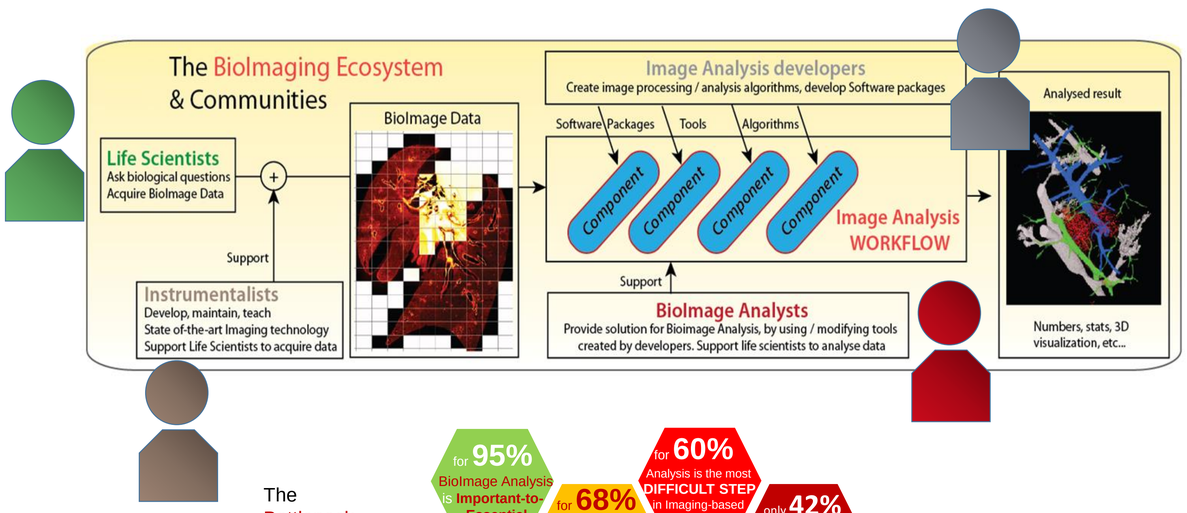
NEUBIAS Working group 4:

Find your way in the jungle of Bioimage Analysis tools and functions

What is WG4 in Neubias in a nutshell:

- **A WEBSITE** — biii.eu
  - Definition of features, web development, web administration
- **2 DATA MODELS**
  - Biii-core-ontology
    - BISE core ontology is a controlled vocabulary aimed at describing the content of the BISE Bio-Imaging Search engine biii.eu.
  - Edam Bio Imaging
    - Bioimage informatics operations, types of data, data formats, and bioimaging topics extension to the EDAM ontology for bioimage analysis, bioimage informatics, and bioimaging.
- **A COMMUNITY OF TAGGERS** — Biologists, Developers, Bio Image Analysts, Microscopists
  - Taggers contribute to the curation of tools, but also to the development of the website and data models.
    OPEN CONTRIBUTIONS all year long
    TAGGATHONS event to gather taggers

Context: Imaging community in life science

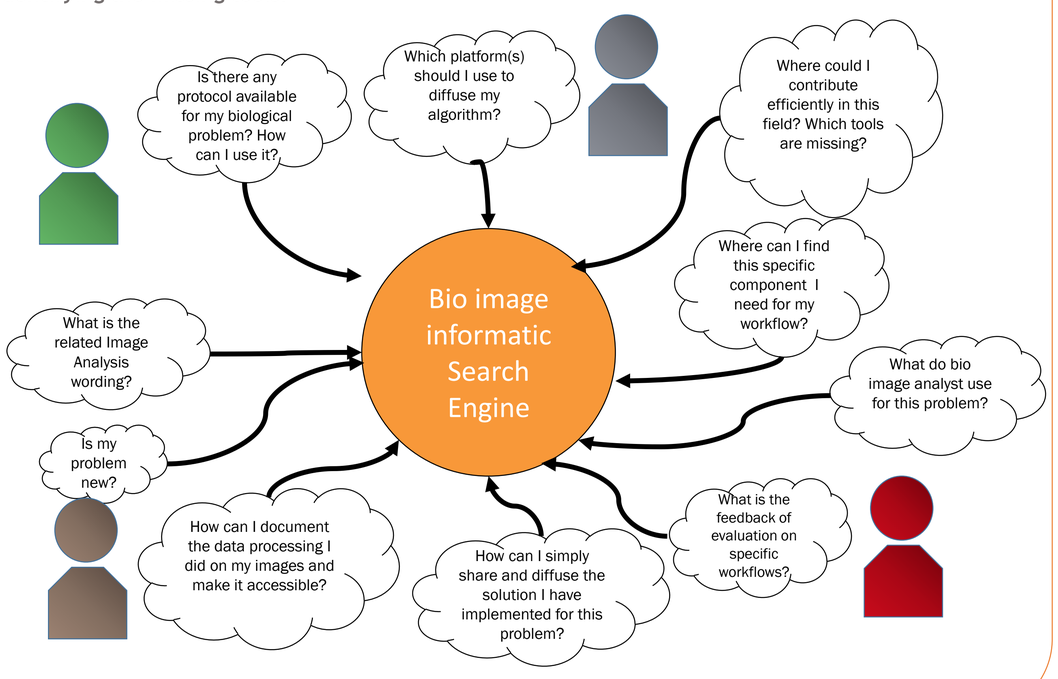


The Bottleneck
(Survey to 1850 scientists March 2015)

- for **95%** BioImage Analysis is **Important-to-Essential**
- for **68%** **Training is lacking** more than Hard-ware capacity
- for **60%** Analysis is the most **DIFFICULT STEP** in Imaging-based projects
- only **42%** of acquired images are quantitatively **Analysed**

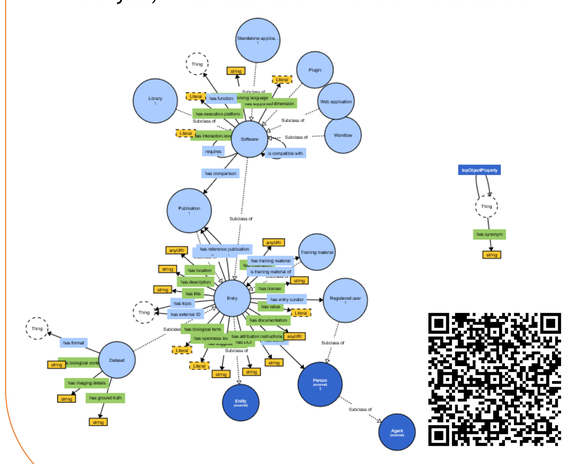
Purpose of BISE: BioImage Informatics Search Engine

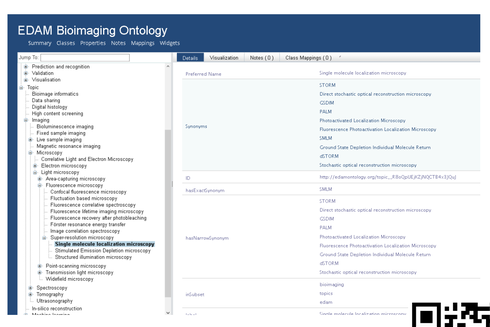
BISE www.biii.eu is a unique repository of bioimage analysis tools based on community usage experiences, to serve and been constructed by the whole community. It matches a biological problems to the relevant tools, foster the dissemination of components or workflows, and help identifying the missing tools.



Data models and ontologies

Two models have been created to make bise as useful as posible, for example trough semantic web requests using standards. BISE core ontology describes the content of the BISE engine: components and workflows. EDAM Bio Imaging provides operations, types of data, and topics extensions to the EDAM ontology for bioimage analysis, in collaboration with Elixir and Euro Bio Imaging





Taggathons

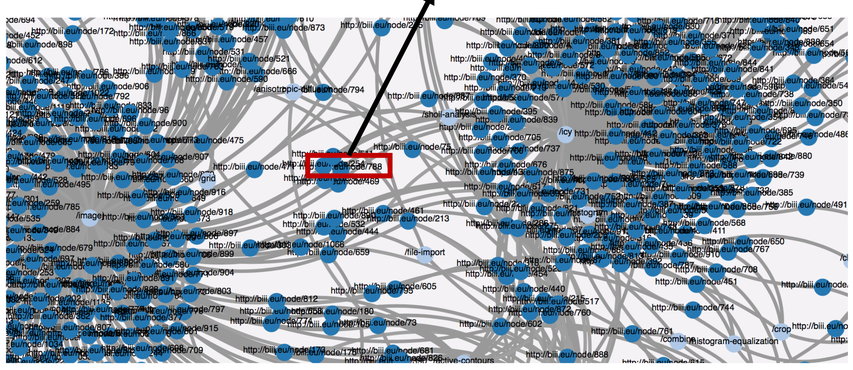
BISE is based on crowd-sourcing techniques fostering exchanges & collaboration, and curation of data all year long, but it boosted by TAGGATHONS: taggers and collaborators gather to contribute to the curation of tools, but also to the development of the website and data models.

Data access and reuse

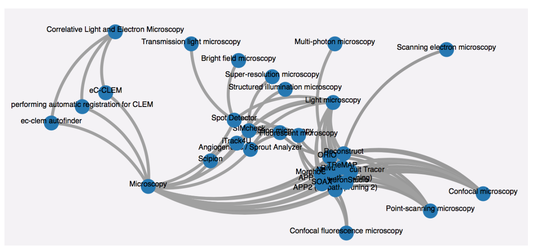
All the content is available under an open data Commons Attribution License(In summary, you are free to share , reuse and adapt BISE, as long as you credit BISE, NEUBIAS and its contributors).
We use standard of semantic web such as JSON and RDF to expose our data, such that other projects (such as plantimageanalysis.org or bio.tools) can be fed by entry in which they got interest and avoid duplicate effort of curation. Our data can also be used to perform more advanced queries, as demonstrated below, that aims to be integrated in biii.eu for advanced search. See also the ABOUT section of biii.eu for further example.

Example 1 of query:
Showing software and their bridges: we search all software and create edges based on their dependencies and compatibilities.

http://biii.eu/import-roi-imagej (Icy plugin to import ROI created in IJ)

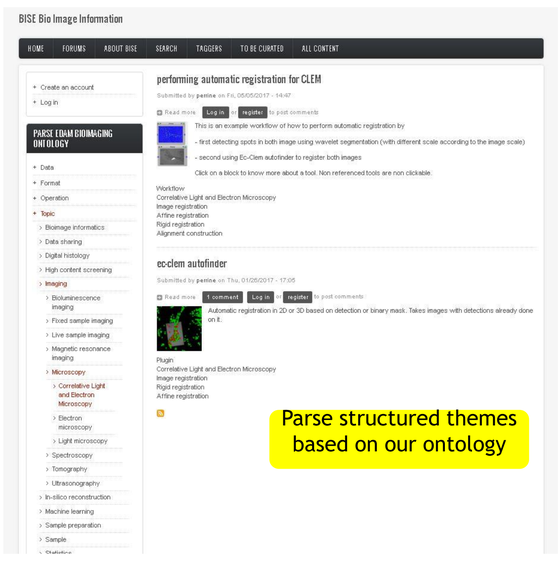


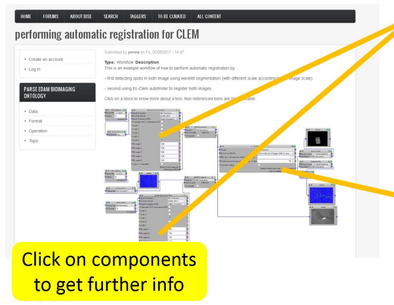
Example 2 of query:
We search an EDAM bio imaging topic (e.g. « Microscopy » and find all corresponding subclass, and the sofwtare annotated with these topics. Finally we display for each matched subgraph an edge between a software label and a topic label

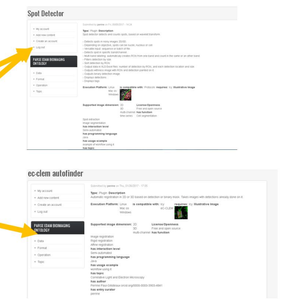


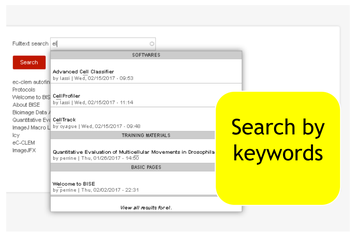
Further info

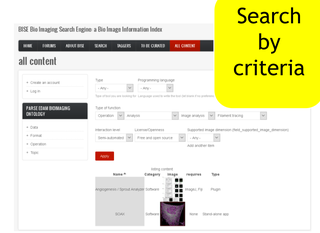
How to search?





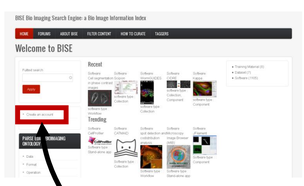






How to contribute?

Our main purpose is to gather the community and bridge the gap between tools and biological problems by fostering the development of new workflows and disseminate the ones already available. But we also aim to contribute to the Open science cloud, by providing a unique reference database of image processing workflows: to justify data integrity and document data deposition for example. We then follow the concept of FAIR data: Findable, Accessible, Interoperable and Reusable. **Do you want to help us?**



Who & why?

Life scientists:
- we need your voice on existing tools usage experiences
- shout your wishlist for: user-friendly tools, missing image analysis functionalities

Bioimage analysts:
- Share your solutions for bioimage analysis problems
- Discover how your fellow bioimage analysts tackle similar problems

Image processing software developer
- Take into account the feedback gathered from BISE
- Identify where you are needed
- Broadcast, improve usability & collect usage statistics of your work

Want to become a tagger?
whenever you want! Just create an account and start tagging.
Join NEUBIAS and WG4 to contribute to taggathons!