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DL4MicEverywhere: deep learning for microscopy made flexible, shareable and reproducible

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Deep learning enables the transformative analysis of large multidimensional microscopy datasets, but barriers remain in implementing these advanced techniques[1,2]. Many researchers lack access to annotated data, high performance computing (HPC) resources and expertise to develop, train and deploy deep learning models. In recent years, several approaches have been developed to democratize deep learning usage in microscopy[2]. Tools such as the BioImage Model Zoo facilitate sharing and reuse of pretrained models, distributing them as one-click image processing solutions[3,4]. Yet often, deep learning models need to be trained or fine-tuned on the end-user dataset to perform well[2,3,5]. We previously released ZeroCostDL4Mic[6], an online platform relying on Google Colab that helped democratize deep learning by providing a zero-code interface to train and evaluate models capable of performing various bioimage processing tasks, such as segmentation, object detection, denoising, super-resolution microscopy and image-to-image translation. Here, we introduce DL4MicEverywhere, an advancement of the ZeroCostDL4Mic[6] framework (Fig. 1).

DL4MicEverywhere is a platform that lets users train and implement their models in different computational environments. These environments include Google Colab, personal computational resources such as a desktop or laptop, and HPC systems. This flexibility is achieved by encapsulating each deep learning technique in an interactive Jupyter Notebook within a Docker container, enabling others to replicate analyses consistently across multiple platforms. DL4MicEverywhere (https://github.com/HenriquesLab/DL4MicEverywhere) enables users to install and interact with a large offering of standardized, user-friendly deep learning workflows, away from the limitations of proprietary platforms such as Google Colab and in a secure computational environment with controlled data privacy and resources. DL4MicEverywhere can be launched graphically, via X11

forwarding, or directly through a command line (headless mode), supporting HPC usage. This cross-platform containerization technology boosts the long-term platform's sustainability and reproducibility, enhancing user convenience[7].

DL4MicEverywhere features a zero-code interface that handles all the behind-the-scenes complexities, so users no longer need to deal with Docker configuration and deployment through a terminal. The intuitive interface abstracts away these technical details while providing a standardized Docker encapsulation for executing advanced techniques reliably. Researchers can select a notebook, choose computing resources and run the corresponding deep learning-powered analysis with just a few clicks (Fig. 1c–e). This allows users to train and apply models on various computing resources they control, eliminating reliance on third-party platforms. Furthermore, researchers can launch a notebook on local or remote systems with GPU acceleration whenever available, without worrying about complex software dependencies, Docker container management, or loss of access to deep learning frameworks (Fig. 1f–h). Compared to ZeroCostDL4Mic, DL4MicEverywhere doubles the number of deep learning approaches and provides new bioimaging analysis tasks, such as semantic segmentation, interactive instance segmentation, image registration, 3D single molecule localization microscopy, temporal and spatial upsampling, and image generation. The platform is designed to encourage the sharing and reuse of deep learning workflows provided as Jupyter Notebooks, which are then integrated into the BioImage Model Zoo. DL4MicEverywhere is strengthened by automated build pipelines[8] that allow tracked versioning of ZeroCostDL4Mic notebooks and the seamless integration of new trainable models contributed by the community as user-friendly notebooks independently of the original ZeroCostDL4Mic framework (Fig. 1b). DL4MicEverywhere handles the corresponding testing and building of fully documented and open-source containers, making

it easy for researchers to share not just the latest method, but the full software environment required to run it reliably.

DL4MicEverywhere is an open-source initiative that aims to make deep learning accessible to everyone by providing a flexible and community-driven platform. Encapsulating software in Docker containers makes it possible to integrate new methods without worrying about complex installation procedures, enriching the microscopy community through support to developers to easily contribute new pipelines, encouraging participatory innovation. Users can rely on shared techniques while customizing models across diverse hardware, retaining control over data and analysis. The platform sets a baseline for the development and use of cutting-edge foundation models[9]. By bundling these sophisticated models into shareable containers, researchers can easily exploit them in their microscopy applications. It is noteworthy that containerization approaches can increase local storage usage. Compared to proprietary platforms, which are not universally accessible, DL4MicEverywhere simplifies complex deep learning workflows through open, easy-to-use graphical user interfaces and automated pipelines. It leverages local computational resources, HPC and cloud-based solutions, which provides flexibility for sensitive biomedical data where privacy risks may limit reliance on public cloud platforms. It also helps with continuously scaling data, such as high-throughput high-content imaging data, whose storage, dissemination and access often rely on institutional infrastructures with specific data-sharing protocols. The containerization of notebooks is secure, as Jupyter Notebook ports are virtualized, private and protected with tokens. DL4MicEverywhere also adheres to FAIR (findability, accessibility, interoperability and reusability) principles, enhancing data-driven scientific discoverability[10]. We expect DL4MicEverywhere to represent an important step toward reliable, transparent and participatory artificial intelligence in microscopy.

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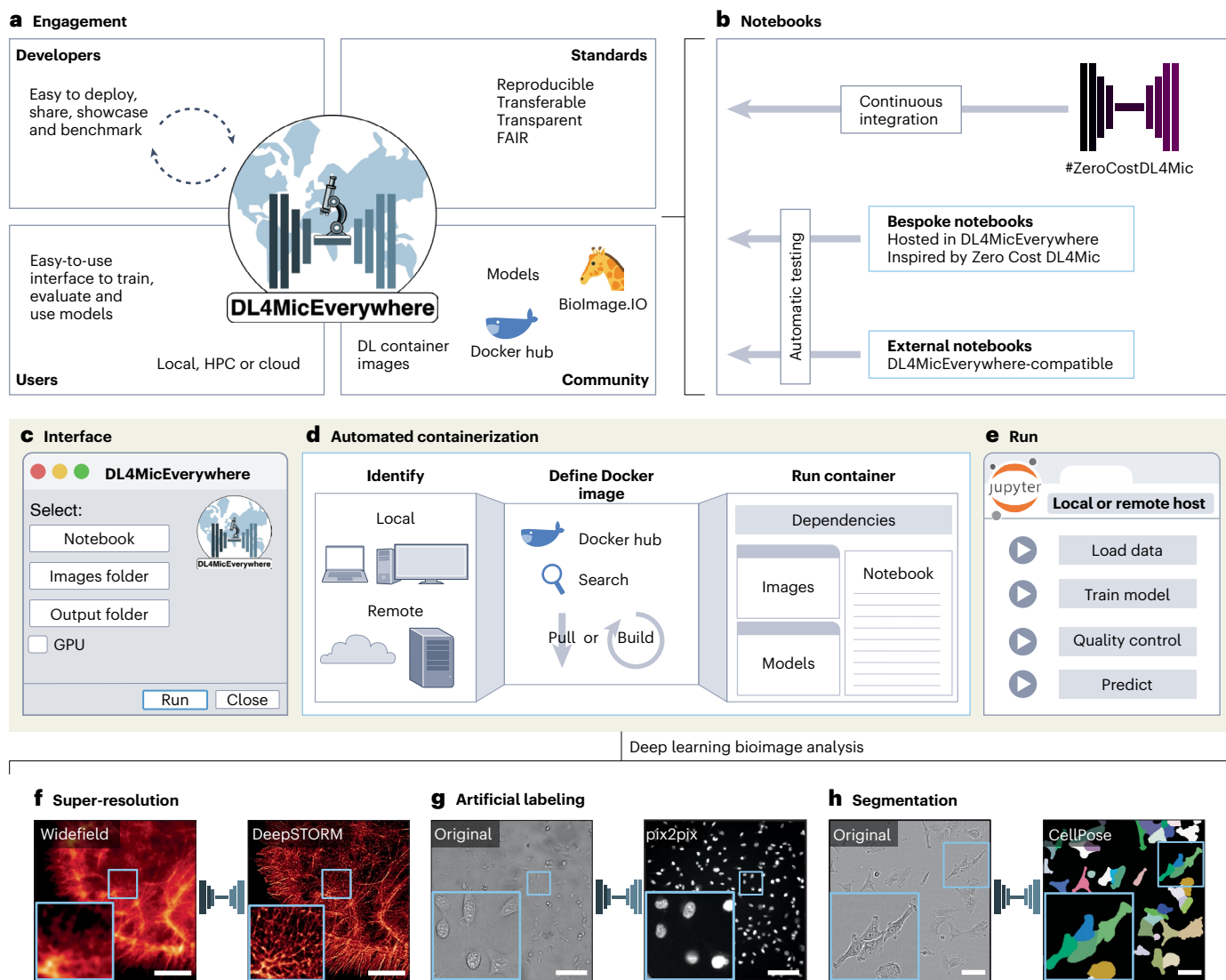
Fig. 1 | The DL4MicEverywhere platform. a, DL4MicEverywhere eases deep learning workflow sharing, deployment and showcasing by providing a user-friendly interactive environment to train and use models. Cross-platform compatibility ensures reproducible deep learning model training. DL4MicEverywhere contributes to deep learning standardization in bioimage analysis by promoting transferable, FAIR and transparent pipelines. The platform exports models compatible with the BioImage Model Zoo[3] and populates free and open source container images in Docker Hub for developers to reuse. **b**, DL4MicEverywhere accepts three types of notebook contribution: ZeroCostDL4Mic[6] notebooks, bespoke notebooks inspired by ZeroCostDL4Mic[6], and notebooks hosted in external repositories that are compliant with our format. The requirements and format of these contributions are automatically tested. **c**, In the DL4MicEverywhere graphical user interface, the user chooses a notebook, images and output folder, and chooses a GPU-running model if possible. **d**, DL4MicEverywhere automatically identifies the system architecture and requirements, checks whether the corresponding Docker image is available in Docker hub to download, and it builds it otherwise. This image is used to create a Docker container: a functional instance of the image that gathers the code environment to use the chosen notebook. **e**, A Jupyter lab session is launched inside the Docker container to train, evaluate or use the chosen model within an interactive notebook, equivalent to ZeroCostDL4Mic[6] notebooks. **f**–**h**, DL4MicEverywhere enables the use of the same notebooks for super-resolution (**f**), artificial labeling (**g**) or segmentation (**h**) pipelines, among many others, in different local or remote infrastructures such as workstations, the cloud or HPC clusters.

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Code availability

The source code, documentation and tutorials for DL4MicEverywhere are available at https://github.com/HenriquesLab/DL4MicEverywhere under a Creative Commons CC-BY-4.0 license.

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Author contributions

I.H.-C., G.J., R.H. and E.G.-d.-M. conceived, designed and wrote the source code of the project with contributions from all co-authors; I.H.-C., J.P.W., M.G.F., C.R., A.S., Y.S., G.J., R.H. and E.G.-d.-M. tested the platform; I.H.-C., J.P.W., M.G.F., G.J., R.H. and E.G.-d.-M. wrote the user documentation; I.H.-C., G.J., R.H. and E.G.-d.-M. wrote the paper with input from all co-authors. F.J. (florian.jug@fht.org) serves as a contact for the consortium.

Competing interests

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