Medical Image Analysis Laboratory (MIALab): An Educational Approach to Medical Image Analysis using Machine Learning

Fabian Balsiger*, Alain Jungo*, Yannick Suter*, and Mauricio Reyes

Institute for Surgical Technology and Biomechanics,
University of Bern, Bern, Switzerland
{fabian.balsiger,alain.jungo,yannick.suter}@istb.unibe.ch
http://www.istb.unibe.ch

Abstract. We present the medical image analysis laboratory (MIALab), an educational approach to medical image analysis using machine learning. MIALab introduces the students to traditional medical image analysis (MIA) pipelines by providing a fully working example on brain tissue segmentation. MIALab aims that students understand, analyze, and improve the whole MIA pipeline, comprising classical steps involved in medical image computing, such as pre-processing, registration, feature extraction, classification, and post-processing. Documentation, including pointers to data source, and source code are publicly available on GitHub.

Keywords: Education · Medical image analysis · Segmentation pipeline.

1 Introduction

The medical image computing and computer-assisted intervention (MICCAI) community has seen enormous progress in image classification, object detection, segmentation, registration, and other tasks during the last years. While this progress is heavily associated with deep learning technologies [3], traditional medical image analysis (MIA) pipeline steps like pre-processing, registration, and post-processing are still required to achieve state-of-the-art results (e.g., [2]). We believe that for students entering the MICCAI community, it is essential to know how such a traditional MIA pipeline works and looks like.

Our submission to the MICCAI educational challenge is termed MIALab (Medical Image Analysis Laboratory), which bases on a lecture at the University of Bern[1]. MIALab introduces the students to MIA by providing a fully working example on brain tissue segmentation aiming that students understand, analyze, and improve the whole MIA pipeline. Our submission includes documentation and source code, which are both publicly available on GitHub. The medical data can be downloaded from the human connectome project [4].

---

* equal contribution
[1] http://www.bme.master.unibe.ch/studies/curriculum/list_of_courses/
medical_image_analysis_lab/index_eng.html

2   Resources

The whole MIALab including documentation and source code is hosted on GitHub in a public repository

`https://github.com/istb-mia/MIALab`,

and the rendered documentation is available at

`https://mialab.readthedocs.io/en/latest/index.html`.

The repository and the rendered documentation are self-containing and we therefore only briefly introduce the content of it and refer the reader to the documentation.

2.1   Documentation

Problem Description As teaching example, the MIA pipeline investigates the problem of segmenting five different brain structures. The clinical background is explained under

`https://mialab.readthedocs.io/en/latest/background.html`.

The MIA pipeline itself is introduced in

`https://mialab.readthedocs.io/en/latest/pipeline.html`,

which does directly relate to experiments we propose such that the students can understand, analyze, and improve the MIA pipeline

`https://mialab.readthedocs.io/en/latest/experiments.html`.

Data and Setup The data itself, the data preparation, and data usage is described under

`http://mialab.readthedocs.io/en/latest/data.html`.

The installation steps proir to running the MIA pipeline are explained at

`http://mialab.readthedocs.io/en/latest/installation.html`.

Miscellaneous The documentation contains other helpful information such as a recommended integrated development environment and a list of recommended software tools (e.g., for viewing medical images).

2.2   Source Code

The source code is modularized and fully documented. MIALab is implemented using Python 3.5, which is now widely used for research due to deep learning libraries such as TensorFlow and PyTorch. It also introduces the student to commonly used Python packages such as scikit-learn and SimpleITK. Furthermore, it makes extensive use of the Python package for medical image analysis *pymia*[2] that is developed and maintained by the same authors as the MIALab.

In addition to the *main* script that contains the entire MIA pipeline including evaluation, the source code also contains a simple *hello world* that verifies the dependencies, and a *toy example* that represents an illustrative example of a random forest classification on sample data [1].

References

1. Criminisi, A., Shotton, J.: Decision Forests for Computer Vision and Medical Image Analysis. Springer London, London, 1 edn. (2013), `http://dl.acm.org/citation.cfm?id=2462584`
2. Kamnitsas, K., Ledig, C., Newcombe, V.F.J., Simpson, J.P., Kane, A.D., Menon, D.K., Rueckert, D., Glocker, B.: Efficient multi-scale 3D CNN with fully connected CRF for accurate brain lesion segmentation. Medical Image Analysis **36**, 61–78 (2017). https://doi.org/10.1016/J.MEDIA.2016.10.004, `http://www.sciencedirect.com/science/article/pii/S1361841516301839`
3. Litjens, G., Kooi, T., Bejnordi, B.E., Setio, A.A.A., Ciompi, F., Ghafoorian, M., van der Laak, J.A., van Ginneken, B., Sánchez, C.I.: A survey on deep learning in medical image analysis. Medical Image Analysis **42**, 60–88 (dec 2017). https://doi.org/10.1016/j.media.2017.07.005
4. Van Essen, D.C., Smith, S.M., Barch, D.M., Behrens, T.E., Yacoub, E., Ugurbil, K., WU-Minn HCP Consortium: The WU-Minn Human Connectome Project: An overview. NeuroImage **80**, 62–79 (oct 2013). https://doi.org/10.1016/j.neuroimage.2013.05.041

---

[2] Python package: `https://pypi.org/project/pymia/`
   Source code: `https://github.com/rundherum/pymia/`