MIRP: A Python package for standardised radiomics

Alex Zwanenburg [1,2] **and Steffen Löck** [2,3,4]

1 National Center for Tumor Diseases Dresden (NCT/UCC), Germany: German Cancer Research Center (DKFZ), Heidelberg, Germany; Faculty of Medicine and University Hospital Carl Gustav Carus, TUD Dresden University of Technology, Dresden, Germany; Helmholtz-Zentrum Dresden-Rossendorf (HZDR), Dresden, Germany **2** OncoRay – National Center for Radiation Research in Oncology, Faculty of Medicine and University Hospital Carl Gustav Carus, TUD Dresden University of Technology, Helmholtz-Zentrum Dresden-Rossendorf, Dresden, Germany **3** German Cancer Consortium (DKTK), Partner Site Dresden, and German Cancer Research Center (DKFZ), Heidelberg, Germany **4** Department of Radiotherapy and Radiation Oncology, Faculty of Medicine and University Hospital Carl Gustav Carus, TUD Dresden University of Technology, Dresden, Germany

Summary

Medical imaging provides non-invasive anatomical and functional visualisation of the human body. It is used clinically for diagnostic, prognostic, treatment planning and other purposes. Many current uses of medical imaging involve qualitative or semi-quantitive assessment by experts. Radiomics seeks to automate analysis of medical imaging for clinical decision support. At its core, radiomics involves the extraction and machine learning-based analysis of quantitive features from medical images (Lambin et al., 2017). However, very few–if any–radiomics tools have been translated to the clinic (Huang et al., 2022). One of the essential prerequisites for translation is reproducibility and validation in external settings (O'Connor et al., 2017). This can be facilitated through the use of standardised radiomics software. Here we present `mirp`, a Python package for standardised processing of medical imaging and computation of quantitative features. Researchers can use `mirp` for their own radiomics analyses or to reproduce and validate radiomics analyses of others.

Statement of need

Lack of standardised radiomics software is one of the reasons for poor translation of radiomics tools to the clinic. The Image Biomarker Standardisation Initiative (IBSI) created two reference standards for radiomics software: firstly, a reference standard for basic image processing and feature extraction steps (Zwanenburg et al., 2020); and secondly a reference standard for image filters (Whybra et al., 2024). There is currently a lack of fully IBSI-compliant radiomics packages in Python, which is important for the radiomics field because Python is used to interface with machine learning and deep learning packages such as `scikit-learn` and `pytorch`. `mirp` is intended to fill this gap. It provides a user-friendly API for standardised image processing for deep learning-based radiomics as well as standardised image processing and feature extraction for machine learning-based radiomics.

`mirp` is intended to be used by researchers in the radiomics field to perform their own radiomics analyses on the one hand, and to externally reproduce and validate results of other researchers. It was originally created in 2016 and regularly updated to conform with the IBSI reference standards and to improve usability. Previous versions of `mirp` were used by e.g. Leger et al. (2017), Zwanenburg et al. (2019), Shahzadi et al. (2022) and Bettinelli et al. (2022). Recently, `mirp` was used as a radiomics engine for the RadTract Python package (Neher et al., 2024). Updates in the recent major release series provide major improvements in user experience with a unified API, better documentation, and easier installation using `pip`.

`mirp` follows an end-to-end design principle and abstracts away intermediate steps for the user. In this sense it is not a toolkit such as `scikit-image` or `opencv`, that offer a set of functions for performing different operations on images. Because of the end-to-end design, relatively few functions are exposed to the user:

- `mirp.deep_learning_preprocessing`: For reading and processing images as input for deep learning networks.
- `mirp.extract_features`: For reading and processing images, and computing radiomics features as input for machine learning algorithms.
- `mirp.extract_images`: For reading and processing images and exporting them.
- `mirp.extract_features_and_images`: For reading and processing images, computing radiomics features and simultaneous export of both processed images and quantitative features computed from them.
- `mirp.extract_image_parameters`: For reading images and extracting their relevant metadata.
- `mirp.extract_mask_labels`: For reading masks and extracting their labels.

Of the above, `mirp.deep_learning_preprocessing`, `mirp.extract_features`, `mirp.extract_images` and `mirp.extract_features_and_images` allow for parallel processing using the `ray` package. These functions also have generator-based variants that yield output one-by-one.

`mirp` supports standard medical imaging formats as input, notably DICOM, NIfTI and NRRD. It also supports `numpy` arrays as a generic fallback option, and has specific routines for handling computed tomography (CT), positron emission tomography (PET), magnetic resonance imaging (MRI) and radiotherapy dose maps. It supports both radiotherapy structure sets (RTSTRUCT) and segmentation (SEG) files as DICOM-based masks.

In conclusion, `mirp` offers a much-needed solution for standardised radiomics. With its user-friendly Python interface, researchers can conduct radiomics analyses and, crucially, reproduce and validate the work of others, bringing us one step closer to harnessing the full potential of medical imaging in improving patient care.

Alternatives

`mirp` is not the only package available for image processing and feature extraction for radiomics analyses. Commonly used alternatives are listed in Table 1.

	mirp	pyradiomics	CERR	LIFEx	radiomics
Version	2.2.4	3.1.0	unknown	7.6.0	unknown
Last updated	6/2024	5/2023	2/2024	4/2024	11/2019
License	EUPL-1.2	BSD-3	LGPL-2.1	custom	GPL-3.0
Programming language	Python	Python	MATLAB	Java	MATLAB
IBSI-1 compliant	yes	partial	yes	yes	no claim

	mirp	pyradiomics	CERR	LIFEx	radiomics
IBSI-2 compliant	yes	no claim	yes	yes	no claim
Interface	high-level API	high-level API, Docker	GUI, high-level API	GUI, low-level API	low-level API
Website	[GitHub](#)	[GitHub](#)	[GitHub](#)	[website](#)	[GitHub](#)
Publication		(Griethuysen et al., 2017)	(Apte et al., 2018)	(Nioche et al., 2018)	(Vallières et al., 2015, 2017; Zhou et al., 2017)

Table 1: Comparison of `mirp` with other popular alternatives. Note that compliance with the first and second set of reference standards of the Image Biomarker Standardisation Initiative (IBSI-1 and IBSI-2, respectively) is based on claims of the developers, and not verified by the authors. API: application programming interface; GUI: graphical user interface.

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