Euro BioImaging
Preparatory Phase II Project

D6.2 Taggathon Meeting, to update the catalogue of image processing and anaylisis tools, including their utility and interoperability and image data repositories, including the imaging domains they cover and their current and planned scale and capabilities

Project N.	688945
Project Title	Euro-BioImaging Preparatory Phase II
Project Acronym	EuBI PPII
Associated Work Package	WP6
Associated Task	Task 6.5
Lead Beneficiary (short name)	CNRS, UNIVDUN
Nature	Report
Dissemination Level	Public
Estimated Delivery Date (Grant Agreement, Annex I)	30/06/2016
Actual Delivery Date	19/09/2016
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Funded by the Horizon 2020 Framework Program of the European Union

Abstract

Despite significant advances in biological and biomedical imaging and analysis, the resources for identifying and accessing the software tools for image processing and analysis are limited. The survey of the Euro-BioImaging community emphasised the importance of such a resource and the requirement for its construction. In this Deliverable, we summarise the technical outputs from a collaborative meeting and follow up work that aims to build the database and tools that are the foundation of the Imaging Resource Portal (IRP). We also provide analysis of the utility of an existing open source tool repository technology, bio.tools, as a foundation for the IRP and an analysis of the existing metadata models and ontologies for use in the IRP.

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1. Preamble

This deliverable focuses on foundation work that we carried out in order to build the EuBI Imaging Resource Portal (IRP) in the way and with the tools described below. The catalogue of image data repositories mentioned in the title of the deliverable has been addressed in the framework of deliverable D6.1.

2. Introduction

Digital imaging is now routinely used across both the life and biomedical sciences and has become an essential tool for all aspects of research, training and clinical practice. Scientists in these disciplines generate a substantial amount of imaging data, and therefore are constant users of software tools that acquire, process and handle imaging data. One of the major challenges for users and technology developers is the large number of software tools that are currently available, as well as new ones that appear every week. For users, it is extremely difficult to identify the range of tools that should be considered for any task and to access any existing knowledge, example applications or publications that use any specific tools. For developers, assessing the current state of the art and identifying opportunities for future development and innovation is challenging. Moreover, once new tools are developed, there isn't a defined mechanism to get them into users hands rapidly and efficiently so that users are guaranteed to be using the latest technologies and new tools are rapidly assessed, tested and used by the community.

These challenges are seen by the Euro-BioImaging community as one of the biggest barriers to scientific progress and one of the most important for Euro-BioImaging to solve. In the survey of the Euro-BioImaging community during Prep Phase I (2010 - 2013), the vast majority of respondents highlighted the difficulty of identifying and accessing software tools for imaging and consistently proposed the development of a single, standardised portal for access to software tools for imaging. Respondents highlighted features including a repository of validated image-analysis tools organized by tasks and well-defined validation protocols (i.e., including test datasets, benchmarking, etc.). Following this strong community recommendation, WP11 in Euro-BioImaging's Prep Phase I defined the requirements for such a resource (see Deliverables 11.2, 11.5, 11.6).[1] Inspired by this community feedback and definition of requirements, Euro-BioImaging Prep Phase II's WP6 aims to establish a public, community-based Imaging Resource Portal ("IRP") that catalogues available tools, applications, datasets and repositories across the full range of the biological and medical imaging communities that make up for the Euro-BioImaging. In this Deliverable, we report on the technical progress towards a fully functional IRP, and in particular the evaluation of technologies that can serve as the database and technical foundation for the IRP.

3.   Previous Work—biii.info

As part of its proof of concept (PoC) work in Euro-BioImaging Prep Phase I, WP11, along with several others, helped sponsor a meeting of image analysts, imaging software developers and users at the 2013 European Biological Image Analysis Symposium (EUBIAS2013; http://eubias2013.irbbarcelona.org/).[2] This first taggathon meeting built a first generation catalogue of image analysis and processing tools for the biological domain, the BioImage Informatics Index (biii.info, http://biii.info). All the resources added in the catalogue were created by community submission, and annotated using a combination of controlled vocabularies and free-text. The result is the first version of vocabulary developed by the community for describing and annotating biological image analysis. Since its establishment, biii.info has evolved through a follow up taggathon meeting organized by France BioImaging (http://eubias.org/eubias2015/?page_id=52) and ongoing curation efforts by a growing community of bioimage analysts (which has subsequently matured into a European COST action Neubias, see below). This ongoing consistent activity demonstrates the commitment of the biological imaging community to the construction such a resource. Biii.info provides the foundation for the work now being undertaken by Euro-BioImaging Prep Phase II, WP6, but will need to be further developed by providing a more structured semantic for annotations and to extend it as Euro-BioImaging needs to also account for the needs of the medical community .

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[1] http://www.eurobioimaging.eu/content-page/documents-gallery
[2] Organized by Sebastien Tosi, Julien Colombelli (both IRB Barcelona) and Kota Miura (EMBL Heidelberg). The list of contributors is available here: http://biii.info/about.

4. Technology for Tool Repositories

A resource like the IRP requested by the community in the Euro-BioImaging surveys requires a combination of defined data structures and relationships (a "data model"), that includes a domain specific vocabulary (a list of semantic terms organized in taxonomy) , a database that supports the data model, a standardised interface for accessing the data in the database and a public-facing usable interface, preferably accessible from a web browser. WP6 aims to assemble all these functions and deploy them into a production Euro-BioImaging IRP. Given the scale of the task, WP6 will need to, wherever possible, re-use existing technologies and interact with other projects and communities to use its resources efficiently, make rapid progress, and develop a resource that has the best chance for community adoption. In particular, this includes a data model, a database that uses this data model, ontologies for annotation, and an interface and framework for building a user interface.

As originally conceived, this Deliverable was focussed on curating and expanding the annotations in biii.info. Curation is necessary because, while many submissions are well-annotated, there are inconsistencies in the annotations used that reduce the value of data in biii.info. A survey of the metadata stored in the current version of biii.info (as of June 2016) is shown in Appendix 1. The annotations are quite comprehensive (2132 tags are included), but inevitably include some duplications (e.g., "voronoi, voronoi diagram, voronoi labelling, voronoi transform"), mis-spellings (e.g., "whatershed thinning" [sic]), poorly defined terms (e.g., "edit"), and inconsistent spelling (e.g., "color", "colour"). These are classic problems in community annotation that can be solved by introducing the use of ontologies and user interfaces that direct data entry and linkage.

Since the original definition of this Deliverable, new technology and resources have become available that Euro-BioImaging can leverage to build the IRP. In particular, WP6 has identified the ELIXIR's Tool & Data Services Registry (https://bio.tools/), which provides essential scientific and technical information about analytical tools and data services for bioinformatics. Its data model and database resources provide a solution that could be adapted to the needs of the Euro-BioImaging IRP. Therefore, instead of the originally planned Taggathon we convened a meeting to analyse and review the existing bio.tools catalogue, its data model and annotation strategy, in order to evaluate its suitability for IRP development and deployment and compare it with the features provided by biii.info. This was a strategic decision to engage with an emerging technology that is actively built and maintained by a partner ESFRI infrastructure. Moreover, the partnering of Euro-BioImaging, bio.tools and Neubias potentially combines existing work and expertise that can potentially synergise to build a comprehensive and useful controlled vocabulary of terms and categories that extend EDAM and underpin the IRP.

5. IRP Data Model and Database—bio.tools

The review meeting was held in Dundee, from June 21-23, 2016. The meeting was attended by IRP project participants and bio.tools developers with the goal of assessing the existing bio.tools data and metadata model, establish how this model aligns with the data already

stored in biii.info (Table 1), and discuss how bio.tools could be extended to support future data submissions and annotations ("tagging"). The meeting produced a full analysis of biii.info, including depth and limitations of its annotations, as well as a full analysis of the current bio.tools data model and how the data model would need to be extended to include imaging tools from both biological and medical domains. This analysis revealed a substantial, useful mapping between existing metadata concepts present in the existing bio.tools data model and those required to support the existing catalogue of tools listed in biii.info (Table 1). Moreover, the requirement for the IRP to implement ontology-based annotations for tools tagging is also satisfied by bio.tools, as this project has standardised on and implemented the EDAM ontology, a community-accepted ontology for defining the components and capabilities of bioinformatics operations, tools, datasets and formats (http://edamontology.org/). The bio.tools development team helps maintain the EDAM ontology, so that updates and changes needed for successful implementation of the IRP can be made easily and quickly. Also, the bio.tools developers indicated that updates of the bio.tools data model planned for 2016 can include support for the specific needs of the imaging community. On this basis, initial work on mapping imaging tool metadata into bio.tools has begun, with the intention of leveraging its ongoing development and its linkage with ELIXIR. Work is continuing through the Summer of 2016, in preparation for a second meeting of the WP6 and bio.tools development teams along with members of Neubias tagging team (see below).

6. **IRP Annotation and "Taggathon"— Global BioImaging and Neubias**

As noted above, the development of the IRP is a strong priority for the Euro-BioImaging community. Other initiatives have also identified the development of a similar resource as a priority in their own projects and for their communities. Euro-BioImaging and Global BioImaging (http://www.eurobioimaging.eu/content-page/global-bioimaging-project) work closely together, and have shared aims to build a usable interface for the IRP. Neubias (http://eubias.org/NEUBIAS/) is a COST Action that is establishing a network of BioImage Analysts across Europe and aims at building a web-based platform for biological imaging. Given these shared interests, Euro-BioImaging Prep Phase II WP6 has partnered with these projects to develop and deliver a coordinated, synergistic effort. The Neubias network is committed to organising community meetings ("taggathons") to assemble and annotate on-line catalogues of data processing tools in biological bioimaging. Therefore, Euro-BioImaging WP6 aims to, wherever possible, work closely with the Neubias community to exchange data and develop compatible solutions, so as to avoid duplication of efforts. To this end, representatives of WP6 and bio.tools will participate in the Taggathon meeting organized by Neubias in Barcelona on 14-16 September 2016 (http://eubias.org/NEUBIAS/?page_id=228).

Similar effort will be put in place to engage the medical community and extend the above mentioned strategy to include medical imaging tools and resources.

Table 1. MODEL COMPARISON | bio.tools vs biii.info

The following main categories of the data model were defined in biii as follow:
Software/Library: A package of various components.
Workflow: Image analysis workflow (a sequence of components) for biological research.
Component: The implementation of image processing and analysis algorithms.

Only a portion of the data model contained in biii.info is decribed in this table, when identified as relevant for the IRP.

1. **SOFTWARE/LIBRARY**

Bio.tools field	Biii.info field	Comments	2.0 (proposed improvements)
Name	Title		-
Language / Resource type	Ecosystem	In biii was a free text with a list of examples.	Extend language CV as needed.
Platform (OS)	Platform (OS)	In biii, selected from a CV (controlled vocabulary) list of platform (see Appendix 1) . Extend Bio.tools CV (Controlled Vocabularies) as needed.	Extend CV from biii input
Homepage (URL)	Link / URL	URLs (components) and Links (libraries	-
N/A	Target audience	In biii was free text with guidelines	Consider extension for small CV (user, analyst, developer, manager) - might be redundant with other existing fields (e.g. Managers need Platforms, etc.)
Resource type	Type	In biii was free text with guidelines	TBC ("Script" is something of an issue. "Examples" could be handled as links.
N/A	Interoperates with	In biii was free text with guidelines	Will be supported in bio.tools by the notion of a relationships by tools entries
EDAM topics, operation, data type (I/O), format	Tags	In biii.info, the tags were selected from a list of terms, (semi-controlled) which could be extended by any curators. The EDAM ontology is structured and controlled and could be completed with selected terms.	In progress
N/A	Rating		Not considered for now in IRP
	Authors		It will be "Credits". Assign to personal credit or institutional credit
License	License		Extend CV as needed and align

			vocabularies
Publication	Reference	DOI in biii, automatically linked to" Biblio" resource in biii, not described here.	Might need choosing DOI/PMID/PMCID
Contact		Overlap with Author in biii.info	Ask/find email address of one of the authors or the Author URL
Short description	Description (Strengths, Limitations)		Need to define guidelines in the long term
EDAM format	Supported formats (not a separate field, part of description)		In progress
Registrant	Submitted by		-
N/A	Image (screenshot)	Extend with tool logo instead (Include image in link)	

2.   WORKFLOWS

Bio.tools field	Biii.info field	Comments	2.0 (proposed improvements)
Name	Workflow		-
Home	Workflow URL		-
EDAM	Tags		In progress
Credit	Workflow author		-
N/A	Dependencies	In biii the selection was linked to the list of "Software/Libraries " Resources (one or several)	Where framework/workbench is required, we can use "Relationship"
Language	Workflow language	In biii the selection was linked to the list of "Language " Resources (one or several), not described here.	Some biii.info entries are just protocols/usage notes and not executable therefore out of scope Extend CV as needed either language or new workflow language
Data type	Dimension	Possibly part of "Data type"	Include dimension in datatype. Capture notion of dimension in EDAM data for images (2D, 3D, time series).
EDAM input type	Input data type	Free text with guidelines in biii	Extend EDAM or use another ontology / CV (OME?) to annotate imaging inputs/outputs

EDAM output type	Output data type	Free text with guidelines in biii	(Look at "Points" format in MULTIMOT project)
N/A	Example Image URL (see http://biii.info/node/2637)	Test data for running the workflow. More EXCELERATE WP2 concern / some data could be in IDR	2.0 will handle test data via links. Links will be typed in 2.0 to provide a hint on what they point to.
	What links here	Link to specific "components" ressources.	Will be handled by "Relationship" between workflow component and workflow
Description	Comments/instructions		-
N/A	Ratings		X
	Applicable to (Sample data)	In biii link to the resource "Sample Data" not described here.	2.0 will handle sample data via links. Links will be typed in 2.0 to provide a hint on what they point to.
Publication	Reference	Converting to DOI or PMID	-

3.   COMPONENTS

Bio.tools field	Biii.info field	Comments	2.0 (proposed improvements)
Name	Title		-
Home	URL / Link		-
N/A	Package/library	In biii linked to the resource "Software/Library"	[component] <is_plugin_for> [workbench|library]
Credit	Author		-
N/A	Workflow	In biii linked to the resource "Workflow"	[component] <is_included_in> [workflow]
Description	Description		-
EDAM	Tags	⌴In biii.info, the tags were selected from a list of terms, (semi-controlled) which could be extanded by any curators. The Edam ontology is structured and controlled and can be extended.	WIP
Publication	Reference	Linked to the resource DOI	-
N/A	Ratings		X

Appendix 1: Biii.info Data (collected Jun 2016)

The initial structure of biii (workflow and component notion in particular) was conceived by Sébastien Tosi (IRB Barcelona) and Kota Miura (EMBL Heidelberg) and subsequently extended during Taggathons.

The list of taggers and supporting institutes are available on biii.info (http://biii.info/about).

Here we provide the flat list of tags published on biii.info which WP6 aims to use as a starting point to extend the EDAM ontology. The tags were extracted using web scraping as the full biii.info database was not available. Due to this limitation, terms are missing and the list is not exhaustive.

All tags (2132)

.1sc, .2fl, .acff, .afm, .aim, .al3d, .am, .amiramesh, .apl, .arf, .avi, .bip, .bmp, .c01, .cfg, .cr2, .crw, .cxd, .czi, .dat, .dcm, .dicom, .dm2, .dm3, .dti, .eps, .epsi, .exp, .fdf, .fff, .ffr, .flex, .fli, .gel, .gif, .grey, .hdr, .hed, .his, .htd, .hx, .ics, .ids, .img, .ims, .inr, .ipl, .ipm, .ipw, .jp2, .jpg, .jpk, .jpx, .l2d, .lei, .lif, .liff, .lim, .lsm, .mea, .mnc, .mng, .mod, .mov, .mrc, .mrw, .mtb, .mvd2, .naf, .nd, .nd2, .ndpi, .nef, .nhdr, .nrrd, .obsep, .oib, .oif, .ome, .ome.tiff, .par, .pcx, .pds, .pic, .pict, .png, .pnl, .pr3, .ps, .psd, .r3d, .raw, .res, .scn, .sdt, .seq, .sld, .sld .fits .pgm .xys .zvi .vws .dv .frm .tfr .html .mdb, .sm2, .sm3, .spi, .stk, .stp, .svs, .sxm, .tga, .tif, .tiff, .tnb, .top, .txt, .v, .vms, .vsi, .wat, .xdce, .xml, .xqd, .xqf, .xv, .zfp, .zfr, 0.2, 0.3, 0.4, 16 bits, 16-bit, 1d, 2-exponential fitting, 2d, 2d 3d, 2d histogram, 2d invariants, 2d viewer, 2d visualization, 2d/3d, 360, 3d, 3d annotation, 3d binary object visualization, 3d color space, 3d geodesic reconstruction, 3d hole closing, 3d labelling, 3d navigation, 3d reslicing, 3d scene, 3d surface collapse, 3d textures, 3d thinning, 3d viewer, 3d viewer plugin, 3d-viewer, 3dview, 4d, 8 bits, 8-bit, aberration compensation, abs, absorbance, abstract types, acceleration, accurate, acquisition, acquisition bleaching, active contours, active meshes, active surfaces, active-learning, adaptative, adaptative thresholding, adaptive, adaptor, add, add noise, administration of users, advanced 2d visualization, advert, affine, affine transform, affine transormation, afin, aggregate, airy unit, algorithms, align images, align planes, alpha dilation, alternate sequential filtering, anaglyph, analysis, analyze, analyzeskeleton, anatomy, andor, angiogenesis, angle, animated gif, animation, anisotropic, anisotropic diffusion, anisotropic filtering, annotate, annotation, anticlockwise, api, application, applied precision, apply deformation, approximate, apps, area, area closing, area opening, area segmentation, area selection, arithmetic operators, arithmetics, arma, arrow, artifact, artificial cells, ascii, assemble, asymetric skeleton, atlas, auto threshold, auto-annotation, auto-tag, autocompletion, autocorrelation, automated, automated analysis, automated tracking, automatic crop, automatic import, automatic tagging, automatic thresholding, automatic tracking, automize, average, avi, axial profile, axiovision, axis transform, axon, b-spline, b. subtilis, background, background leveling, background removal, background shading, bacteria, barycenter, baseline subtraction, basic, basic image processing, basic registration, basic statistics, basic visualization, batch, batch copy rendering settings, batch-processing, bayes, bead, beads, behaviour, benchmark, bernsen thresholding, best focus, beta dilation, big data, big images, bigger, bimodal, binarized, binary, binary image, binary image processing, binary mask, binary morphology, binary patterns, binary stack, binning, bioconductor, bioformats, biomedical, biorad, biovision, bisector, bitplane, black tophat, bleach, bleach correction, bleaching, blend, blending, blind, blind deconvolution, blob, blobs, block matching, blocks, blood vessel, bmp, boolean, bounding box, boxplot, branch, branches, branching, branching points, brightfield, browse images, browser, browsing, brushes, bubble graph, bug, bug report, building gui, bulk annotations, button, bwlabel, c, c library wrapper, c#, c++, c++-templates, c-elegans, c.elegans, calculator, calibration, calibrator, caller, camera, camera calibration, canny, canvas, capture, carl zeiss, cascade, cell, cell assay, cell biology, cell counting, cell cycle, cell descriptors, cell detection, cell division, cell dynamics, cell migration, cell mitosis, cell polarization, cell profiler, cell segmentation, cell tagging, cell tracking, cell-based assays, cell-lineage, cellh5, cellprofiler interoperable, cells, cellular subcomponents, celsis, center of mass, centroid, challenge, channel, channel shift, chart, checkmate, chess, children, chromatic aberration, chromatic aberration correction, chromatic shift, chronometer, cicardian, circadian, circle fit, circle identification, clahe, classification, classify, classify cell, client, client-server, clip, clipper, clockwise, clojure, close, closeball, closed curve fitting, closing, cloud, cluster, cluster support, clustering, cmyk, co-localization percentages, co-localized voxels, code sample, codec, coder, collaboration, collaborative, collection, colocalisation correction, colocalization, color, color alignment, color analysis, color based threshold, color blind, color code, color combination, color compensation, color deconvolution, color distribution, color histogram, color image, color manipulation, color measurement, color processing, color profile, color quantization, color restoration, color separation, color space, color space transformation, color splitting, color stack, color thresholding, color unmixing, color-coding, colortable, colour conversion, colour extraction, colour mode, combine, combine channels, combine images, combine z slices, combo, command line interface, command line tool, command-line, commercial, commerical, communicator, comparator, compare, compiled matlab, complex imaginary, complex modulus, compose, composite channels, compression, comptage, computation, compute cumulated intesity, compute deformation

from beads, computefeatures, computer aided diagnosis, computer-vision, concatenation, configure, confocal, confocal microscopy, conformation, connect to server, connected components, connected particles, connected sets, consistent, constrained collapse, content database, contour, contour map, contrast, contrast enhancement, control, conversion, convert, converter, convex hull, convolution, correction, correlation, correlation analysis, cost matrix, costes, costes algorithm, count, count cells, count chromosomes, count neighbours, count nuclei, count objects, counter, counting, counting per, counting spots per cells, countours, cover, cplex, create dataset, create project, create roi, create tags, creating, crop, cropping, cross correlation, cross-language, cross-section, crosshair, csv, ct, cuda, curvature, curve, curve analysis, curve evolution, curve extraction, curve fitting, curve point detection, curve to spline conversion, curve2spline, curvilinear skeleton, customizable, customization, cut, cutting, cutting plane, cytofluorogram, cytology, cytoplasm, dab, daemon, dalaunay triangularization, damas, darkfield, data, data analysis, data exchange, data formats, data interpretation, data organization, data processing, data protection, data sharing, data storage, data visualization, data-exporter, data-importer, database, datatype, daubechies, daubechies wavelets, deblurring, debugging, decay, decision tree, decoder, deconvolution, deformable models, deformation, delaunay, delaunay triangulation, delauney, delete component, delineation, deltavision, demo, dendrite, dendritic tree, denoise, denoising, density, density counting, density filtering, density plot, deph of field, deprecated, depth, depth field, derivatives, design, desktop interface, detect objects, developer, developmental biology, dialog generator, dialogue, diameter, difference, differentiation, diffraction, diffusion, digital connectivity, digital histology, digital phantom, digital slide, digital topology, dilate, dilation, dimensions, direction, directional, directional filter, discrete mathematics, dispersion, displacement, display, distance, distance analysis, distance map, distance of histograms, distance transform, distortion, distortion correction, distributed computing, distribution, distribution estimation, distro, dithering, divide, division, django, doc, documentation, domain, dose response, double labelling, downsample, draw, draw a ball, draw arrow, draw curve, draw ellipse, draw field, draw line, draw rect, draw spline, draw torus, draw triangulation, drawing, drg, drift, drift correction, drop, dual-screen, duration, dye, dynamic, dynamic range, e-coli, e.coli, easy, ebimage, ec50, eccentricity, eclipse, ecology, edge, edge detection, edge enhancement, edge preserving, edges, edit, edit roi, editing, editor, effcient, eigenvalues of hessian, elastic, elastic alignment, elastic deformation, electron microscopy, elements, elevation, ellipse, ellipse fit, ellipse identification, ellipsoids, emai generator, encoder, end point assays, end point detection, end-point voxel, ending points, endosomes, endothelial tube formation assayenhance, enhance contrast, enhancement, enlarge, entropy, eosin, equalization, equation, equivalence, erode, erosion, error correction, euclidean binary skeleton, euclideian ball, event classification, event detection, event management, evolution, example, excel, execnet, expand, experiment design, exponent, exponential, export image, export metadata, export of results, export to omero, exporter, expression level, extended depth of field, extended view, extensible, extensible/plugin-ins/modules, extract, extract tags from names, ezplug, f-factor, fading, faking, farenheit, fast, fast marching, fast marching algorithms, fast prototyping, feature, feature calculation, feature descriptor, feature detection, feature selection, feature tables, ffmpeg, fft, fiber, fiber analysis, fiber detection, fiducial, fiducial markers, field, figure, figure creation, figure preparation, fiji, filament tracer, filament tracing, filaments, file, file formats, file importer, file input, file management, fill, fill holes, fill regions, filler, filter, filter noise, filter operations, find, finite, finite elements, first order statistics, fish, fisheye, flat field correction, flat zones, flatfield, flatten, flattening, flexible, flickr, flimfit, flip, floating-point, flop, flow, flow map, fluorescence, fluorescence decay, fluorescence lifetime imaging, fluorescent in-situ hybridization, fluoview, fly-through, flycam, flying camera, fmri, focus, focus quality, focusing, follow, format and type conversions, formats, forrest, forums, fourier shift theory, fourier space, fourier transform, framework, france, frap, free rotate, freeform roi, freehand contour, frequency, frequency analysis, fret, friendly, full width at half maximum, function, fuse images, fusion, fwhm, ga to latex, gabor, gallery, gamma correction, ganglion, ganglion explant, gatan, gatan's 3view, gate, gaussian, gaussian convolution, gaussian filtering, gaussian model, gaussian noise, gaussian smoothing, gene expression, general filter, general image analysis, general purpose, generator, generic, generic programming, geodesic dilation, geodesic distance, geodesic erosion, geodesic operations, geodesic propagation, geodesy, geometrical transformation, geometry, gestures, gibson & lanni, giemsa, global, global fitting, global threshold, global thresholding, golgi, golgi segmentation, google maps, gpgpu, gpu, gpu support, gradient, granularity, granulometry, graph, graph cut, graph-cut, graphic card, graphic tool, graphical, graphical output, graphical programming, gray level morphology, grayscale, grey image, greyscale, greyscale morphology, grid, grid access, grid computation, grid of images, grouping, grow, gtk, gui, guided skeleton, h&e, h-maxima, h-minima, h2, h2database, haar transform, haar wavelets, halftone thresholding, hamamatsu, haralick, haralick features, hardware control, hdf5, headless, heatmap, height, height maxima, height minima, height segmentation, helmoholtz, help, help and support, helper, hematoxylin, hessian, hidden markov models, hide tokens, high-throughput, highlight, hindlimb, histogram, histogram based, histogram based streching, histogram calculation, histogram classification, histogram distance, histogram equalization, histogram matching, histogram matching method, histogram operations, histogram output, histogram partitioning, histological slices, histology, hit or miss, hl60, hole, holes, homogeneity, homotopic cutting, horizontal, horn, horn-schunck, hough, huang, huygens, hyperstack, hysteresis thresholding, icy, ide, identify line, identify parabola, identify plane, ihc, ihc membrane stainings, ihc nuclear stainings, ilastik, illumination, illumination correction, illustration, illustrator, image, image acquisition, image analysis, image annotation, image arithmetics, image calculator, image calibration, image classification, image combination, image conversion, image convolution, image database, image denoising, image editing, image enhancement, image export, image features, image filtering, image

format, image fusion, image generation, image grid, image import, image inspection, image manipulation, image math, image measure, image merge, image noising, image normalizer, image operation, image overlap, image perception, image processing, image projection, image publishing, image pyramid, image quality, image representation, image rotation, image scaling, image segmentation, image sequence, image smoothing, image stack, image streching, image summary, image to graph conversion, image transformation, image translation, image variance, image visualization, image-guided therapy, imagej, imagej plugin, imagej2, imaris, imate stitching, imglib2, immunostain, imod, import, import as, import for another user, import image, import plate, importer, improve resolution, ims, imview, in focus, inf, influence zone, inpainting, inpector, input/output, insert image, instrument response function, integer linear programming, integer medial axis, integral, integral image, integration platform, intelligent imaging systems, intensity, intensity based, intensity conservation equation, intensity histogram, intensity presevering, intensity profile, intensity view, inter-class entropy, interaction, interaction with images, interactive, interactive display adjustment, interactive machine learning, interactive operators, interactive parameter manipulation, interactive segmentation, interactive visualization, interest point dectection, interesting pixels, interface, interior point detection, interior points, interleave, intermodes, internalization, internet, interoperability, interpolate, interpolation, intracellular, intraclass variance, invert, io, isbi, ischemia, isnull, iso, isodata, isolated point detection, isometries, isosurface, isotropic scaling, isthmuses, iterative, iterator, iteratoradapters, itk, java, javadoc, javascript, jfreechart, jitter removal, jpeg, junction point detection, junction voxel, jython, k-means, k-nn, kalman, kapur, kdtree, keep borders, kelvin, kernels, keyframes, keypoints, khalimsky, khalimsky order, khalimsky watershed, kidney tubules, kinetics, king, kirsch, knime, knn, kuwahara, kymograph, label, label cells, label image, label objects, label regions, labeled images, labeling, lambda medial axis, lan, landmark, landmark cloud, language bindings, lantuejoul skeleton, laplace, laplacian, laplacian of gaussian, large image block processing, large image handling, large images, large parameter set, large specimen, larva tracking, lateral view, ldap, learnable segmentation, least squares, leica, length, lens, lens distorsion, level, level sets, li, lib, library, ligand, ligand-receptor, light microscopy, light-sheet, limited focus, lims, line, line alignment, line roi, lineage, lineage tracking, lineage tree, linear, linear filter, linear filtering, linear kernel, linear regression, linear stretch, linear transformation, lines, link, linux, list of features, live, live cell imaging, load background, load images, load time varying background, loading, local, local background, local circle fitting, local extrema, local features, local structure analysis, local thickness, local threshold, local thresholding, localization, loci bio-formats, log, logarithmic, lookup table, loop, low-level features, lsm, lsm file, lsm510, lucas-kanade, lung, lut, mac, machine learning, macroscopy, magenta, magic mouse, magnification, manage groups, manage users, manager, manders, manders coefficient, manipulate, manual, manual contour, manual delineation, manual edit, manual editing, manual segmentation, manual tracing, manual tracking, manually, manupulation, map, marching cubes, mark, mark cells, marker, mask, masking, match query images with different rresolution, matching, math, mathematica, matlab, matlab common runtime environment, matlab exporter, matlab importer, matlab toolbox, matlab-clone, matrix, maven, max, max diameters, max filter, max homogeneity, maxentropy, maxima, maximum, maximum correlation thresholding, maximum entropy, maximum flows, maximum intensity projection, maximum likelihood, maximum projection, maxlocal, mcib3d, mean projection, mean square displacement, meanfilter, measure, measure angle, measurement, measurement display, measuring, measuring intensity, median, medical, medical image, medical image analysis, medical imaging, membrane, menu, mereo, mereotopology, merge, merge color, merging, mesh, mesh flattening, mesh noising, mesh smoothing, metadata, metadata viewer, metamorph, meyer watershed 4d, mice, micro-manager, micrograph, microscopy, microscopy simulator, microsope format, microtiter plate, microtubules, middlebury, migration, min, minerror, miniature, minima, minimum, minimum length, minimum projection, mip, mip-rendering, mirror, mitosis, mixture, mixture of gaussians, mobile device access, model, model analysis, model fitting, model-based, modeling, modelism, modellling, molecular devices, moment features, moments, monitor, monitoring, montage, mops, morphing, morphogenesis, morphological dynamics, morphological filters, morphological operations, morphological reconstruction, morphological transforms, morphology, morphology demo, morphometric, morphometric analysis, mosaic, motion, motion analysis, motion model, motion quantification, mouse, move, move data between groups, movement, movement analysis, movement filtering, movie, moving average, moving cell, moving roi, mpeg, mr, mri, msd, msrcr, mult, multi raw, multi touch, multi-channel, multi-core, multi-dimensional, multi-dimensional images, multi-dimensional plots, multi-methods, multi-modality, multi-platform, multi-roi, multi-threaded, multi-threading, multi-view, multiclass, multilevel thresholding, multiple point detection, multiply, multiresolution, multiscale, muti-processing, mycosis, mycosis detection, mysql, n-dimensional, navigation, nd filters, nd images, nd2, nearest neighbor, need seedpoint, nerve cells, network, neural networks, neurite, neurite length, neurite tracer, neurite tracing, neuroanatomy, neuron, neuron cell morpholgy, neuron tracing, neuroscience, newspaper, nikon, no blur, nodes, noise, noise estimation, noise reduction, noise simulator, non linear, non quantitative, non-linear, non-linear distorsion, non-mage data fitting, non-rigid, non-uniform, nonlinear filter, normalization, normalize, normalize layers, nucleus, nucleus classification, nucleus detection, number of neighbors, numpy, object, object analysis, object border, object classification, object detection, object features, object filtering, object generation, object hierarcy, object measurements, object overlap, object relations, object removal, object separation, object statistics, object substraction, object thickness, obsolete, olympus, ome, ome-tiff, omero, omero.insight, omero.searcher, omero.web, open, open image, open image in imagej, open source, opencl, opencv, opengl, opengray, opening, operation, operators, opertaor, optical artifact, optical density correction, optical flow, optimal, optimization, optimized, organelle, organism tracking, organization, orientation, oriented, origin, ortho-slice,

orthogonal, orthogonal slicing, orthogonal sub image, orthogonal view, orthoviewer, otsu, out-of-scope, outdated, outlining, output, output image, overlap, overlapping tiles, overlay, package, paint, paint cells, palm, pan and tilt, paper, parabola fit, parallel, parallel 2d binary skeleton, parallel directional constrained collapse, parallelization, parents, parse file path, parse names, parser, parsing mathematical equation, particle analysis, particle image velocimetry, particle tracking, parts, path, pca, pde, pdf, pdf extractor, pearson, pearson coefficient, percentile, perkinelmer, perreault, persistent movement, perspective, perspective transform, perspective transformation, perturb, pet, pgm, phagokinetic tracks, phantom, phantom generation, phase contrast, phenotyping, photography, photoshop, picker, pincushion, pink, pipe programming, pipeline, piv, pixel, pixel by pixel fitting, pixel classification, pixel features, pixel graph, pixel iterator, pixel size, pkt, plane, plate, platform, plot, plots, plotting, plotting function, pluggable, plugin, plugin concept, plugin distribution, plugin list, plugin suite, png, png file, point, point correspondence, point tool, poisson, poisson noise, polarized, polygon editor, pool, position, postprocessing, powerwatershed, prairie technologies, precision, prediction/correction, preprocessing, presentation, preserve edges, prewitt, print, printing, probabilistic, probability image, processing, profile, programming, programming tool, projection, propagate, propagation, proprietary format, protein localization, protocol, protocol editing, prototyping, protractor, provider, pruning, psf, psf 3d, psf generator, psf model, psf theoritical generator, publication, publish, publishing, pure-let, pyqt, python, qt, quality control, quantification, quantify, quantile filter, quantization, quasi shear rotation, queen, r, radial opening, rand index, random, random forest, random image, random number generator, random walk, rank order filter, rankfilter, raster, raster image, rasterize, ratio, ratio acquisition, ratioed images, raw, raw image, read image, reader, real-time applications, real-time feedback, recall, receptor, reconstruct, reconstruct big images, reconstruction, recorder, rectangle fit, red, reduction, reference points, refine search, reflection, refractive index, region growing, region merging, region summary, regional thresholding, regions, regions of influence, register, registration, regularity, relation, relationships, remote, remote access, remote-execution, remote-processing, remove cells, remove noise, remove objects, remover, render, rendering, renyientropy, reporting, reproducible research, resample, resampling, resizing, reslice, reslicing, resolution, response, restoration, restore-tools, results, retina, retinex, rgb, rgbimage, rhino, richards & wolf, ridler-calvard, riesz, riesz transform, rigid, rigid registration, rigid transform, ring, ripley's k function, roberts, rodent, roi, roi importer, roi measurement, rolling ball, rotate, rotation, ruler, s.pombe, saturation, save images, save locally, save roi, save to server, scala, scalable, scale, scale bar, scaling, scatter, scattergram, scatterplot, scene animation, schunck, scientific computing, scoring, screen, screen capture, screen shot, script editor, scripting, scripts repository, sdk, search, search multiple databases, seed, seed point, seeded, seeds, segement, segment cells, segment nucleii, segmentation, segmentation result, select component, selection, semi automated, semi-automatic, semi-automatic tracing, semi-manual, separable, separate cells, separate channels, separating cells from nuclei, separating point detection, sequence, sequential filter, series, server, server-client, set to background, shanbag, shape, shape analysis, shape context, shape descriptor, shape distance, shape features, shape filtering, shape fitting, shape matching, sharing, sharp, sharp edges, sharpening, shepp-logan, shift, shock, sholl, sholl analysis, shortest path, show off, sieving, sift, sigma filter, signal processing, signed, signed curvature, similarity, similarity transform, simple, simulate cell image, simulate focus, simulate noise, simulate optical path, simulation, simulator, sinusoid, size, size filtering, skeleton, skeleton decomposition, skeleton pruning, skeleton smoothing, slab voxel, slic superpixels, slice, slice viewer, slicing, slide scanner, slidebook, slope, smaller, smooted histogram, smooth, smoothing, snake, snap, snapshot, sobel, sobel filter, socket, software, soma, sort, space partition, space-time plot, sparse, sparsity, spatial, spatial calibration, spatial colocalization, spatial distribution, spatial randomness, spatial statistics, spatial transformation, specific application, speckles, speckling, spectral, spectral decomposition, speed, speed measurements, sphere, sphere structuring element, spherical aberration, spim, spine tracking, spinning disk, splash, splash screen, spline, spline drawing, spline gradient, spline interpolation, split, split channels, split colours, split objects, split spectral channels, split view, split view figure, spot detector, spot segmentation, spreadsheet, sqlite, squared roi, squeeeze, ssim, stabilization, stabilize, stable, stack, stack rotation, stain, stain quantification, stain separation, staining, stand alone, stand-alone application, standard, star wars, statistical analysis, statistical modelling, statistical significance, statistical test, statistics, statistics to object link, steerable, steerable wavelets, stereo, stereo view, stereo vision, stereoscopic 3d, stereoscopy, stitch, stitching, stk, stk file, stl-like, storage, stretch, structure, structure analysis, structuring element, structuring element editor, subpixel, substance, substraction, subtract, super resolution, supervised, supervised learning, supervised segmentation, support vector machines, sure, surf, surf features, surface, surface rendering, svm, swap dimensions, swap time and channels, swap time and z, swimming pool, swing, synapses, table, tag, tag on import, tagger, tagging, teams, temperature, template, test, text, text analysis, text block, texture, texture features, theoretical point spread function, theoritical deconvolution, theoritical psf, theoritical psf generator, theory, theta-connected component labeling, thick, thicken, thickness, thin, thread, threshold, threshold adjacency statistics, threshold tests, thresholded landweber, thresholding, tiff, tiff file, tiled, tiles, tiling, till photonics, time, time delay, time lapse analysis, time lapse sequences, time series, time stamp, time-lapse, time-lapse microscopy, tissue, tissue analysis, tissue segmentation, tissue slides, tk/pil, tnt, tomography, tool, toolbox, toolboxes, toolkit, tooltip, top-hat, topography, topological watershed, topologically controlled dilation, topologically controlled erosion, topologically correct marching cubes, topology, topology controlled sequential filter, touchpad, toxicity, tracing, track, track manager, track number, track processor, track-importer, tracker, tracking, tracking analysis, traffic, train, trainable, trajectories analysis, trajectory, trakem2, transformation, translate, translation, translocation, transpose, tree-like structure, triangle, triangulation, tube-

like structures, tubular structures, turboreg, tutorial, two photon, uneven illumination, ungerflow, unique label, unmixing, unsigned, untile, unwarp, update, upsample, usability, user-friendly, utility, v factor, vaa3d, valley, variable number, variance, variance filter, vascularization density, vector graphics, vector map, velocity, velocity measurements, vertical, vessicle tracking, vessles, vicinity, video, video importer, video microscopy, video recorder, view image, view plate per row, view roi, viewing, views, vigra, virtual camera, virtual memory, virtual optics, virtual stack, visualbasic, visualization, visualize, volocity, volume, volume based filtering, volume closing, volume measurements, volume opening, volume rendering, volume thickness, voronoi, voronoi diagram, voronoi labelling, voronoi transform, vtk, warping, watershed, wavelength, wavelet, wavelet transform, web, web browser, web frontend, web interface, web-tool, webcam, well, whatershed thinning, white tophat, whole-organism, widefield, widefield microscopy, widget, windows, windows os, windows vista, windows xp, windows/linux, workbooks, workflow, workflow database, workflow engine, workflow management, workspace, wormatlas, write image, wxwidgets, x server, x-server, xls export, xls output, xml, xuggler, yen, z, z factor, z stacks, z-stack, zeiss, zernike, zoom, zvi