Reproducible user-friendly deep learning workflows for microscopy image analysis with deepImageJ

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Abstract

In the last decade, advances in Deep Learning (DL) methodologies have enormously contributed to improving the solution of several bioimage analysis tasks such as denoising, super-resolution, segmentation, detection, tracking, response prediction, or computer-aided diagnosis. These techniques support automatic image processing workflows and have demonstrated the potential to surpass human-level performance in common tasks[1]. Consequently, they profoundly impact how life-science researchers conduct their bioimage data analysis. However, integrating this breakthrough technology into research pipelines remains a challenge for the scientific community. Training and evaluating DL models requires previous programming expertise and technical knowledge. Therefore, the transfer of this technology to the daily practice of life-sciences researchers remains a bottleneck[2]. Pioneering works have recently targeted the very need to make DL solutions accessible through user-friendly software[3-8]. Moreover, the bioimage analysis community is increasingly interested in spreading general knowledge about DL and supporting its democratization[9-12].

Here, we present our latest contribution to this effort: deepImageJ[3], a user-friendly plugin of ImageJ/Fiji[13,14], to run trained DL models in one click. DeepImageJ is designed to deploy DL models regardless of their architecture or the task for which they were trained. It has been developed to import TensorFlow (Keras) and PyTorch models -the most extensively used DL environments by bioimage processing developers. This allows the integration of DL methodologies into complex analysis pipelines by connecting with any ImageJ/Fiji ecosystem method. Of note, the deepImageJ bundled model format is subject to the specifications defined in the BioImage Model Zoo (https://bioimage.io/), which seeks to define DL models in a standard manner, and hence, contribute to the democratization of DL in the bioimage analysis.

Most DL models trained for bioimage analysis cannot easily generalize to data acquired in different laboratories or under experimental conditions (e.g., image acquisition device, cell type, fluorochromes, media). Hence, (re-)training and fine-tuning will play a vital role in integrating DL in daily bioimage analysis routines. As deepImageJ operates with models that are already trained, its existing connection with ZeroCostDL4Mic4 is very relevant for its usability. Currently, this connection enables the (re-)training, fine-tuning, full assessment and deployment of models such as StarDist[5], 2D and 3D U-Net[15], and DeepSTORM[16]. Thanks to the ZeroCostDL4Mic - deepImageJ connection, researchers can train their models and get a fully documented model package ready to be shared and deployed in either Python or ImageJ. Importantly, deepImageJ reproduces the pre- and post-processing steps of the entire DL inference pipeline in ImageJ. Interestingly, both tools (deepImageJ, ZeroCostDL4Mic) give access to different DL workflows without any particular infrastructure besides a standard laptop.

DeepImageJ stands as a key solution for easily applying DL models to imaging data. Together with ZeroCostDL4Mic and the BioImage Model Zoo, it has the potential to make available some of the most powerful machine-learning algorithms to be applied in microscopy image processing.

References

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