

Bioimaging requires novel computer vision approaches and open software

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Biological image data, especially from fluorescence microscopy, are very different from the photographs or satellite imagery traditionally considered in computer vision. Biological images are often three- or even higher-dimensional, and not standardized. Moreover, they frequently only become interpretable when considering additional prior knowledge, e.g., about the labeled structures or the optics of the microscope. We hence need to develop computer vision algorithms that provide principled ways of including prior knowledge in a modular fashion. This is necessary in order not to develop a separate “algorithm” for each problem. Microscopy and biological research are rapidly moving forward, and we cannot afford developing new methods from scratch every time the data change. This can only be achieved in a multi-disciplinary community effort and with user-friendly, open-source software to which everybody can contribute. As an example, we show how recent progress in computer vision enabled both user-friendly and optimal segmentation, as implemented in the open-source MOSAIC suite for Fiji and ImageJ.