

Deliverable D4.3

Release of human-in-the-loop interfaces (accessible from the AI4Life website)

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Authors	Nils Mechtel and Wei Ouyang
Contributors	Estibaliz Gómez de Mariscal
Reviewers	Joanna Hård, Beatriz Serrano-Solano, Florian Jug, Arrate Muñoz-Barrutia, Dorothea Dörr



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Change Log

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v0.4	04.09.2024	Nils Mechtel, Wei Ouyang	Final draft approved for submission

Acronyms and Abbreviations

AI	Artificial Intelligence
BMZ	BiolImage Model Zoo
D	Deliverable
EOSC	European Open Science Cloud
FAIR	Findable, Accessible, Interoperable, Reusable
RPCs	Remote Procedure Calls
SAM	Segment Anything Model
UI	User Interface
v	Version
WP	Work Package

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Executive summary

The AI4Life project is dedicated to democratising Artificial Intelligence (AI) methods for biological imaging, bridging the gap between life sciences and computer vision to make cutting-edge techniques more accessible. Within this framework, Work Package 4 (WP4) plays a crucial role in developing services that integrate reproducible deep-learning algorithms into the BioImage Model Zoo (BMZ), a central component of AI4Life.

Deliverable 4.3 (D4.3) details the creation of a scalable, user-friendly human-in-the-loop collaborative annotation tool within the AI4Life project. The collaborative annotation tool expands the usability of the BioEngine by integrating AI models following the specifications of the BioImage Model Zoo, such as the microSAM model, into the Kaibu web image annotation interface. The newly developed BioImage.IO Colab web tool (available at <https://bioimage-io.github.io/bioimageio-colab/>) enables users to manage annotation sessions directly from their browsers. This facilitates real-time, AI-assisted image annotation without the need for complex installations. This system supports both manual and AI-assisted segmentation. This allows users to interactively refine AI-generated results and improve the quality of the annotations through human feedback. By leveraging Kubernetes for scalability, this framework ensures robust performance under high user demand, enabling large-scale dissemination and simultaneous use of the resources, thus advancing AI4Life's mission to enhance AI-driven bioimage analysis.



1. Introduction

The AI4Life project, part of the European Union's Horizon Europe research and innovation programme, is coordinated by Euro-BioImaging and involves ten partners, five of whom are European Research Infrastructures. The project started in September 2022 and will continue until September 2025, aiming to democratise the accessibility of state-of-the-art AI-based image analysis for life scientists. AI4Life focuses on establishing and supporting innovative services that cater to life scientists and AI method developers.

Work Package 4 (WP4) is dedicated to "Contributor Services" and supports several core objectives of AI4Life:

- Objective 1: Democratise the availability of AI-based image analysis methods as a FAIR service, accessible through the AI4Life service landscape and powered by the European Open Science Cloud (EOSC) infrastructure.
- Objective 2: Establish standards for the submission, storage, and FAIR access to reference data, annotations (ground-truth), trained AI models, and trainable AI methods.
- Objective 3: Simplify the deployment, sharing, and dissemination of AI-based methods as a new developer-facing service within the BioImage Model Zoo (BMZ).
- Objective 5: Empower common image analysis platforms with AI tools.

The rapid increase of data generated in life science research has exposed the limitations of conventional desktop applications used for bioimage analysis. These tools struggle with the memory demands of high-throughput data and the complexity of AI-driven image analysis, often requiring substantial hardware and intricate software setups. Additionally, existing machine-learning model zoos tend to be inaccessible to a broader audience, requiring advanced programming and computer science knowledge. These challenges underscore the need for a scalable, efficient, and user-friendly solution for AI model storage and serving.

In response to these challenges, AI4Life has developed the BioEngine, a cloud-based infrastructure designed to scale and simplify the complex landscape of bioimage analysis by enabling user-friendly model deployment in the cloud. The BioImage Model Zoo builds upon the BioEngine to enable non-expert users to test-run pre-trained AI models on their own images without requiring any local installations. The BioEngine integration within existing software platforms like Fiji, Icy, or napari eliminates the need for multiple dependencies.



For developers, the BioEngine provides a scalable platform that judiciously utilises limited GPU resources, featuring a simple API accessible via HTTP or WebSocket. This enables the integration of cloud-based models into Python scripts, Jupyter notebooks, or web-based applications, which, in turn, democratises access to advanced AI tools for a wider audience.

As part of the evolving landscape of AI in bioimage analysis, models such as cellpose¹, the Segment Anything Model (SAM)², and, more recently, microSAM³ for microscopy image segmentation, have demonstrated high generalisation capabilities. These models can be used on unseen images to produce reliable segmentation results interactively and can be deployed within the BioEngine for easy access. This provides a unique opportunity for speeding up the annotation process, as users can automatically obtain initial guesses for large datasets with these models and rapidly curate the annotations by making minor corrections. This human-in-the-loop approach is emerging as a highly efficient way to build high-quality annotation datasets.

To further enhance the efficiency and scalability of this annotation process, we used Hypha⁴ as a central communication hub in the BioEngine, which supports real-time collaboration through Remote Procedure Calls (RPC) mechanism. This integration enables further integrations such as Kaibu⁵, an annotation tool in a web browser. With Hypha, users can generate shareable URLs to distribute annotation tasks among multiple users or collaborators, significantly increasing the speed and efficiency of the annotation process while fostering community interaction. Researchers can train or fine-tune AI models within the BioImage Model Zoo with the annotations collected through this system. Moreover, by enabling URL connection with the platform, researchers can use the complementary tools developed within AI4Life, such as the DL4MicEverywhere⁶ platform—another service offered by AI4Life—, to access cutting-edge deep learning techniques for bioimage analysis through interactive Jupyter notebooks with user-friendly graphical interfaces. This platform ensures portability and reproducibility, allowing execution across various computing environments, further reinforcing the project's mission to democratise AI-driven bioimage analysis.

¹ <https://www.cellpose.org/>

² <https://segment-anything.com/>

³ <https://github.com/computational-cell-analytics/micro-sam/>

⁴ <https://github.com/bioimage-io/hypha/>

⁵ <https://kaibu.org/docs/#/>

⁶ <https://github.com/HenriquesLab/DL4MicEverywhere/>



2. Description of Work

2.1 Collaborative Annotation Workflow Integration

The collaborative annotation workflow has been significantly enhanced by the introduction of a web-based BioImage.IO Colab interface (accessible from <https://bioimage-io.github.io/bioimageio-colab/>), enabling image annotation through the integration of the microSAM model and the human-in-the-loop system. This platform is built on scalable infrastructure using Kubernetes and BioEngine⁷ to manage and deploy microSAM as a BioEngine application, ensuring robust performance and ease of use. Additionally, the workflow integrates DL4MicEverywhere, a tool within the BioImage.IO environment, to enable the fine-tuning of models using the collected annotations. Once a substantial number of annotations are gathered, a model trainer can use DL4MicEverywhere to pull pairs of source images and annotation masks, fine-tune a model, and then push the updated model back to the BioImage Model Zoo.

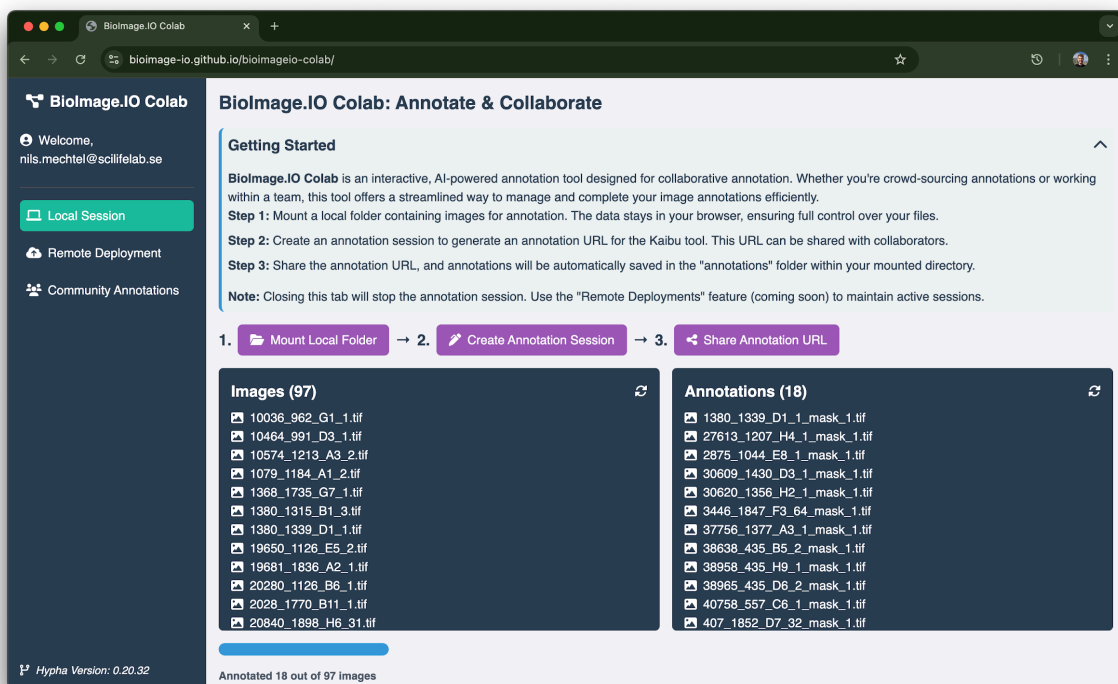


Figure 1: BioImage.IO Colab for collaborative annotation. The tool offers an intuitive platform for initiating and managing local annotation sessions. Users can mount a local folder to store images, deploy an annotation session that creates an "annotations" folder for storing results, and share the Kaibu interface URL for annotation. The interface is entirely browser-based, ensuring ease of use without the need for complex

⁷ <https://github.com/bioimage-io/bioengine/>

installations. The user interface features a sidebar for navigation, with tabs for "Local Sessions," "Remote Deployment," and "Community Annotations", enabling flexible session management and community contributions for crowdsourcing annotations.

The BiImage.IO Colab offers a user-friendly platform for initiating and managing annotation sessions (see Figure 1). The interface is designed to guide users by setting up a collaborative annotation session. Providers can mount a local folder for storing images, ensuring that data remains within their control throughout the process. This local deployment setup is intuitive, requiring no installations—users interact with the system entirely through a web browser.

Once the local folder is mounted, the provider can create an annotation session through BiImage.IO Colab. This automatically creates an "annotations" folder in the mounted directory, storing all annotations. A unique URL is generated for the annotation tool featuring the Kaibu interface, which the provider can share with annotators.

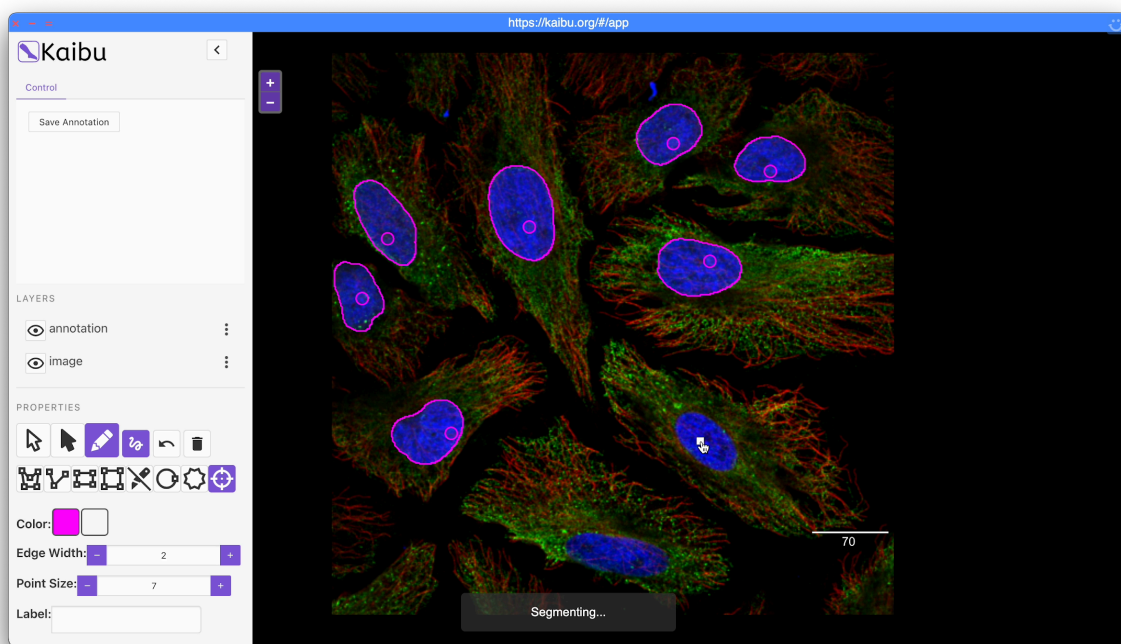


Figure 2: Kaibu Annotation Interface. The Kaibu Annotation Interface provides annotators with a versatile and user-friendly tool for image segmentation. Annotators can either manually draw polygons to define regions of interest or utilise the microSAM service, where placing point coordinates sends the image to microSAM deployed on the Kubernetes cluster. The model returns a segmentation result, drawing a polygon around the target area, which the user can further refine. This interface supports a hybrid approach, allowing users to combine manual annotations with AI-assisted segmentation for precise and efficient results.

In the Kaibu interface (see Figure 2), annotators have two primary methods for interacting with the images:

- 1. Manual Annotation:** Annotators can manually draw polygons around the regions of interest in the image, allowing for precise control over the segmentation process.
- 2. microSAM-Assisted Segmentation:** Alternatively, annotators can place point coordinates on the image, which are sent to the microSAM service running on the Kubernetes cluster. microSAM uses these points as reference targets to perform the segmentation, generating a polygon on the image. This automatic segmentation can be further refined by the annotator if necessary.

These methods can be combined, giving the annotators flexibility in approaching the task. For example, an annotator might use the microSAM service to quickly generate a segmentation and then manually adjust the results. Kaibu also includes a polygon cutter tool that allows annotators to correct or split existing annotations, further enhancing the precision and quality of the results.

2.2 Scalability and Performance Enhancements

Integration of Kubernetes for deploying the microSAM model as a BioEngine application was essential to address performance challenges encountered during high-demand scenarios. Initially, the segmentation model was deployed on a local workstation, but this setup struggled under the load of multiple simultaneous annotations, leading to system failures.

To resolve these issues, the microSAM model was migrated to the Kubernetes cluster (deployed at KTH) and deployed as a BioEngine application (see Figure 3). This architecture allows for dynamic scaling of computational resources, ensuring that the annotation service remains responsive even under heavy user loads. The Kubernetes cluster automatically adjusts resources to match demand. This prevents bottlenecks and enhances the overall efficiency of the system. Additionally, using Ray⁸ clusters within this setup provides significant advantages in terms of parallel processing and resource management, allowing for efficient handling of large-scale annotation projects.

⁸ <https://www.ray.io/>



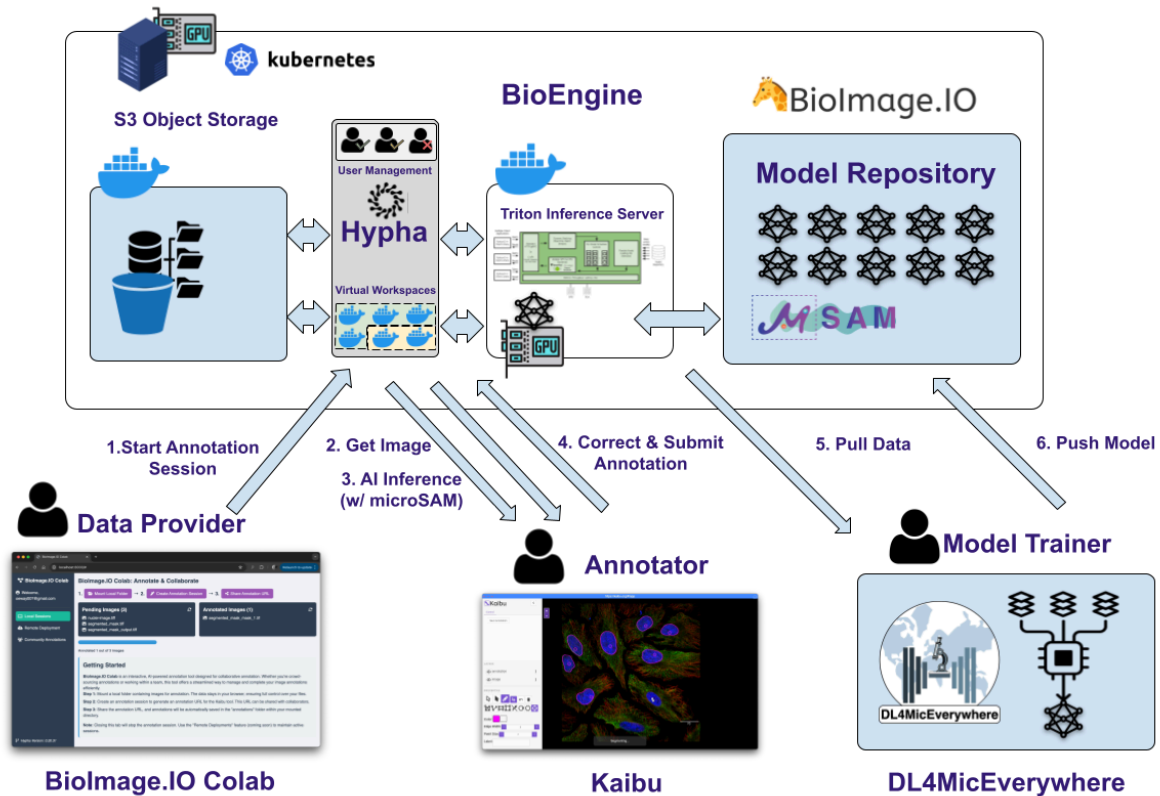


Figure 3: Workflow diagram of the human-in-the-loop annotation platform. The workflow diagram illustrates the end-to-end process of human-in-the-loop annotation and model training. It begins with the provider using BiImage.IO Colab to create an annotation session, which generates a Kaibu interface URL. Annotators access the Kaibu interface to perform image segmentation, either manually or with the assistance of microSAM, which runs as a BioEngine application on the Kubernetes cluster. The annotated data is saved directly to the provider’s mounted folder. Once a sufficient amount of annotations is collected, a model trainer can pull the data into DL4MicEverywhere, fine-tune a model using the annotations, and then push the updated model back to the BiImage Model Zoo. The integration of these components ensures a scalable, efficient, and user-friendly annotation process, leveraging both human expertise and AI capabilities.

2.3 Technical Framework and Integration

The human-in-the-loop system is deeply integrated with the BiImage.IO environment, leveraging BioEngine for managing interactive segmentation and data-providing services. The technical framework is composed of several key components:

1. BiImage.IO Colab: This tool is the central tool for data providers to manage their annotation sessions. It features a sidebar with navigation options and a simple intuitive layout that guides users through the process of mounting a local folder, deploying an annotation session, and sharing the annotation URL. The interface runs in the browser, using Pyodide to execute Python code for managing the session deployment and data

flow. This ensures that the entire process is accessible and easy to manage without requiring any local installations. The source code is available at <https://github.com/bioimage-io/bioimageio-colab/>.

2. Hypha & BioEngine Integration: The microSAM model is deployed as a BioEngine application within the Kubernetes cluster. Built on top of Hypha, the BioEngine uses Remote Procedure Calls to enable real-time communication between different clients in the collaborative annotation, including the BioImage.IO Colab web client, the Kaibu interface and the computational backend, which runs microSAM. This framework ensures that all operations are performed securely and efficiently in real-time. BioEngine is available at: <https://github.com/bioimage-io/bioengine/>.

3. Kaibu Interface: The Kaibu web interface remains the primary tool for annotators to interact with images. It provides essential tools for precise segmentation, and the annotations are saved in real-time to the data provider's local storage. The integration with the Kubernetes cluster allows for real-time feedback, making the annotation process smooth and responsive. Kaibu source code is available at: <https://github.com/imjoy-team/kaibu>, and the tool itself is accessible from <https://kaibu.org>.

4. DL4MicEverywhere: DL4MicEverywhere is integrated into the workflow to support the fine-tuning of AI models using the collected annotations. After an annotation session, users can leverage DL4MicEverywhere to refine existing models or train new ones using the annotated data. A sample notebook is provided to fine-tune a CellPose model with the collected annotations. The notebook can be configured by downloading the provided configuration file. Users can then open DL4MicEverywhere, select the advanced options, and specify the local path to the downloaded config YAML file. This approach ensures reproducibility and easy deployment through containerization. The configuration file is available at:

<https://github.com/bioimage-io/bioimageio-colab/blob/main/notebooks/config.yaml>

2.4 AI Models and human-in-the-loop

The integration of the microSAM model with the human-in-the-loop system showcases the application of AI to enhance image annotation workflows. The model provides initial segmentation results that can be refined through human input, combining the speed and efficiency of AI with the accuracy and expertise of human annotators. This iterative process, where annotated data is used to fine-tune the AI models, leads to continuous improvements in model performance and accuracy.



The system has a user-friendly design, where data providers can manage their sessions entirely through a web interface and annotators only need a browser to participate. This eliminates technical barriers and enhances accessibility. The transition to Kubernetes and the deployment as a BioEngine application ensures scalability and robustness, making this system well-suited for large-scale image annotation projects. Taken together, the design reflects AI4Life's commitment to democratise access to advanced AI tools in bioimage analysis.

3. Conclusion

Deliverable 4.3 marks a significant advancement in the AI4Life project by integrating AI models within a scalable, user-friendly framework for collaborative image annotation. The development and deployment of the human-in-the-loop system, powered by microSAM as a BioEngine application on a Kubernetes cluster, showcases a new era in bioimage analysis. This system combines AI efficiency with human expertise, enabling the rapid creation of high-quality annotation dataset directly from a web browser. This setup significantly enhances the speed and accuracy of the annotation process.

The transition to a Kubernetes-based infrastructure was crucial for addressing scalability and performance challenges, particularly during high-demand scenarios. The system dynamically allocates resources to maintain responsiveness and efficiency, even under heavy workloads, supporting AI4Life's mission to democratise bioimage analysis.

Looking ahead, the annotations generated by this system will contribute to refining and training more powerful AI models within the BioImage Model Zoo. The real-time collaboration enabled by the Hypha platform fosters greater community engagement, accelerating scientific discovery and promoting collective contributions. This work underscores AI4Life's commitment to creating a FAIR and accessible ecosystem for AI-driven bioimage analysis, paving the way for future innovations and ensuring broad accessibility to cutting-edge tools.

