

# New Cytomine architecture & modules for AI in digital pathology



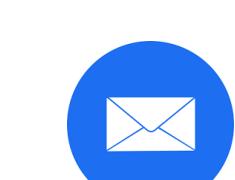
doc.cytomine.org



@cytomine\_uleige



github.com/cytomine-uleige  
(Apache 2.0 license)



info@cytomine.org

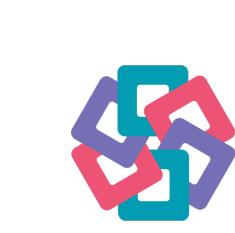
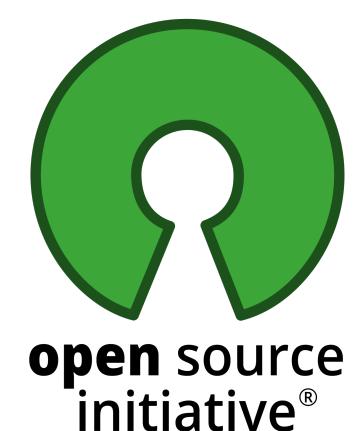
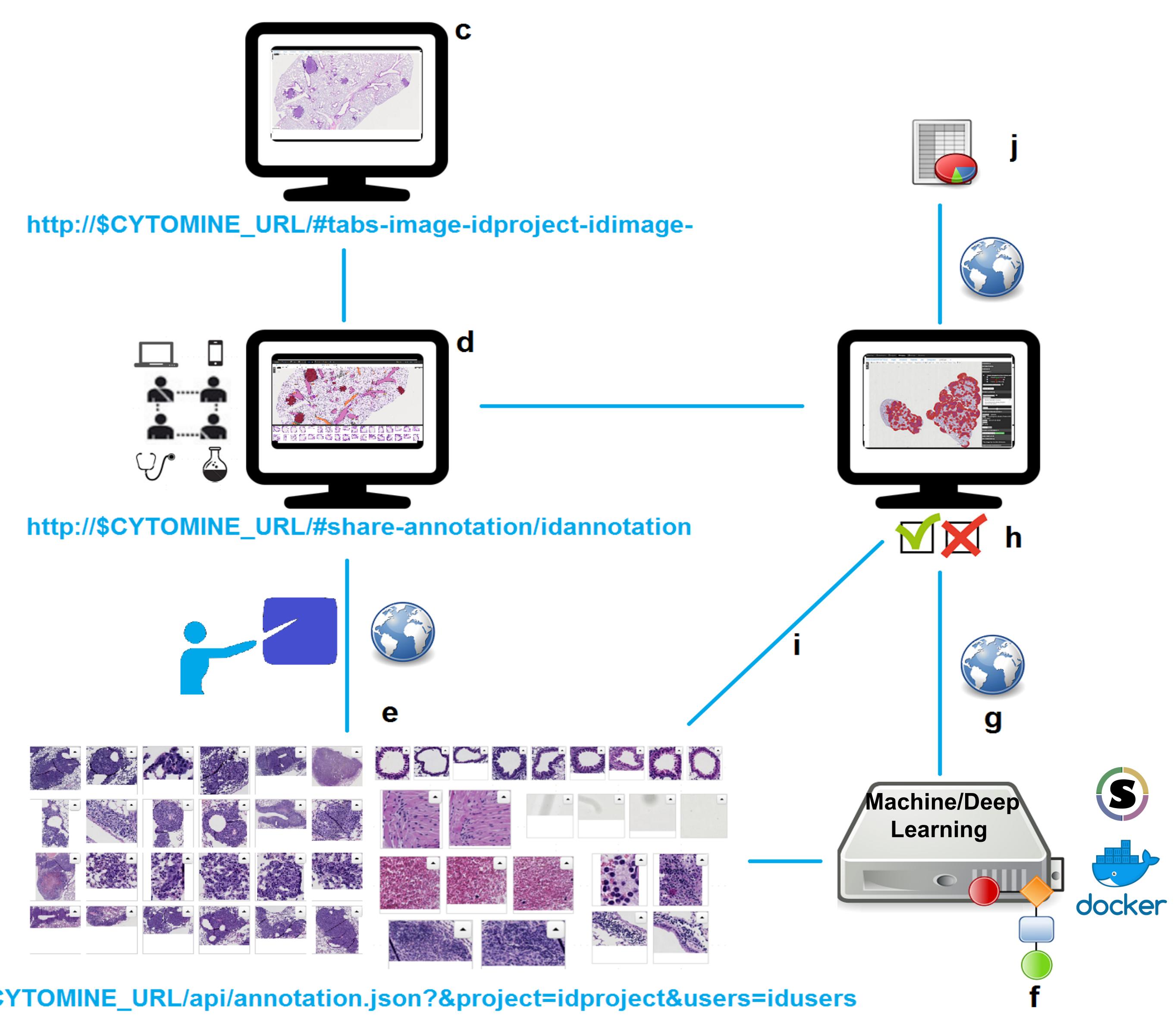
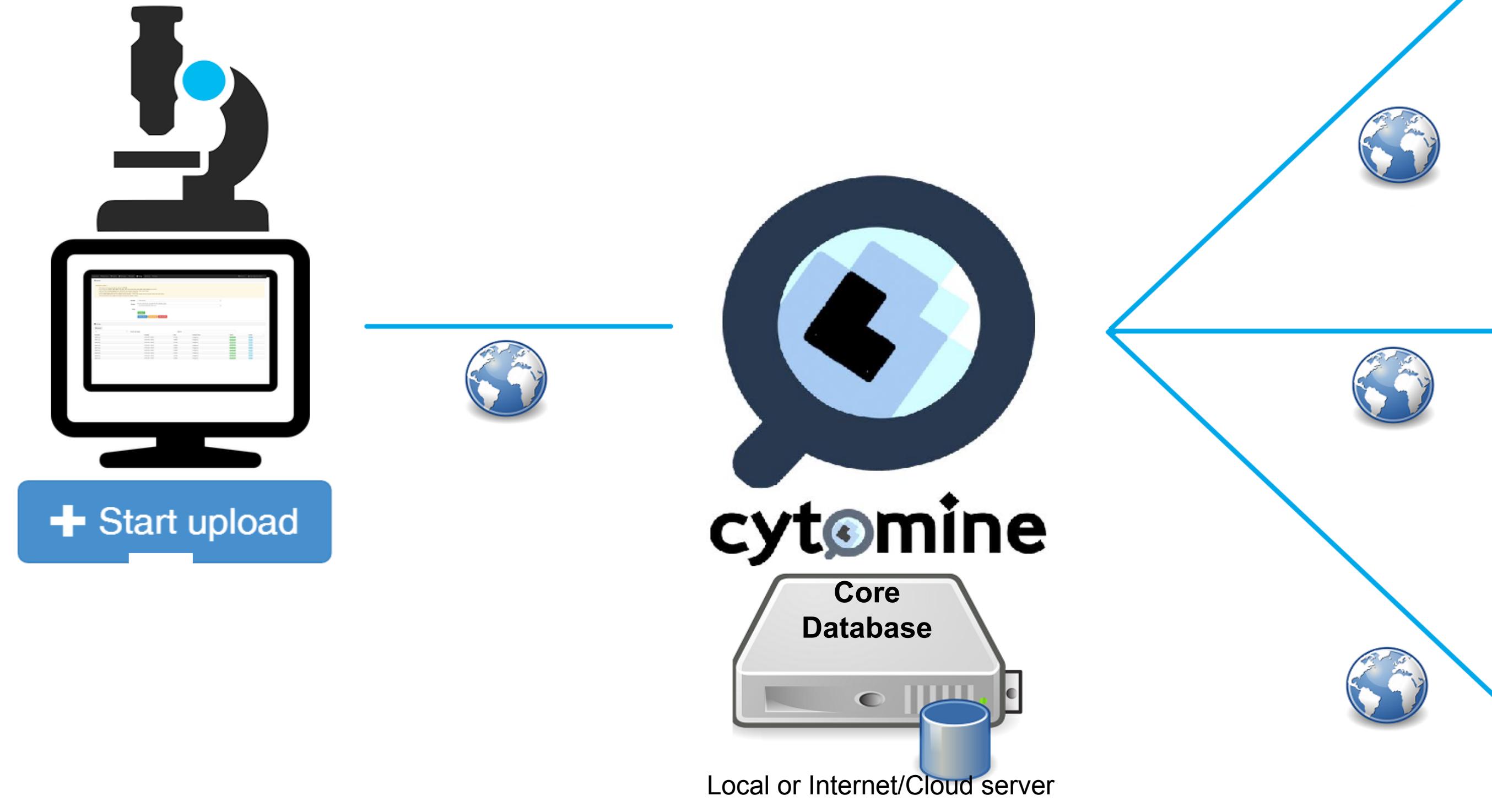


image.sc (tag Cytomine)

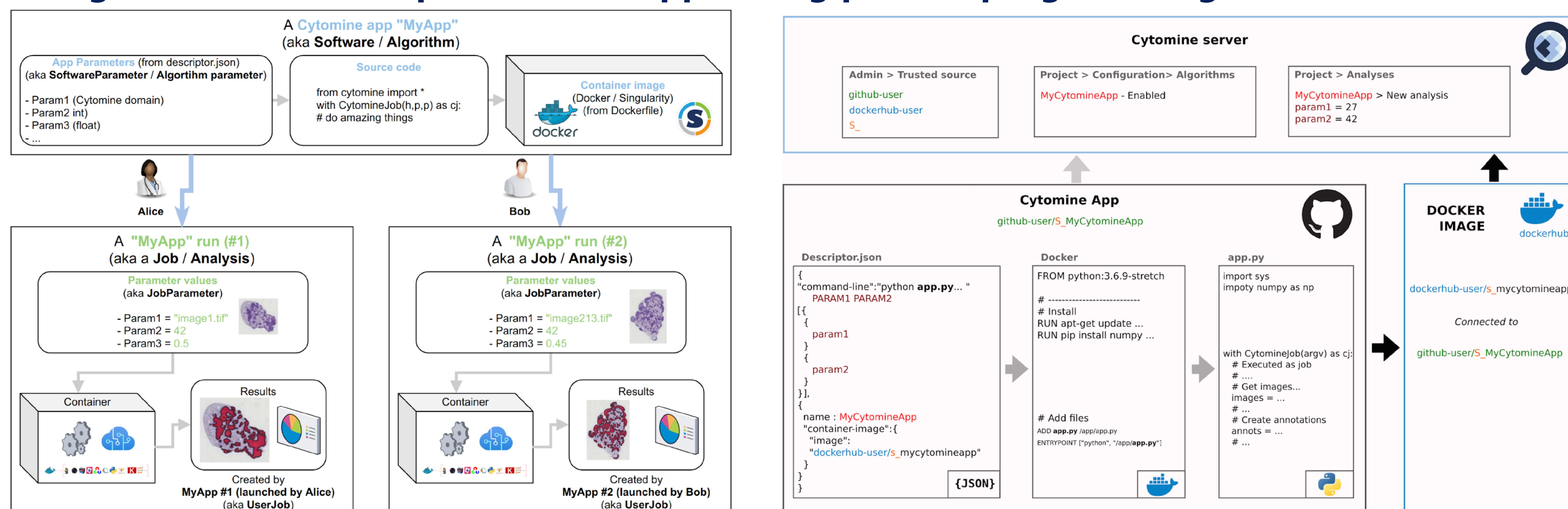


**CYTOMINE is open-source (Marée et al., 2016) and offers WEB REMOTE VIEWING, SEMANTIC ROI ANNOTATION, DATA SHARING, AND QUANTITATIVE ANALYSIS**

with WEB SERVICES (RESTful APIs)



**Our new software execution architecture (Rubens et al., 2020) enables WEB execution of heterogeneous AI or computer vision apps using precise programming conventions:**



\*compatible with:

**Example with seamless integration of StarDist cell detection algorithm (other example apps using U-Net, Random Forests, etc. are available on our GitHub):**

Launch new analysis

Algorithm: CellDetect\_StarDist\_HE\_ROI (v1.0.3)

Name	Value
Cytomine Image ID	CMU-1.svs
Cytomine ROI term ID	ROI
Cytomine Cell term ID	Nuclei_predict

Pre-filled parameters (hide)

- StarDist Probability Threshold: 0.5
- StarDist Non-Maximum Suppression Overlap threshold: 0.5
- StarDist Image Normalization Percentile Low: 1
- StarDist Image Normalization Percentile High: 99.8

Cancel Launch new analysis



## References

- Marée et al., Collaborative analysis of multi-gigapixel imaging data using Cytomine. Bioinformatics, 2016.  
 Rubens et al., Toward an Open and Collaborative Software Platform for Digital Pathology Bridged to Molecular Investigations, Proteomics: Clinical Applications, 2019.  
 Rubens, Mormont, et al., BIAFLOWS: A collaborative framework to benchmark bioimage analysis workflows, Cell Patterns, 2020.