Biolmage.IO Chatbot: A Personalized Assistant for Biolmage Analysis Augmented by Community Knowledge Base

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Abstract

The rapidly expanding landscape of bioimage analysis tools presents a navigational challenge for both experts and newcomers. Traditional search methods often fall short in assisting users in this complex environment. To address this, we introduce the BioImage.IO Chatbot, an Al-driven conversational assistant tailored for the bioimage community. Built upon large language models, this chatbot provides personalized, context-aware answers by aggregating and interpreting information from diverse databases, tool-specific documentation, and structured data sources. Enhanced by a community-contributed knowledge base and fine-tuned retrieval methods, the BioImage.IO Chatbot offers not just a personalized interaction but also a knowledge-enriched, context-aware experience. It fundamentally transforms the way biologists, bioimage analysts, and developers navigate and utilize advanced bioimage analysis tools, setting a new standard for community-driven, accessible scientific research.

Main

The exponential growth in bioimage data volume and diversity presents both a challenge and an opportunity for researchers¹. While the community has responded by developing an impressive array of bioimage analysis tools, software libraries, and workflows, these resources have proliferated to a point where they can overwhelm users. From standalone desktop tools like ImageJ², llastik³, and napari⁴ to plug-ins, pipelines, and specialized notebooks, the landscape of bioimage analysis is incredibly rich but equally complex. Traditional search engines like Google often fall short in helping users navigate this maze, especially when users may not even know the appropriate keywords to initiate their search. Moreover, the high variability in documentation styles and technical language barriers exacerbate the situation. For those less familiar with technical jargon, navigating the specialized documentation can be a significant challenge, making it more difficult to fully utilize advanced tools. On the flip side, developers face challenges in creating documentation that balances technical accuracy with accessibility, thereby inadvertently contributing to the confusion⁵. This lack of clear, easily understandable documentation also impacts collaborative efforts among developers, who may end up reinventing the wheel due to difficulty in locating or understanding existing solutions.

In parallel, AI-driven conversational agents, notably GPT-based models⁶ like ChatGPT, have gained traction as transformative technologies across multiple sectors. Recent advancements, such as reinforcement learning from human feedback (RLHF)⁷ and the introduction of GPT-4⁸, have further enhanced their capabilities. These models have streamlined tasks in areas ranging from education and customer service to e-commerce, democratizing access to information and specialized services. Applied to various domains like language learning, event planning, and technical support, such intelligent systems are democratizing complex processes, making them more accessible and manageable for a diverse range of users. Moreover, emerging studies have proposed a vision for using chatbots in tasks as specialized as smart microscopy⁹. Additionally, there are ongoing efforts to perform image analysis tasks using the code generation capabilities of GPT models¹⁰, further showcasing the growing versatility and applicability of these technologies in bioimage analysis.

Building on existing visions and preliminary efforts in the field, we introduce the BioImage.IO Chatbot as a comprehensive solution to the challenges facing biologists, bioimage analysts, and developers. This specialized conversational assistant is engineered to serve the diverse needs of the bioimage community, bridging gaps in knowledge and accessibility. This chatbot leverages the power of large language models (LLMs) to provide personalized answers and is enhanced by a dynamic, community-driven knowledge base (**Fig. 1a**). Our system aggregates information from various existing databases like ELIXIR bio.tools (https://bio.tools) and the ImageJ Wiki (https://imagej.net), tool-specific documentation such as deepImageJ¹¹, ilastik³ and ImJoy¹², as well as structured databases like the repository of the BioImage Model Zoo¹³. Importantly, the knowledge base is open for community contributions, making it a continuously expanding resource. Unlike traditional search engines, our context-aware chatbot understands conversational flow and can refine vague queries through clarifying questions, offering more nuanced and accurate information retrieval than existing tools. Additionally, the chatbot is

designed to be personalized; it can use user profiles to tailor responses according to the user's specific background. This way, the BioImage.IO Chatbot serves as a highly accessible and customized guide, assisting users in seamlessly navigating the complex landscape of bioimage analysis tools and documentation.

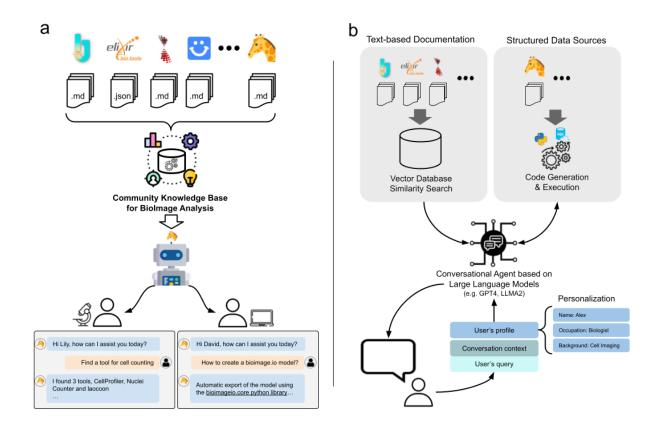


Figure 1. Architecture and Functionality of the BioImage.IO Chatbot for Bioimage Analysis

a) The Biolmage.IO Chatbot integrates text documentation and structured data from diverse sources into a community knowledge base. This enriched knowledge base augments the Large Language Model (LLM) based conversational agent. The chatbot serves both non-expert users looking for suitable bioimage analysis tools and developers seeking technical guidance. b) Operating as a conversational agent built on top of LLM, the chatbot functions within a schema-based agent framework designed for efficient information retrieval. It employs two primary methods to find the information you need: For text-rich databases (e.g. markdown or pdf files), the chatbot utilizes vector databases and conducts similarity searches in a language-embedded space; And for databases with structured data (e.g. csv file or SQL database), it leverages code generation features to, for example, automatically create Python scripts for API calls or data manipulations. When the chatbot receives a user query—which includes the user's profile, past interactions, and current question—it may seek additional clarification, provide a direct response, or use database or code-driven methods to fetch the required information. The responses are then summarized and conveyed in terms suited to the user's expertise level and background.

Our system is designed to be a versatile solution for information retrieval, leveraging the power of advanced large language models like GPT-4. Utilizing two complementary retrieval methods, our chatbot adeptly addresses a variety of user queries-from straightforward text-based questions to complex data retrieval operations (See Fig. 1b). To enable this versatility, we employ the function call capabilities of specialized, fine-tuned GPT models to craft structured inputs and outputs within a data schema-based framework. This unique feature streamlines the information retrieval process while minimizing noise. Our first retrieval method relies on a text-based search from an extensive knowledge base, which consolidates resources from bio.tools, imagej.net, ImJoy, DeepImageJ, and BioImage.io. This database is organized using an augmented vector database implemented with Faiss for rapid and precise text retrieval. The second approach is optimized for structured data sources, leveraging the chatbot's code-generation capabilities to create Python scripts for tasks like API calls or processing structured data objects. User profiles enrich both retrieval methods, fostering a highly personalized and context-aware user experience. When a user does not explicitly specify a retrieval channel, the system intelligently defaults to the most appropriate method. This ensures not only accurate but also individually tailored responses. Our chatbot aims to serve a wide audience—be it biologists, developers, or researchers—by making complex and varied information sources accessible and user-friendly. We provide more details about the implementation and example conversations in our Github repository.

While our approach incorporates robust measures to mitigate issues like hallucinations and noise, it's crucial to acknowledge the inherent limitations and ethical considerations of large language models like GPT-4. Even with precautions such as a schema-based approach, conversational chat history, and user profiles, the chatbot may produce inaccurate or biased responses. Users should exercise critical thinking and seek verification from trusted sources. We remain committed to continuous improvements to address these challenges, emphasizing the need for user vigilance.

Looking ahead, we aspire to democratize access to a plethora of scientific information and tools, not only through conversational assistance but also through intelligent code generation for smart microscopy control and autonomous bioimage analysis. We envision a future where the BioImage.IO Chatbot can be intricately customized, seamlessly integrating into specific scientific workflows, projects, or websites. This will empower a diverse and growing community of researchers, developers, and scientists. As we stand on the cusp of an era of fully automated AI systems in scientific research and data analysis, our chatbot serves as a critical bridge, synergizing human intelligence with AI capabilities to lay the groundwork for unprecedented advances in life sciences.

Code availability

The source code for the BioImage.IO Chatbot is available at <u>https://github.com/bioimage-io/bioimageio-chatbot</u>.

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Author contributions

Conceptualization was led by WO, with supporting code and design contributions from WL and CFB, as well as input from AMB. The development and implementation of the BioImage.IO Chatbot were carried out by WL and WO. CFB organized the documentation, while the manuscript was organized and written by CFB, WL, AMB, and WO. Funding and project administration were managed by AMB and WO.

Competing interest

WO is a co-founder of Amun AI AB, a commercial company that builds, delivers, supports and integrates AI-powered data management systems for academic, biotech and pharmaceutical industries.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Li, X., Zhang, Y., Wu, J. & Dai, Q. Challenges and opportunities in bioimage analysis. *Nat. Methods* 20, 958–961 (2023).
- 2. Schneider, C. A., Rasband, W. S. & Eliceiri, K. W. NIH Image to ImageJ: 25 years of image analysis.

Nat. Methods 9, 671–675 (2012).

- Berg, S. *et al.* Ilastik: Interactive machine learning for (bio)image analysis. *Nat. Methods* 16, 1226–1232 (2019).
- Ahlers, J. et al. napari: a multi-dimensional image viewer for Python. (2023). doi:10.5281/zenodo.7276432.
- 5. Levet, F. *et al.* Developing open-source software for bioimage analysis: opportunities and challenges. *F1000Res.* **10**, 302 (2021).
- 6. Brown, T. B. et al. Language Models are Few-Shot Learners. arXiv [cs.CL] (2020).
- Ouyang, L. *et al.* Training language models to follow instructions with human feedback. *arXiv* [*cs.CL*] (2022).
- 8. OpenAI. GPT-4 Technical Report. *arXiv* [cs.CL] (2023).
- Carpenter, A. E., Cimini, B. A. & Eliceiri, K. W. Smart microscopes of the future. *Nat. Methods* 20, 962–964 (2023).
- Royer, L. A. Omega Harnessing the Power of Large Language Models for Bioimage Analysis.
 (2023). doi:10.5281/zenodo.8240289.
- Gómez-de-Mariscal, E. *et al.* DeepImageJ: A user-friendly environment to run deep learning models in ImageJ. *Nat. Methods* 18, 1192–1195 (2021).
- 12. Ouyang, W., Mueller, F., Hjelmare, M., Lundberg, E. & Zimmer, C. ImJoy: an open-source computational platform for the deep learning era. *Nat. Methods* **16**, 1199–1200 (2019).
- 13. Ouyang, W. *et al.* BioImage Model Zoo: A Community-Driven Resource for Accessible Deep Learning in BioImage Analysis. *bioRxiv* 2022.06.07.495102 (2022) doi:10.1101/2022.06.07.495102.