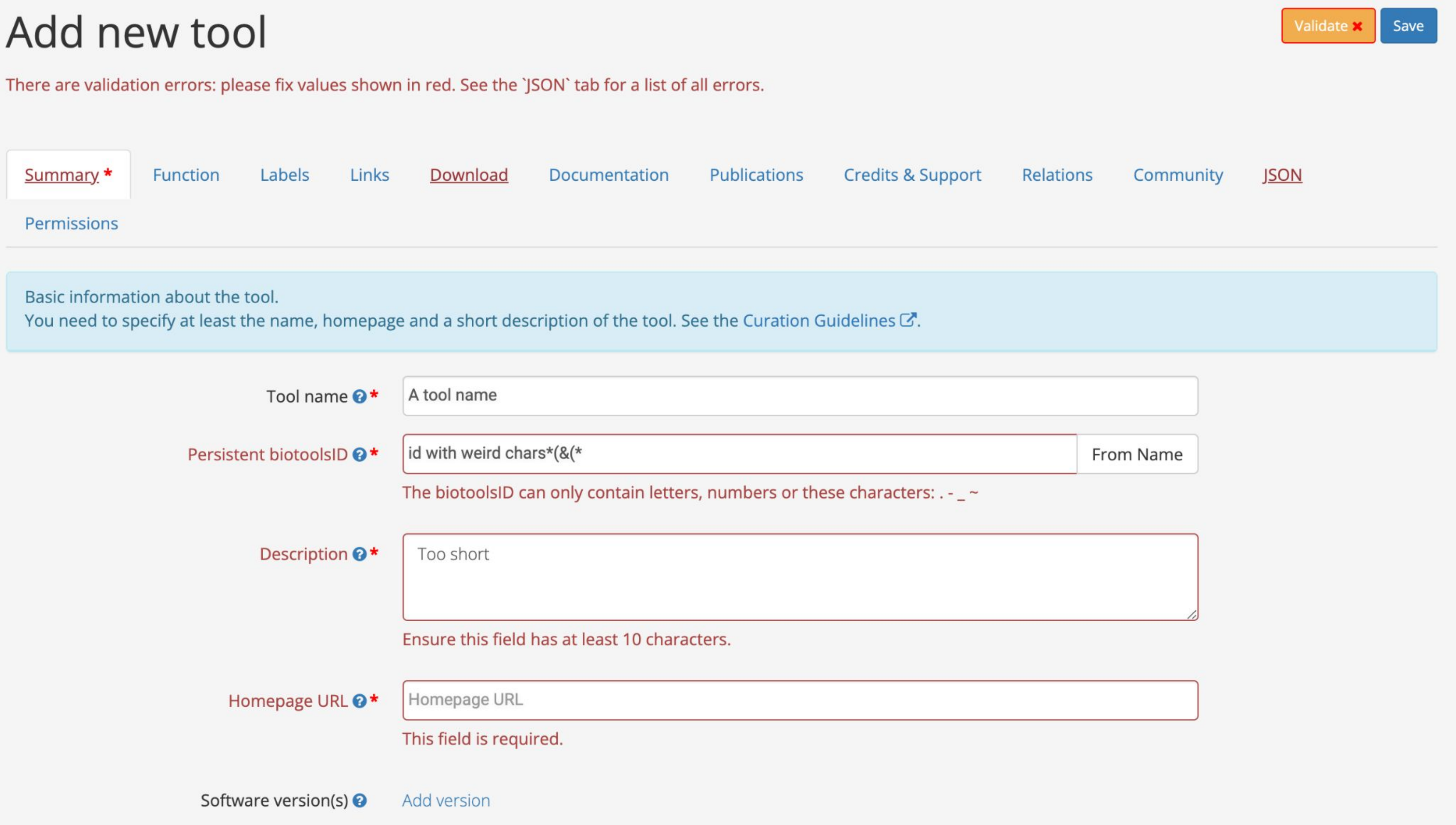


A publication about the tool.
We recommend you specify at least the primary publication, i.e. the one that should be cited when the tool is used. Use "Add publication" for each individual publication and specify one or more of DOI, PMID and PMCID (ideally the DOI). See the Curation Guidelines.

Details for a single publication

Digital Object ID: 10.1093/nar/gkv1116
PubMed ID: 26538599
PubMed Central ID: PMC4702812
Publication type: Add publication type
Version: e.g. 1.1, beta01, 2.0 - 2.7
Note: Note about the publication

New tool: errors



Add new tool

There are validation errors: please fix values shown in red. See the `JSON` tab for a list of all errors.

Basic information about the tool.
You need to specify at least the name, homepage and a short description of the tool. See the Curation Guidelines.

Tool name *: A tool name

Persistent biotoolsID *: id with weird chars*(&(*

The biotoolsID can only contain letters, numbers or these characters: . - _ ~

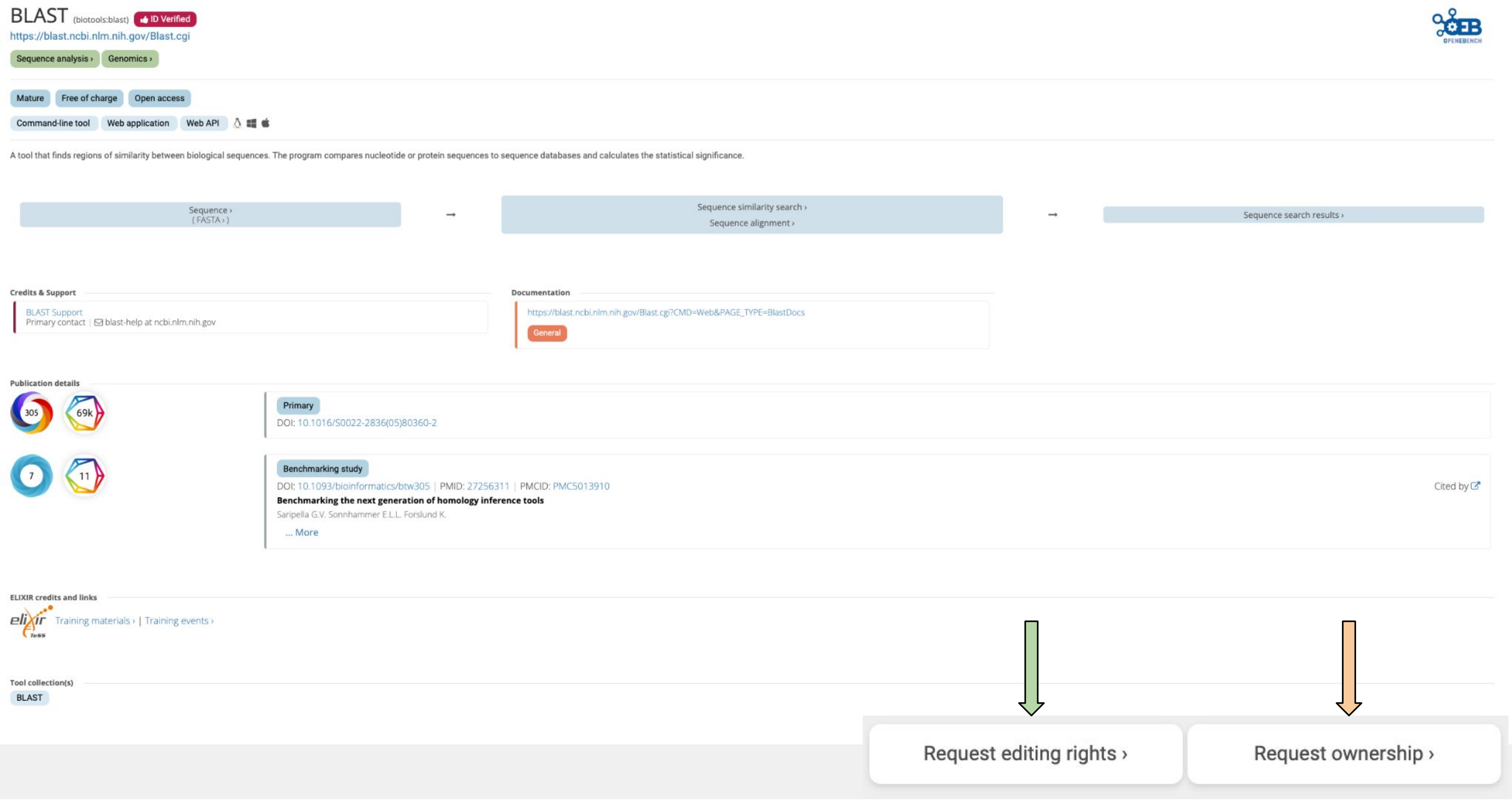
Description *: Too short

Ensure this field has at least 10 characters.

Homepage URL *: Homepage URL

This field is required.

Software version(s)



BLAST (biotools:blast) ID Verified

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Sequence analysis › Genomics ›

Mature | Free of charge | Open access

Command-line tool | Web application | Web API

A tool that finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

Sequence › (FASTA ›) → Sequence similarity search › Sequence alignment › → Sequence search results ›

Credits & Support

BLAST Support
Primary contact | blast-help at ncbi.nlm.nih.gov

Documentation

https://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastDocs
General

Publication details

Primary
DOI: 10.1016/S0022-2836(05)80360-2

Benchmarking study
DOI: 10.1093/bioinformatics/btw305 | PMID: 27256311 | PMCID: PMC5013910
Cited by
Benchmarking the next generation of homology inference tools
Saripella G.V. Sonnhammer E.L.L. Forslund K.
... More

ELIXIR credits and links

Training materials › | Training events ›

Tool collection(s)

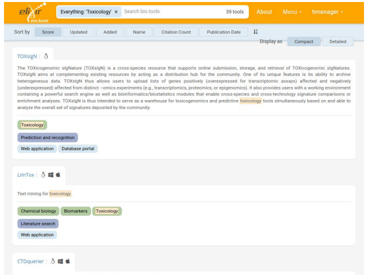
BLAST

The "ELIXIR Tools Platform" from a user's perspective

FIND → **EVALUATE** → **DEPLOY** → **RUN**

FIND

bio.tools registry
WorkflowHub registry



Everything: 'Toxicology' × Search bio.tools 39 tools About Menu hmenager

Sort by Score Updated Added Name Citation Count Publication Date

Display as Compact Detailed

TOXsIgN

The TOXicogenomic sIgNature (TOXsIgN) is a cross-species resource that supports online submission, storage, and retrieval of TOXicogenomic sIgNatures. TOXsIgN aims at complementing existing resources by acting as a distribution hub for the community. One of its unique features is its ability to archive heterogeneous data. TOXsIgN thus allows users to upload lists of genes positively (overexpressed for transcriptomic assays) affected and negatively (underexpressed) affected from distinct −omics experiments (e.g., transcriptomics, proteomics, or epigenomics). It also provides users with a working environment containing a powerful search engine as well as bioinformatics/biostatistics modules that enable cross-species and cross-technology signature comparisons or enrichment analyses. TOXsIgN is thus intended to serve as a warehouse for toxicogenomics and predictive toxicology tools simultaneously based on and able to analyze the overall set of signatures deposited by the community.

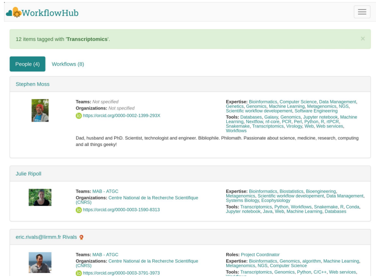
Toxicology
Prediction and recognition
Web application Database portal

LimTox

Text mining for toxicology.

Chemical biology Biomarkers Toxicology
Literature search
Web application

CTDquerier



WorkflowHub

12 items tagged with '**Transcriptomics**'.

People (4) Workflows (8)

Stephen Moss

Teams: *Not specified*
Organizations: *Not specified*
https://orcid.org/0000-0002-1399-293X

Expertise: Bioinformatics, Computer Science, Data Management, Genetics, Genomics, Machine Learning, Metagenomics, NGS, Scientific workflow developement, Software Engineering
Tools: Databases, Galaxy, Genomics, Jupyter notebook, Machine Learning, Nextflow, nf-core, PCR, Perl, Python, R, rtPCR, Snakemake, Transcriptomics, Virology, Web, Web services, Workflows

Dad, husband and PhD. Scientist, technologist and engineer. Bibliophile. Philomath. Passionate about science, medicine, research, computing and all things geeky!

Julie Ripoll

Teams: MAB - ATGC
Organizations: Centre National de la Recherche Scientifique (CNRS)
https://orcid.org/0000-0003-1590-8313

Expertise: Bioinformatics, Biostatistics, Bioengineering, Metagenomics, Scientific workflow developement, Data Management, Systems Biology, Ecophysiology
Tools: Transcriptomics, Python, Workflows, Snakemake, R, Conda, Jupyter notebook, Java, Web, Machine Learning, Databases

eric.rivals@lirmm.fr Rivals

Teams: MAB - ATGC
Organizations: Centre National de la Recherche Scientifique (CNRS)
https://orcid.org/0000-0003-3791-3973

Roles: Project Coordinator
Expertise: Bioinformatics, Genomics, algorithm, Machine Learning, Metagenomics, NGS, Computer Science
Tools: Transcriptomics, Genomics, Python, C/C++, Web services,

EVALUATE

OpenEBench

Scientific Benchmarking Technical Monitoring Statistics About Docs

JASS

http://statistical-genetics.pages.pasteur.fr/jass/

biotools

CMD SOAP WEB

Version : 1.0.1._2.0

Description : software package that handles the computation of the joint statistics over sets of selected GWAS results, and the interactive exploration of the results through a web interface.

OS : Linux

Metrics

Brief description of metrics collected

Accessibility : Bioschema SSL

License : Open Source OSI

Documentation : Manual General FAQ Terms of use

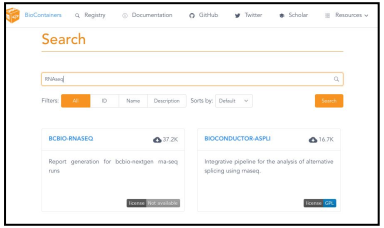
Distribution : Sourcecode

Uptime / Accesstime

Displays if the service is currently available

DEPLOY

Bioconda
BioContainers



BioContainers Registry Documentation GitHub Twitter Scholar Resources

Search

RNAseq

Filters: All ID Name Description Sorts by: Default Search

BCBIO-RNASEQ 37.2K

Report generation for bcbio-nextgen rna-seq runs

license Not available

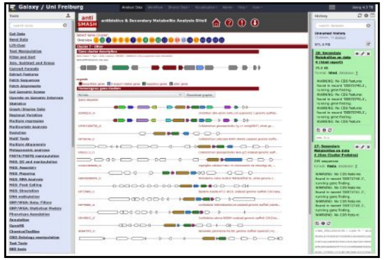
BIOCONDUCTOR-ASPLI 16.7K

Integrative pipeline for the analysis of alternative splicing using rnaseq.

license GPL

RUN

Galaxy



- Facilitate curation (metadata)
- Facilitate navigation (linking)

The “tools ecosystem”

- Open (meta)data
- Standards-based
- Enables data exchange
- Facilitates curation
- Improves the sustainability of the tools resources

Useful links

- **bio.tools APIs**
  - https://biotools.readthedocs.io/en/latest/api_reference.html
  - https://biotools.readthedocs.io/en/latest/api_usage_guide.html
- **Documentation**
  - https://biotools.readthedocs.io
  - https://biotoolsschema.readthedocs.io
- **Curation guidelines**
  - https://biotools.readthedocs.io/en/latest/curators_guide.html
- **Contact:**
  - help@bio.tools
  - https://github.com/bio-tools/biotoolsRegistry/issues
- **EDAM:**
  - https://github.com/edamontology/edamontology
  - https://bioportal.bioontology.org/ontologies/EDAM/?p=classes

Thank you! Questions?