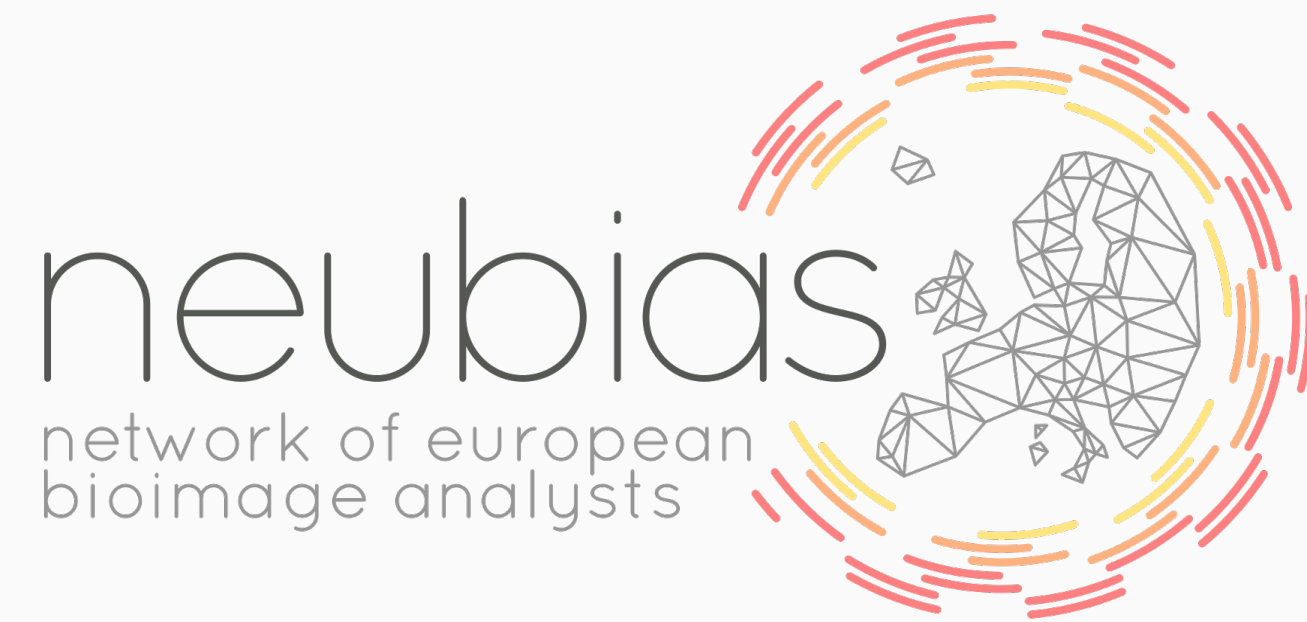


# NEUBIAS WG5 WEBTOOL

## BENCHMARKING BIOIMAGE WORKFLOWS

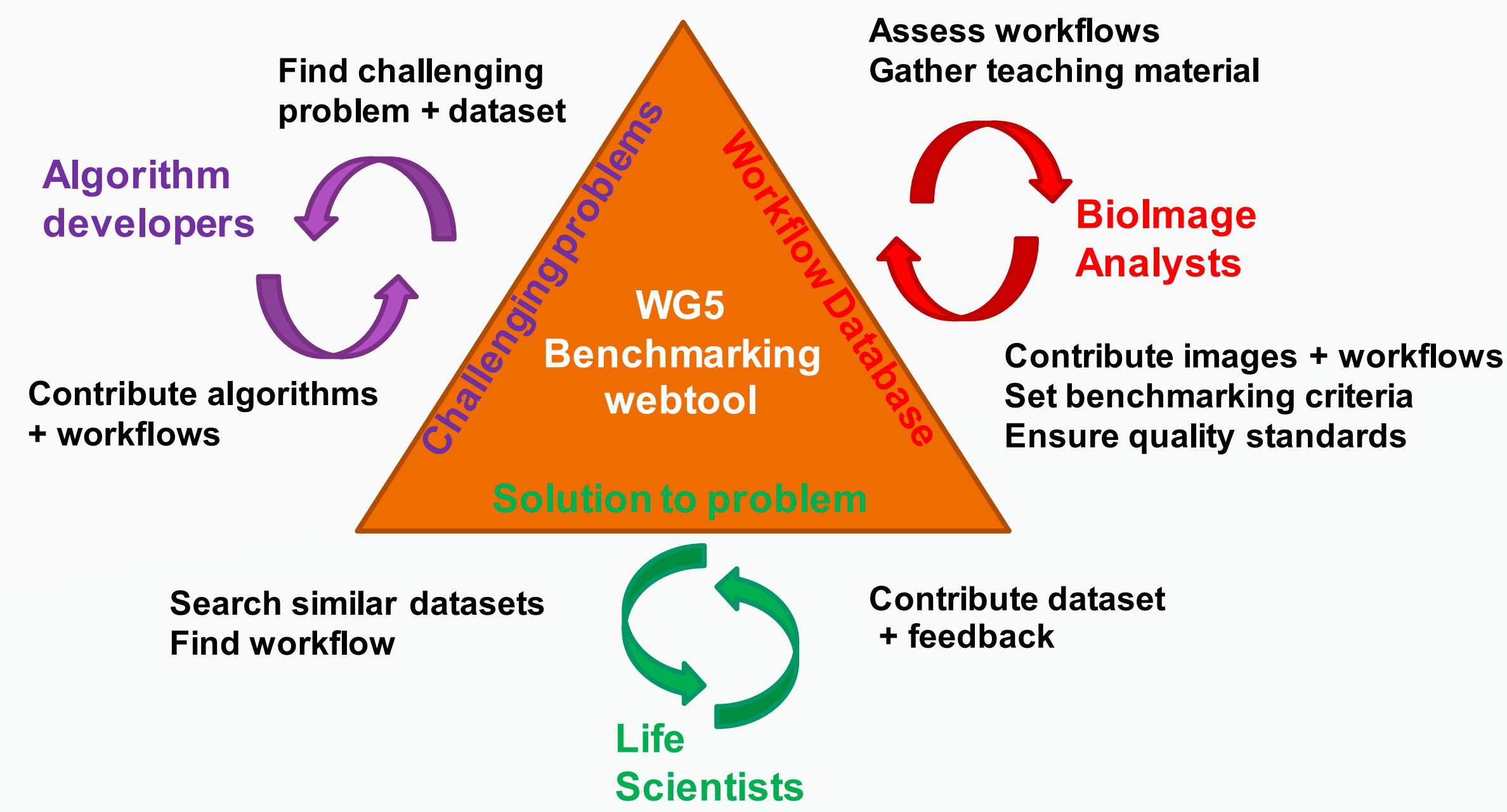


### INTRODUCTION

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

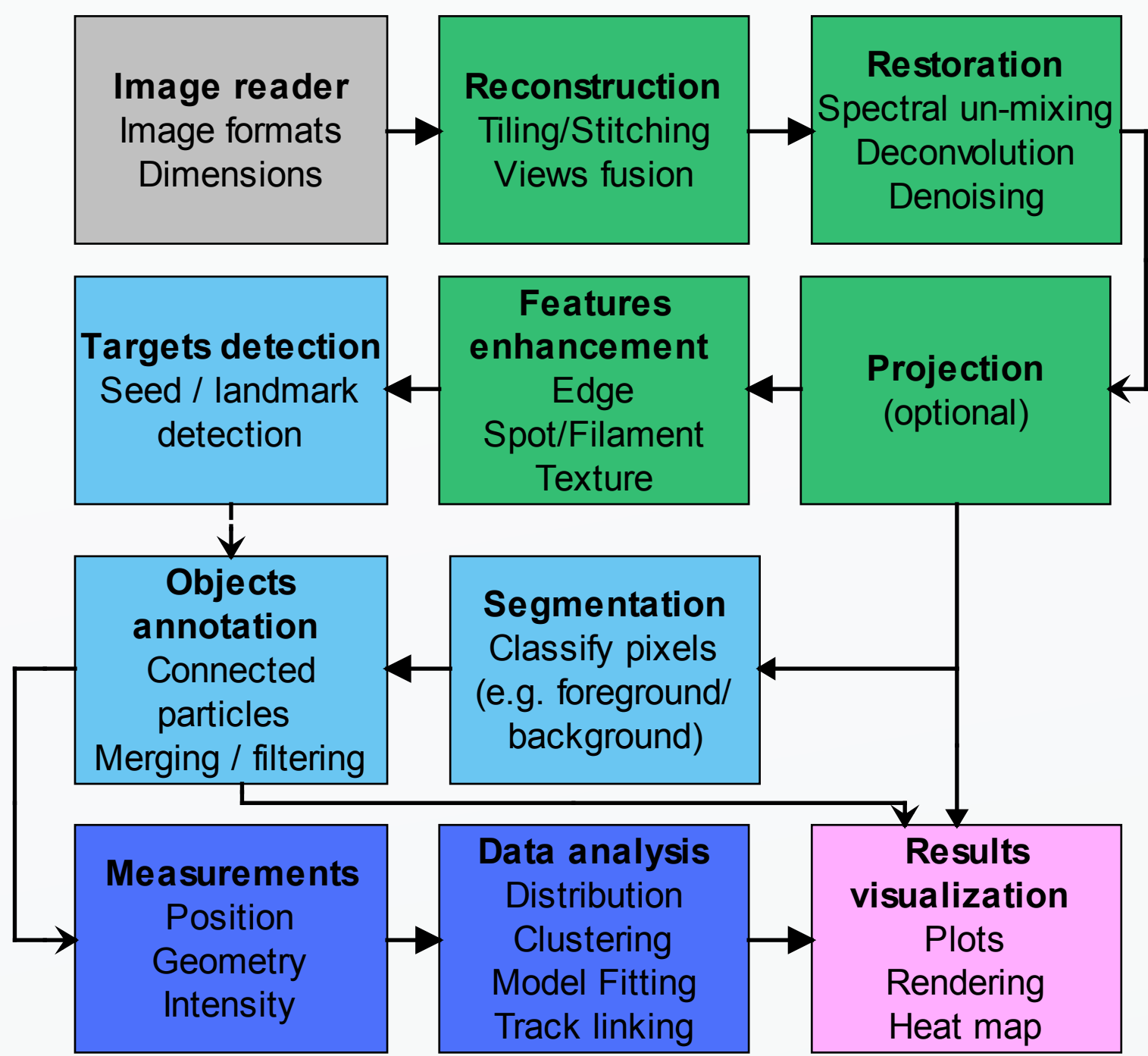


### BIA PROBLEMS TAXONOMY

IVG6-T21 BIAS problems														relations to other datasets	
File Edit View Insert Format Data Tools Add-ons Help														Customize	
Last visit was on 14 February															
Core Image Analysis															
Core Image Analysis															
Problem class															
Structure of interest															
Sample															
Imaging															
Markers															
Output															
Additional															
Isolated object detection															
Name ID															
Autophagy vesicles Spots 10-15 px Live seeded cells Link Fluo 30X0 mRFP-GFP-LC3 Autophagy intermediates LC3 Coordinates BS															
Lipid droplets Spots 10-15 px Live seeded cells Link Fluo 30X0 Nile Red Lipid droplets (neutral lipids) Coordinates BS															
Chol. droplets 2-5 px Fixed seeded cells Link WFI Fluor 100X Brooker Chl. DNA CHNARNA Coordinates BS															
Nuclei Ellipses 10-15 px Histology section Link WFI Color 20X H DAB Nuclei Coordinates BS															
Single molecule FISH Spots 10-15 px Fixed seeded cells Link Fluo 30X Cy3 mRNA Coordinates BS															
Isolated object segmentation															
Mitochondria Filament-like 10-20 px Live seeded cells Link Fluo 30X0 JC-9 Mitochondria RCIs Link															
Nuclei Ellipsoids 15-20 px Fixed seeded cells Link CF Fluor 20X DAPI Nuclei DNA RCIs Link															
Cells Polygon packing 15-20 px Live seeded cells Link Spide-GFP / Ha2A-mRFP1 Cell membrane / nuclei RCIs Link															
Cells Ellipsoids 10-20 px Tissue histology section See article Color 20X H DAB Nuclei / cell membrane RCIs Link															
Tissue Range 5-20 px 10-100 px Fixed seeded cells Link Fluo 20X DAPI RCIs Link															
Disaggregated adhesion ring Range 5-20 px 10-100 px Fixed seeded cells Link Fluo 20X 20dH1 Cell junction RCIs Link															
Cells Polygon packing 5-10 px Disaggregated vesicles Link Fluo 30X DAPI Cell junction RCIs Link															
Yeast Ellipsoids 20-100 px Live seeded cells Link Fluo 30X DAPI Cell junction RCIs Link															
Immunogold particles Spots 5-12 px Mice tissue Link Fluo 20X DAPI RCIs Link															
Cells Ellipsoids 7-10 px Live seeded cells Link Fluo 20X DAPI RCIs Link															
Artery Ellipsoids 10-20 px Histology section Link Color 20X HSE Artery walls RCIs Link															
Neurons Filament-like 10-20 px Mice tissue Link Fluor 20X DAPI Cell membrane RCIs Link															
Connective tissue Ellipsoids 10-20 px Connect. tissue, also single-cell gel Link Fluor 20X DAPI Cell membrane RCIs Link															
Cells Ellipsoids 10-20 px Histology section Link Color 20X HSE Cell Junction type RCIs Link															
Filament tracing															
Blood vessels Lumpy network 3-15 px wide Mice tissue Link LS Fluor 100 Lactin Vessel walls Networks Link															
Blood vessels Lumpy network 3-15 px wide Mice tissue Link WFI / CT 100 Vessel walls Networks Link															
Neurons Filament-like 10-20 px Fluor white mount Link Fluo 30X DAPI Vessel walls Trees Link															
Case A problems															
Composite A problems															

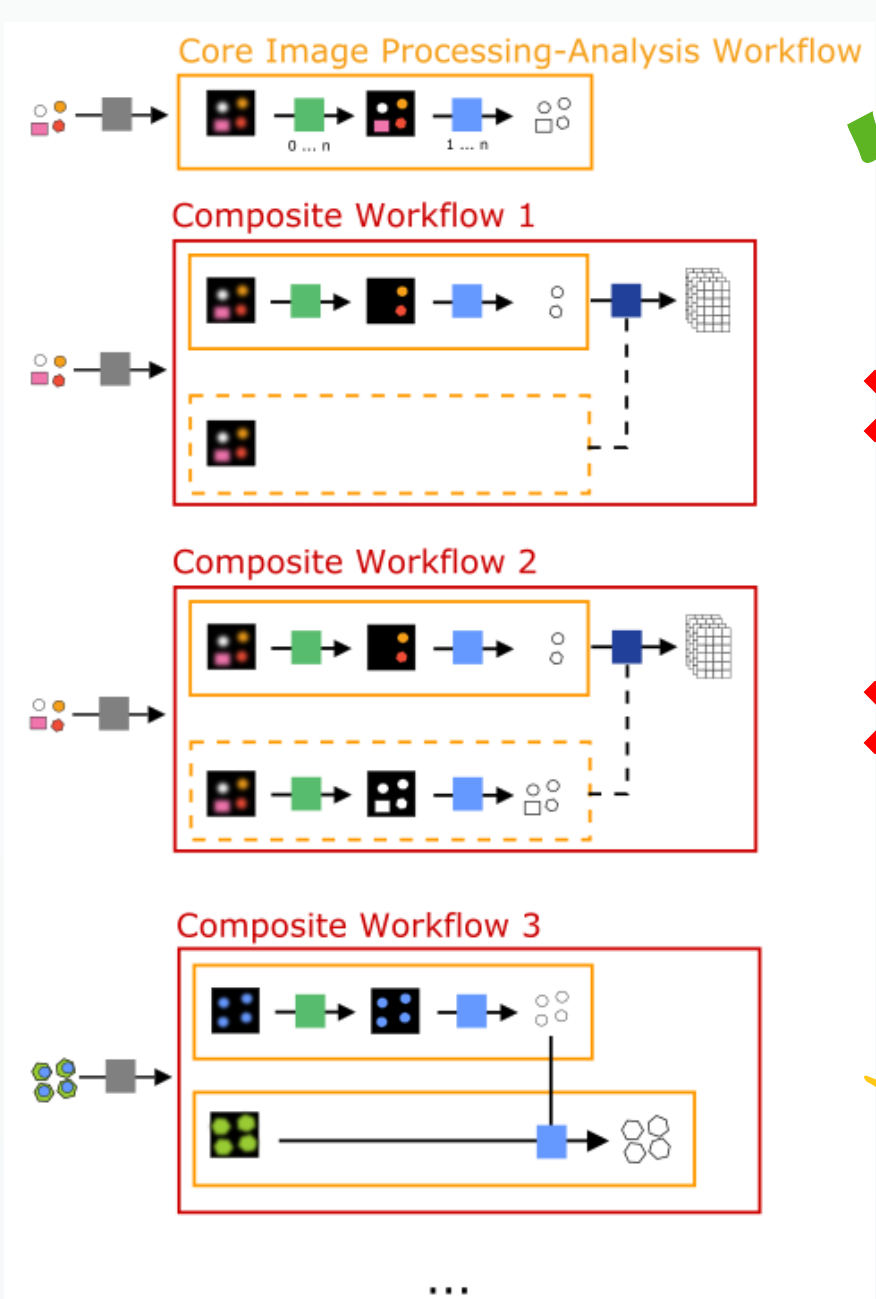
Problems were grouped by problem classes and subdivided by object geometry, sample labeling and imaging modality. They were also linked to sample images and articles describing the applications. Sample images should be annotated in a standard format that is problem class dependent and set by WG5.

### BIA WORKFLOWS



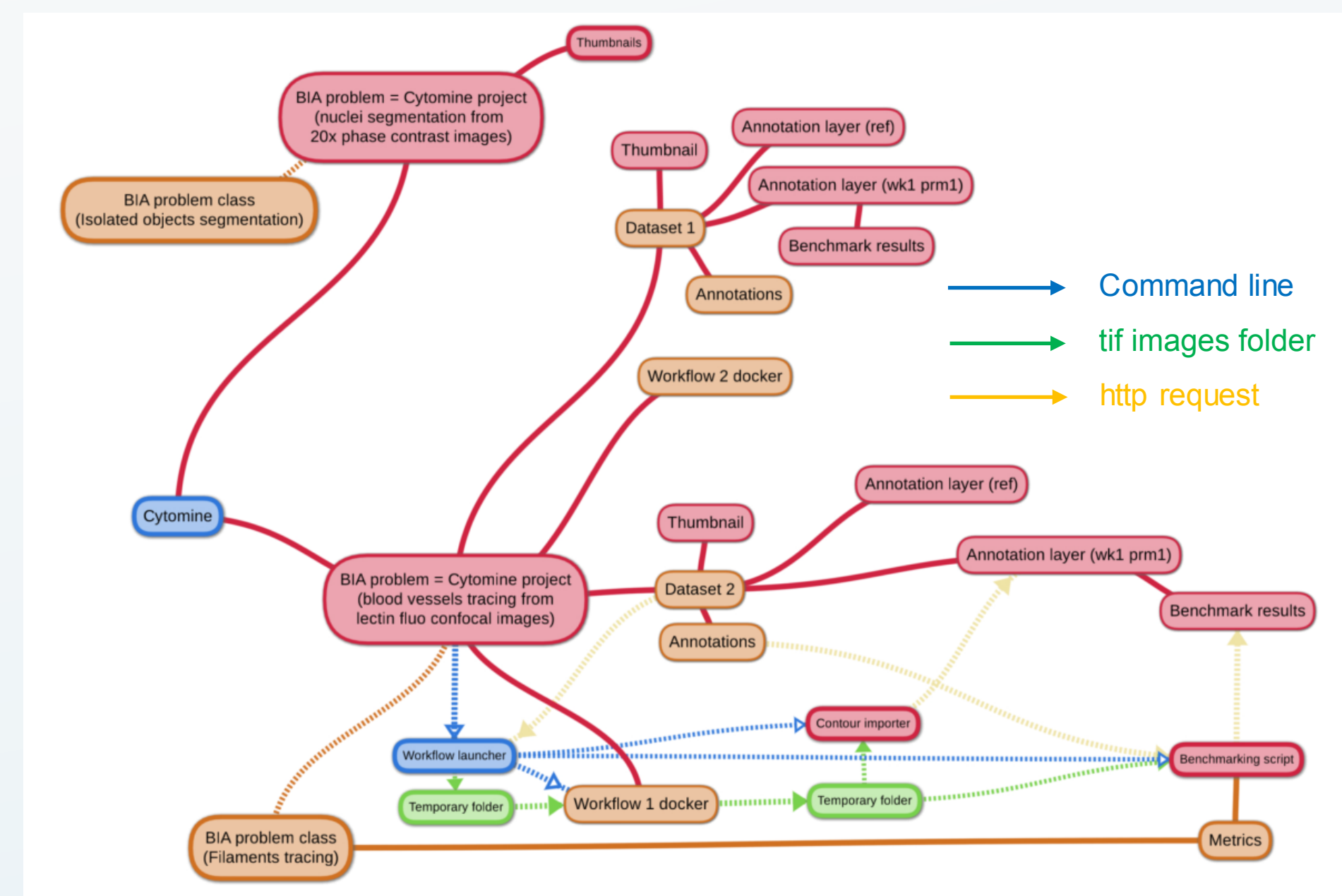
A problem can be addressed by a workflow, a sequence of operations often mapping to this diagram. Many workflows can address the same problem and we plan to compare their efficiency.

### CORE BIA WORKFLOWS



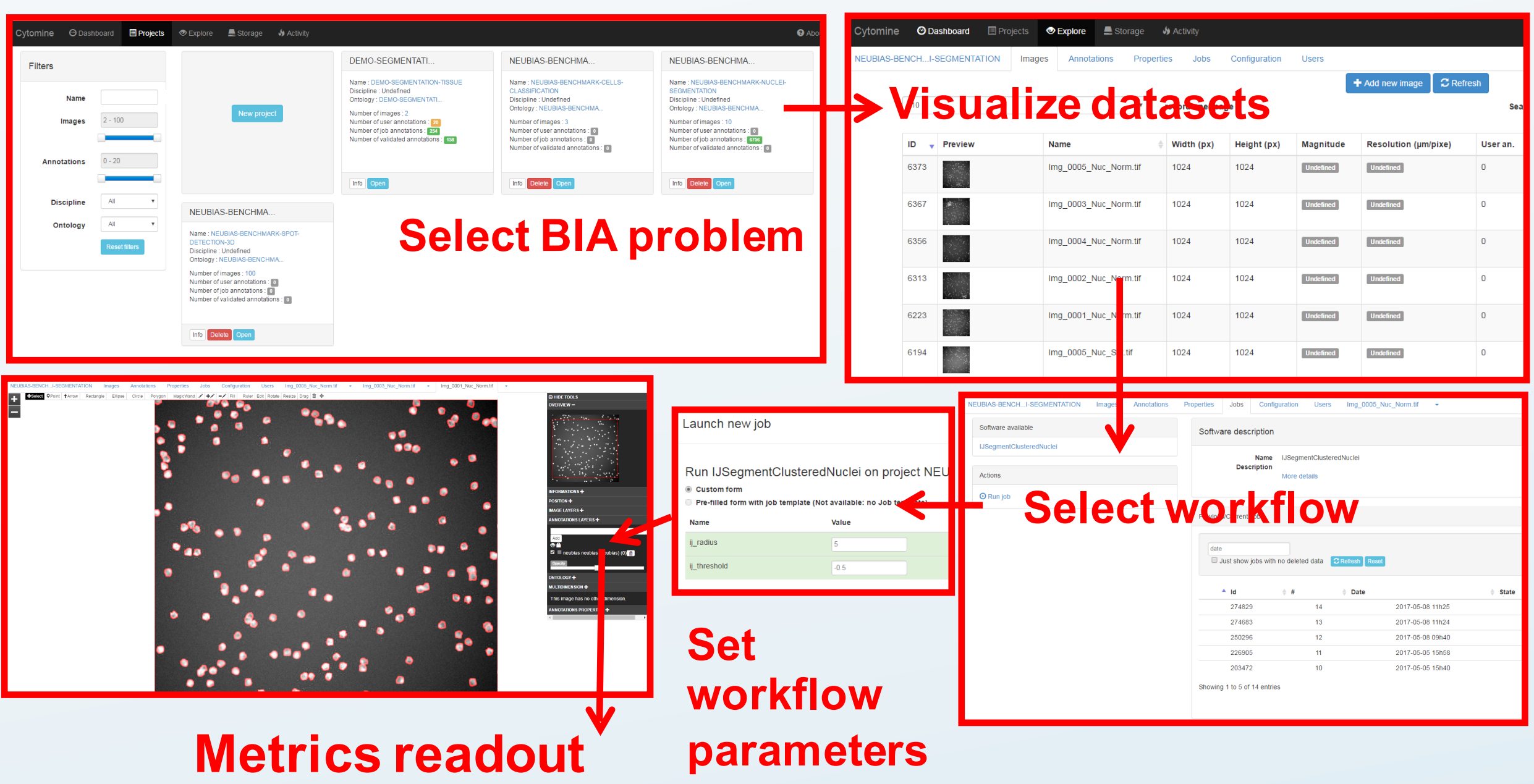
Core workflows are a subset of workflows aiming at identifying a single type of biological object; they do not perform any data post analysis. Only core workflows will be benchmarked. To be integrated to the webtool, core workflows should run in one of the supported platforms (ImageJ, Icy, Python, CellProfiler, 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<sup>1</sup> to handle OME-tiff<sup>2</sup> multi-dimensional images (importations, annotations) and interact with BIA workflows encapsulated in Docker containers<sup>3</sup>.

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 quantitatively 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>