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BiaPy: accessible deep learning on bioimages

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Bioimage analysis is a cornerstone of modern life sciences, powering discoveries and insights derived from biological image data. Deep learning has become an invaluable tool for analyzing microscopy datasets, and its application is increasingly widespread in biomedical research[1]. However, its prerequisite for high-level programming skills has often acted as a barrier, limiting accessibility for researchers without a specific computational background[2].

The rapid evolution of deep learning methods, along with the diverse range of bioimage analysis applications, has created a dynamic landscape that requires researchers to adapt continuously. These applications often involve navigating multiple tools and integrating workflows that handle tasks such as image segmentation, object detection, tracking, image classification and reconstruction. To support this diversity, many solutions now either build on or integrate deep learning approaches in some form (Supplementary Table 1). For example, deepImageJ[3] allows users to apply (but not retrain) pretrained deep learning models within Fiji[4], leveraging resources like the BioImage Model Zoo[5] for model sharing. Web-based platforms such as ZeroCostDL4Mic[6] and ImJoy[7] provide easy access to deep learning workflows, though their reliance on cloud-based services can limit flexibility and reproducibility. Alternatively, tools like Ilastik[8] offer intuitive graphical interfaces that make deep learning-based image analysis more accessible to non-expert users.

Some of these tools provide features for building workflows in a pipeline-based paradigm through plug-ins, whereas others prioritize accessibility with graphical interfaces that lower the barrier for users without a computational background (Supplementary Table 1). Web-based platforms attempt to mitigate the barriers of software installation, though this comes with trade-offs, such as reduced flexibility. For example, ZeroCostDL4Mic[6] relies on Google Colab, which requires ongoing updates to align with changes in the platform. To improve portability and reproducibility, the same authors
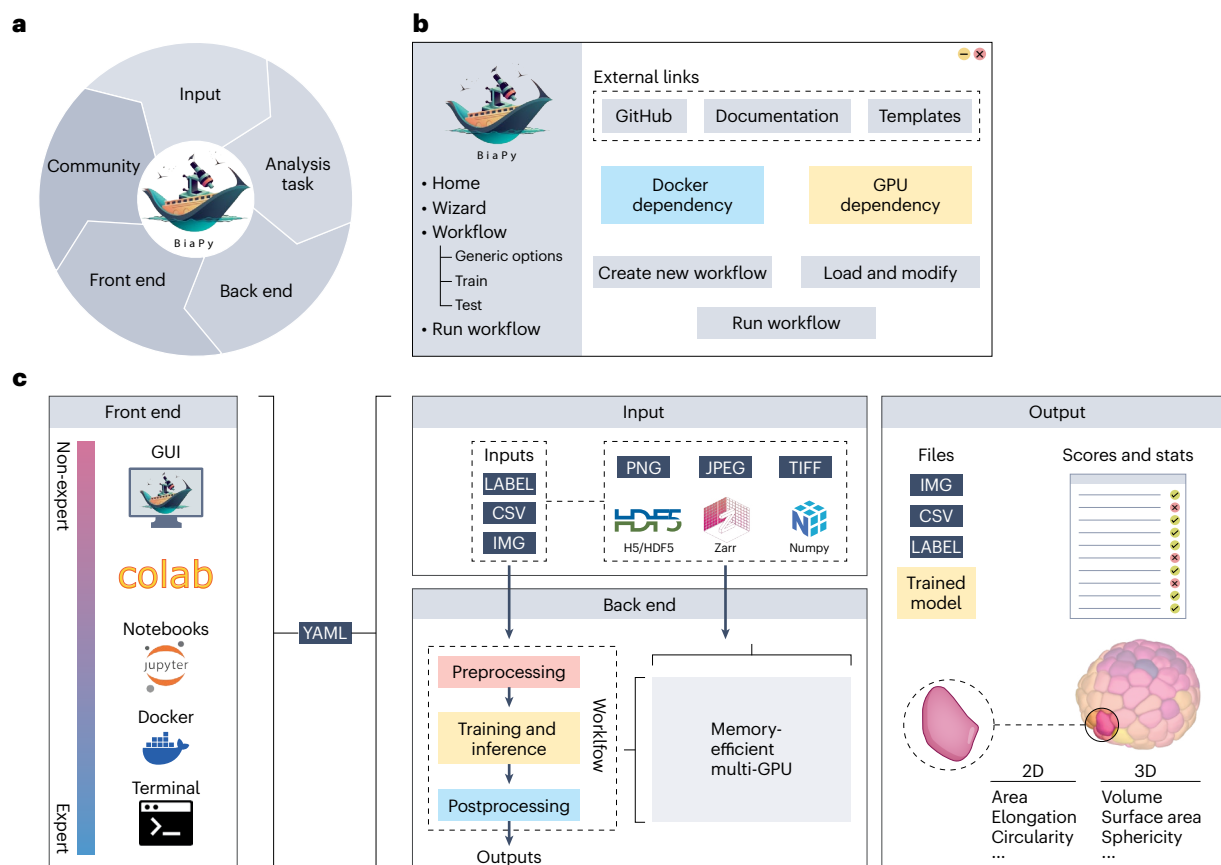

Fig. 1 | BiaPy environment and scope. a, Overview of BiaPy's workflows for 2D/3D microscopy data, supporting model customization and integration with the BioImage Model Zoo[5]. **b**, GUI with a wizard for guided workflow setup. **c**, BiaPy offers multiple installation methods and generates a YAML configuration file during execution. Workflows consist of three stages: preprocessing; model training and inference (supporting multi-GPU); and postprocessing. Outputs include images, tables and evaluation metrics.

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introduced DL4MicEverywhere[9], which uses Docker containers to encapsulate the notebooks along with their dependencies.

To address specific gaps in the current bioimage analysis landscape, we present BiaPy (https://biapyx.github.io), an open-source library designed to streamline a variety of bioimage analysis tasks for multichannel, multidimensional microscopy data (Fig. 1a). BiaPy simplifies the analytical process by supporting both traditional convolutional neural networks and modern transformer architectures within a single unified interface. This mix of established and advanced models allows researchers to apply deep learning consistently, accurately and flexibly, aligning with the rapidly evolving methods of bioimage analysis.

Unlike many tools reliant on command-line interactions, BiaPy offers a user-friendly interface (Fig. 1b) and zero-code online notebooks (Fig. 1c), lowering the entry barrier for researchers. A single-container installation improves accessibility, as compared with that of frameworks that require multiple containers per workflow[9]. The design prioritizes ease of use while maintaining efficiency.

Designed for both local computational environments and large-scale imaging facilities, BiaPy supports multi-GPU setups and handles large file formats (for example, Zarr and H5), ensuring scalability for computationally intensive analyses (Fig. 1c). Its integration with the BioImage Model Zoo[5] and TorchVision (https://pytorch.org/vision/stable/index.html) allows users to import, execute, fine-tune and export pretrained state-of-the-art deep learning models within a unified framework, capitalizing on its computational infrastructure (Fig. 1a).

Built on Python and PyTorch, BiaPy provides an accessible and widely adopted deep learning environment. It optimizes memory usage through automatic mixed precision and chunked multi-GPU operations, improving performance across diverse hardware configurations (Fig. 1c).

To streamline workflow development, BiaPy follows a structured pipeline with three key elements: data preprocessing; model training and inference (including microscopy-specific data augmentation methods); and postprocessing (Fig. 1c). This structure facilitates the prototyping of new workflows by enabling users to easily select pre- and postprocessing methods suited to their specific data and tasks.

Workflows are configured via a single YAML file, editable in a text editor, graphical user interface (GUI) or notebooks (Fig. 1c). Sharing workflows is facilitated by sharing this configuration file, along with model weights if needed for inference or retraining. BiaPy workflows are designed to process raw images and corresponding labels or annotations, producing outputs such as predicted annotations, analysis reports or pretrained models, depending on the task at hand. The wizard feature further simplifies the setup by guiding users through task-oriented questions[10]. The final configuration is based on user input, supplemented by default settings to foster optimal performance across a range of scenarios, making it easier for users to generate configuration files without needing advanced technical expertise.

In its current release, BiaPy supports various workflows for both 2D and 3D image data, including instance and semantic segmentation, object detection, image denoising, single-image super-resolution, self-supervised learning, image classification and image-to-image translation (see Supplementary Information).

In conclusion, BiaPy offers a versatile and portable solution, providing a range of workflows for bioimage analysis. Its combination of an intuitive GUI, zero-code notebooks and Docker integration makes it accessible to users with different levels of technical expertise. This combination ensures accessibility across a range of hardware configurations, from high-performance machines with GPUs to basic setups without GPU support. BiaPy is designed with a focus on reproducibility and flexibility, making it a valuable tool for both computer vision experts and life scientists. While it does not aim to replace existing platforms, it complements current tools by addressing specific gaps, such as multi-GPU support and adaptability to large datasets. As an open-source initiative, BiaPy encourages collaboration and contributions from the scientific community with the goal of empowering researchers and supporting advances in bioimage analysis.

Code availability

The complete source code for the BiaPy platform, encompassing the library's main code, GUI and associated documentation, is accessible at https://github.com/BiaPyX. For comprehensive documentation, video tutorials and use-case examples, please refer to BiaPy's documentation website (https://biapy.readthedocs.io/en/latest/).

Daniel Franco-Barranco[1,2,3,4],
Jesús A. Andrés-San Román [5,6],
Ivan Hidalgo-Cenalmor [4,7],
Lenka Backová[4,8], Aitor González-Marfil [3,4],
Clément Caporal [9], Anatole Chessel [9],
Pedro Gómez-Gálvez[1,2,5,6],
Luis M. Escudero [5,6], Donglai Wei[10],
Arrate Muñoz-Barrutia [11,12] &
Ignacio Arganda-Carreras [3,4,8,13]

[1]MRC Laboratory of Molecular Biology, University of Cambridge, Cambridge, UK. [2]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK. [3]Donostia International Physics Center (DIPC), San Sebastian, Spain. [4]Department of Computer Science and Artificial Intelligence, University of the Basque Country (UPV/EHU), San Sebastian, Spain. [5]Instituto de Biomedicina de Sevilla (IBiS), Hospital Universitario Virgen del Rocío/CSIC/Universidad de Sevilla and Departamento de Biología Celular, Facultad de Biología, Universidad de Sevilla, Seville, Spain. [6]Biomedical Network Research Centre on Neurodegenerative Diseases (CIBERNED), Madrid, Spain. [7]Instituto Gulbenkian de Ciência, Oeiras, Portugal. [8]Biofisika Institute (CSIC-UPV/EHU), Leioa, Spain. [9]Laboratoire d'Optique et Biosciences, CNRS, Inserm, Ecole Polytechnique, Institut Polytechnique de Paris, Palaiseau, France. [10]Department of Computer Science, Boston College, Boston, MA, USA. [11]Departamento de Bioingenieria, Universidad Carlos III de Madrid, Madrid, Spain. [12]Area de Bioingenieria, Instituto de Investigación Sanitaria Gregorio Marañón, Madrid, Spain. [13]IKERBASQUE, Basque Foundation for Science, Bilbao, Spain.
✉e-mail: mamunozb@ing.uc3m.es; iargandacarreras@gmail.com

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Correspondence

Author contributions

Conceptualization: D.F.-B., A.C., L.M.E, D.W., A.M.-B. and I.A.-C. Software: D.F.-B., J.A.A.-S.R., I.H.-C., L.B., A.G.-M., P.G.-G., C.C. and I.A.-C. Validation: D.F.-B., I.H.-C., L.B., A.G.-M., P.G.-G., C.C. and I.A.-C. Writing — initial outline: D.F.-B., A.M.-B. and I.A.-C. Writing — original draft: D.F.-B., A.M.-B. and I.A.-C. Writing — review and editing: all authors. Visualization: D.F.-B. and I.A.-C. Supervision: L.M.E, D.W., A.M.-B. and I.A.-C. Funding acquisition: A.C., L.M.E., D.W., A.M.-B. and I.A.-C.

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