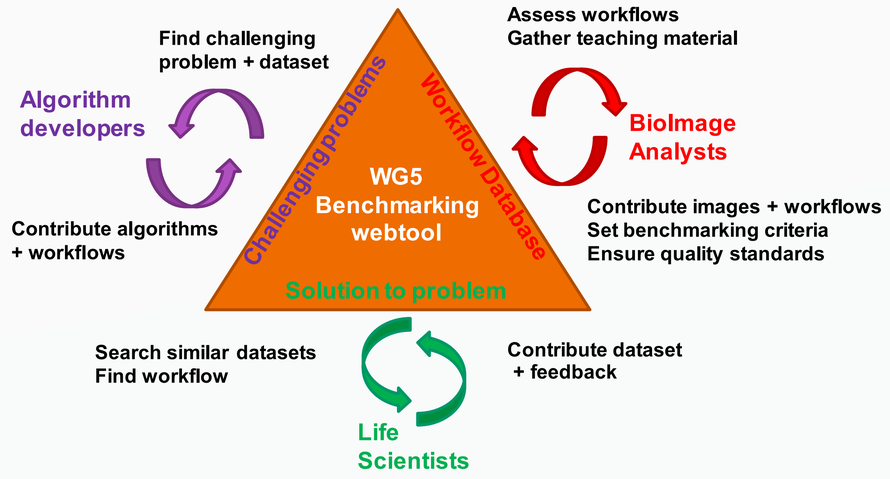
NEUBIAS WG5 WEBTOOL
BENCHMARKING BIOIMAGE WORKFLOWS

INTRODUCTION

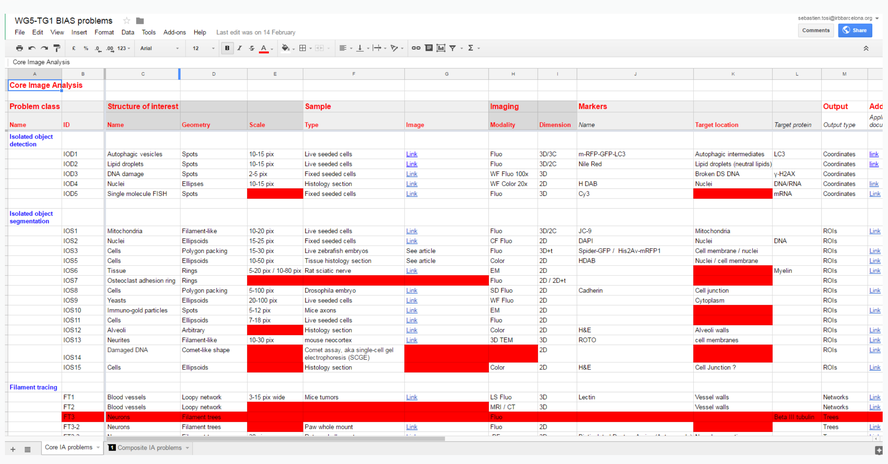
The mission of WG5 is to build an online platform (webtool) enabling to run and benchmark BioImage Analysis (BIA) workflows addressing common image analysis problems faced by Life Scientists; the workflows will be tested and benchmarked on ground truth annotated images stored on the server. This online platform has been identified as a critical resource to:

1) Formalize the concept of BIA workflows and review common BIA problems
2) Compare workflows in fair settings and on representative images
3) Link to WG4 webtool to enhance BIA tools search
4) Help Life Scientists identify the most efficient workflows addressing the BIA problems they face
5) Highlight complex problems for which current solutions are not fully satisfying

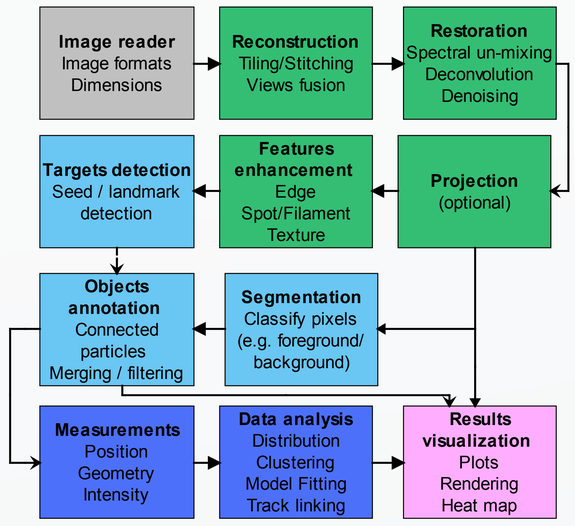
GATHERING THE BIOIMAGING COMMUNITY



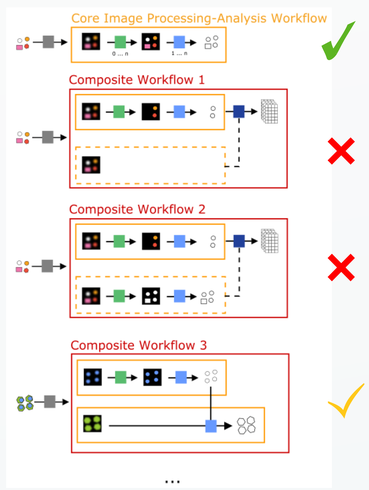
BIA PROBLEMS TAXONOMY → BIA WORKFLOWS → CORE BIA WORKFLOWS



Problems were grouped by problem classes and subdivided by object geometry, sample labeling and imaging modality. They were also linked to sample images and articles describing the applications. Sample images should be annotated in a standard format that is problem class dependent and set by WG5.

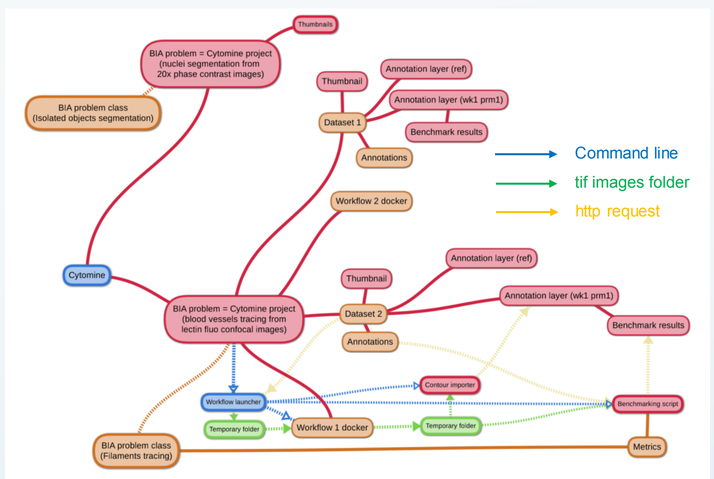


A problem can be addressed by a workflow, a sequence of operations often mapping to this diagram. Many workflows can address the same problem and we plan to compare their efficiency.



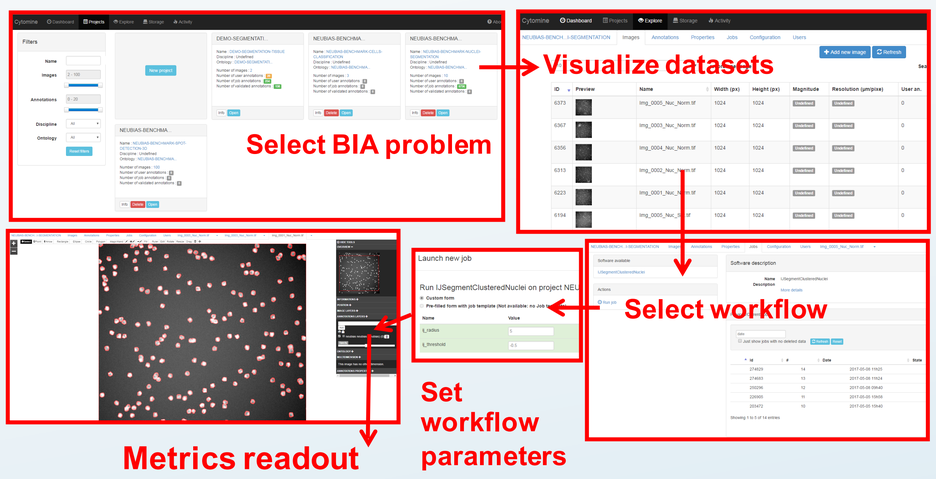
Core workflows are a subset of workflows aiming at identifying a single type of biological object; they do not perform any data post analysis. Only core workflows will be benchmarked.
To be integrated to the webtool, core workflows should run in one of the supported platforms (ImageJ, Icy, Python, CellProfiler, Matlab) and comply with the standard output format for their associated problem class.

WEB INTERFACE: EXTENDING CYTOMINE



As infrastructure for the webtool, we are extending Cytomine[1] to handle OME-tiff[2] multi-dimensional images (importations, annotations) and interact with BIA workflows encapsulated in Docker containers[3].

We are also developing a module to import workflow results as Cytomine annotation layers and a module to compute benchmarking metrics by comparing workflow results to ground truth annotations.



From Cytomine UI, a user can browse through existing BIA problems, visualize associated datasets, select a BIA workflow associated to the problem, adjust input parameters, and launch the workflow.

Upon workflow completion, the identified objects can be visualized as an overlay layer on the original images, and the results quantitavely compared to ground truth (benchmarking metrics).

Annotation layers and metrics from past benchmark runs (different workflow or parameter set) and ground truth annotation layer can also be displayed.

CONCLUSION

Overall, WG5 benchmarking webtool should bring the community an excellent opportunity to encompass current BIA problems, help formalizing the concept of BIA workflows, and assist scientists in efficiently leveraging image analysis to improve the outcome of their research projects.
It should also boost the development of new workflows by providing developers with challenging datasets and aims, as well as a public platform to fairly compare their implementations on community selected datasets.
The webtool could also straightforwardly be used for batch benchmarking (exploring workflows input parameters space); and identifying families of robust and effective workflows to tackle specific problem class.

REFERENCES

1 http://www.cytomine.be/
2 https://www-legacy.openmicroscopy.org/site/products/ome-tiff
3 https://www.docker.com/what-container

cost
EUROPEAN COOPERATION IN SCIENCE AND TECHNOLOGY