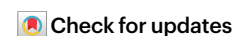


JDLL: a library to run deep learning models on Java bioimage informatics platforms



The advancements in artificial intelligence (AI) technology over the past decade have been a breakthrough in imaging for life sciences, paving the way for novel methods in image restoration¹, reconstruction² and segmentation³. However, the wide adoption of deep learning (DL) techniques by end users in bioimage analysis is hindered by the complexity of their deployment. These techniques stem from a variety of rapidly evolving frameworks (for example, TensorFlow 1 or 2, PyTorch) that come with distinct and often conflicting setups, which can discourage even proficient developers. This has led to integration difficulties or even absence in mainstream bioimage informatics platforms such as ImageJ, Icy and Fiji, many of which are primarily developed in Java.

We present JDLL (Java Deep Learning Library), a Java library that provides a comprehensive toolkit and application programming interface (API) for crafting advanced scientific applications and image analysis pipelines with DL capabilities. JDLL streamlines the installation, maintenance and execution of DL models across any major DL frameworks. JDLL is based on two main components (Fig. 1). The first, the DL-engine-installer, acts as a framework manager. It facilitates the download and integration of leading DL frameworks such as Tensorflow 1 and 2, PyTorch (from v1.4) and ONNX (from v1.3). It is capable of functioning with both CPU and GPU across a vast array of supported versions. Notably, DL-engine-installer automatically identifies the required engine and version from the model specifications, handling downloads or loads seamlessly for the end user. The second component, DL-model-runner, offers a Java API for performing inference on models built on the aforementioned DL frameworks. It can work around memory (CPU or GPU) limitations when processing large images, thanks to its tiling feature. Furthermore, it offers a user-friendly API for model loading or downloading, presenting comprehensible details about its training process and the underlying DL framework.

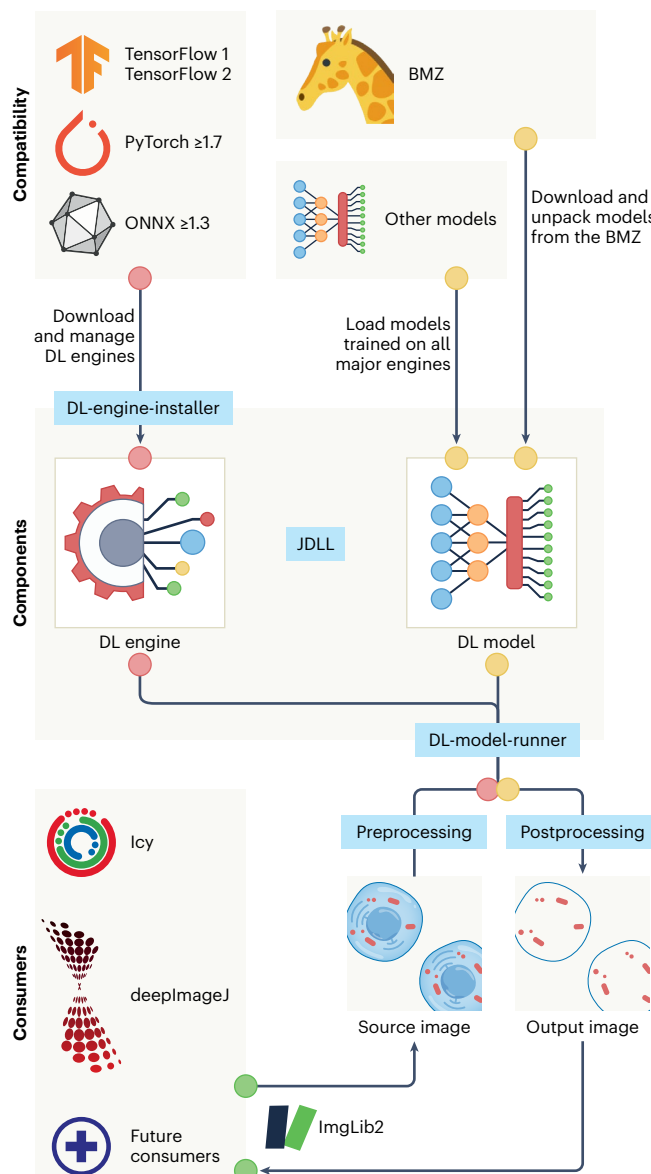


Fig. 1 | The JDLL architecture. JDLL is a Java API that can manage and load models created with a wide range of DL frameworks or engines (top). It can also download and deploy the models shared on the BMZ repository following BMZ conventions. These models are unpacked with JDLL, along with the engines required to run inference with the models, in a manner transparent to API consumers. JDLL provides to these consumers (such as Icy and deepImageJ, bottom) a simple and unified API to run inference on images via a custom ImgLib2 wrapper for their specific image data models. Because the API is generic and relies on an ImgLib2 component, JDLL can be used by any Java software platform, fostering the reproducibility of DL model deployment.

The flexibility and adaptability of these components are pivotal in facilitating the effortless installation and utilization of the full spectrum of DL models prevalent in the life sciences. JDLL is streamlined, carrying minimal dependencies – namely, *ImgLib2* (ref. 4) and specific libraries for processing JSON and YAML files, commonly used for DL model specifications. It is built to be compatible with existing and potential future DL frameworks, leveraging *ImgLib2* to create a framework-agnostic tensor implementation. Consequently, applications built on JDLL will not require engine-specific code. JDLL offers a universal, singular implementation compatible with all engines across their various versions. Its cutting-edge management of DL engines empowers it to operate multiple models within a single program, even if they were trained on normally incompatible DL engines. For example, JDLL can effortlessly sequence a style-transfer model operating on TensorFlow 2 with an instance segmentation model running on TensorFlow 1 within a single script.

The Bioimage Model Zoo (BMZ)⁵ represents a collaborative endeavor aimed at streamlining the utilization and sharing of DL models in life sciences, facilitating their download or retrieval and running inference easily. It provides specifications for the models and the engines they require to run, along with pre- and postprocessing steps. Several community partners in BMZ, such as *Icy*, *ImageJ/Fiji* (via *deepImageJ*), *ZeroCostDL4Mic* and *ImJoy*^{6–9}, already target end-user applications. JDLL aspires to serve as the common core component for DL across the Java-based platforms in this list, introducing distinctive features to support this integration. The BMZ specifications detail both pre- and postprocessing steps, and for true reproducibility, it is imperative that these steps yield consistent outputs across all platforms. Whereas the existing Java platforms rely on their own custom implementations, these processing steps are now addressed generically thanks to the universal tensor capabilities provided by JDLL and *ImgLib2*. As a result, platforms incorporating JDLL can depend on a shared code base for all processes tied to running a


DL model. This approach minimizes redundant coding efforts and ensures pixel-by-pixel reproducibility.

JDLL serves as a foundational library designed to support a growing community of developers in creating scientific tools for end users (such as bioimage analysts or biologists). Furthermore, its efficient and streamlined API reduces the complexities of executing a DL model to just a handful of code lines. This makes it compatible for use in analysis scripts (such as those in MATLAB, Fiji or Icy) or through connectors that integrate it with visual programming languages (we can foresee KNIME and Icy Protocols). This positions JDLL as an asset for the biological community. Thanks to its generality and versatility, JDLL offers the means to imbue scientific Java image analysis platforms with DL capabilities. Given the popularity of these platforms within the biological research community, JDLL stands poised to bolster the widespread adoption of DL in life sciences.


Code availability



The source code, documentation, tutorials and examples implementing JDLL can be found at <https://github.com/bioimage-io/JDLL>. JDLL is made available under the open-source Apache software license.


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Stéphane Dallongeville ^{1,2},


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Code concept and design were done by C.G.L.d.H., J.-Y.T., S.D. and J.-C.O.-M., with contributions from E.G.d.M., D.S., W.O. and A.M.-B. JDLL coding development and implementation was done by C.G.L.d.H., J.-Y.T., T.M. and S.D.; manuscript organizing and writing by C.G.L.d.H., J.-Y.T., A.M.-B. and J.-C.O.-M. with all authors contributing comments and revisions; funding and project administration by J.-Y.T. and J.-C.O.-M.

Competing interests

The authors declare no competing interests.

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