# NEUBIAS: BIOIMAGE ANALYSTS NETWORK TO SUPPORT LIFE SCIENTISTS THROUGH TRAINING, ONLINE TOOLS REPOSITORIES AND BENCHMARKING DEPLOYMENT FOR BIOIMAGE ANALYSIS WORKFLOWS

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Image Analysis is now perceived by a large majority of Life scientists as the narrowest bottleneck in their bioimage-based projects. While open software tools for analysis, management or visualization of bioimages become more advanced, more powerful or more accessible, the lack of knowledge and training in image analysis is often the main explanation for the too small fraction of data being analyzed and quantitated. The reality is that despite huge investments in Imaging infrastructures in Europe, the ever increasing data production and complexity are not adequately balanced our the ability to process data. Moreover, the integration of advanced image analysis technology in Life Science is hampered by the lack of recognition of the specialized professionals entitled to support scientists in the use, tuning and development of bioimage analysis workflows. These specialists are bioimage analysts and NEUBIAS, a European initiative recently funded by COST (CA15124), was founded to support the recognition of their activity in Life Science and bridge software/algorithms developments with Life Scientists. NEUBIAS aims to promote the career path of image analysis experts that support Life Scientists and to empower those specialists with a solid forum where to efficiently develop their profession. On behalf of an emerging community of 250 members, we report here on three current developments of NEUBIAS that will contribute to improving the output of imaging-based research in Life science:

- The establishment of a European multi-level Training programme in Bioimage Analysis to support early careers and consolidate the skills of confirmed experts, in parallel to the release of open access online training material.
- The implementation of a unique online repository of bioimage analysis tools, functions and workflows, based on community usage experiences, to ease the search of image analysis knowledge and solutions. This bioimaging search engine (BISE) is a crowd-sourced webtool fed by the communities of analysts, developers and life scientists, and constructed on dedicated ontology/controlled vocabularies enabling multiple experts to search tools and their applications in their own language.
- The implementation of an open online benchmarking platform, BIAFLOWS, to enable life scientists and bioimage analysts to compare existing workflows on representative datasets and visualize workflows results for user defined parameters, compare results to annotations and sort/explore/export benchmarking results. The current workflows in BIAFLOWS identify specific types of biological objects in 2D/3D (e.g. vesicles, cells, filaments, …) in the context of a selection of advanced bioimage analysis problems (e.g. object tracking, filament network tracing, …), and aim to run in batchmode, online or deployed locally. In the midterm, it will enable users and developers to integrate their code/algorithms with minimal effort with Dockers.