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AI AND DEEP LEARNING

Integrating Radiomic Image Analysis in the Hero Imaging Platform

Keywords:
Radiomics, medical imaging, computer vision, visual programming, artificial intelligence.

We present the integration of radiomic image analysis in the Hero Imaging platform. We created a SPAARC node on Hero Imaging Platform, which facilitates access to SPAARC's cutting-edge functionality with the visual programming simplicity of the Hero Imaging platform. Subsequently, we validated the reliability of the $\text{SPAARC}_{\text{Hero}}$ using the IBSI validation dataset of multimodal imaging (CT, F18-FDG -PET, and T1w MRI) comprising 51 patients with soft-tissue sarcoma. This validation involved evaluation of the ICC of $\text{SPAARC}_{\text{Hero}}$ and two other IBSI compliant software, MIRP and $\text{SPAARC}_{\text{MATLAB}}$ using IBSI 2 phase 3 configuration and Test cases. Out of the 486 extracted features, 462 were found to be reproducible across the three software, with lower bounds of 95% confidence intervals (CIs) of ICCs greater than 0.75. Our results verify the compliance of SPAARCHero with IBSI standard for Radiomics feature extraction.

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P. Oyibo, P. Brynolfsson, and E. Spezi, 'Integrating Radiomic Image Analysis in the Hero Imaging Platform', *Proceedings of the Cardiff University School of Engineering Research Conference 2024*, Cardiff, UK, 2024, pp. 23-27.

doi.org/10.18573/conf3.g

INTRODUCTION

Typical user interactions in medical image processing often involve utilizing command-line inputs or scripting within text editors [1]. While expert engineers and computer scientists may find it straightforward to leverage text-based coding to develop complex algorithms from a series of basic image processing steps, non-experts and clinicians may find this difficult. This challenge is evident in the field of radiomics, a rapidly growing area of research focused on extracting quantitative metrics from medical images, known as radiomic features. These features include characteristics such as tissue and lesion heterogeneity and shape. They show potential for aiding clinical diagnosis or prognosis, either on their own or when combined with demographic, histologic, genomic, or proteomic data. [2]. Despite their potential in quantifying medical imaging characteristics, the requirement of image processing knowledge as well as the absence of standardized definitions and validated reference values has hindered their clinical utility.

Recently, a collaboration involving twenty-five research teams contributed to a significant joint effort known as the Image Biomarker Standardization Initiative (IBSI). This initiative aimed to address critical challenges within the field of radiomics, particularly focusing on the reproducibility and reliability of common radiomic features. In its initial effort, the IBSI standardized procedures for computing a comprehensive set of 169 radiomics features, facilitating the validation and calibration of various radiomics software tools [3]. Subsequently, the IBSI further defined and standardized eight convolutional filter types intended to enhance specific structures and patterns in medical imaging. This standardization supported reproducible radiomics analyses, thereby improving consistency and reliability for more robust clinical insights [4]. The outcomes of the IBSI have significantly influenced the development of various radiomics frameworks, including LIFEx [5], Pyradiomics [6], Medical Image Radiomics Processor (MIRP) [7] and SPAARC [8].

SPAARC[1] stands for Spaarc Pipeline for Automated Analysis and Radiomics Computing. SPAARC is a rigorously tested package designed for reproducible extraction of radiomic features from both 2D and 3D image arrays [9, 10]. For radiomic features to be beneficial, they must be applied clinically, requiring an adequate level of visualization and interaction. Consequently, a substantial advancement in medical image analysis is expected if these algorithms can be smoothly integrated into clinical environments, with reasonable effort dedicated to validating their relevance, thereby ultimately enhancing healthcare.

In this work, we present and validate the integration of radiomic image analysis in the Hero Imaging Platform by developing a SPAARC node (SPAARC$_{Hero}$) which allows an easy combination of the IBSI compliant radiomic feature extraction algorithms with visualizations created by the Hero Imaging platform to facilitate ease-of-use in both clinical and research settings without the requirement of computer programming knowledge.

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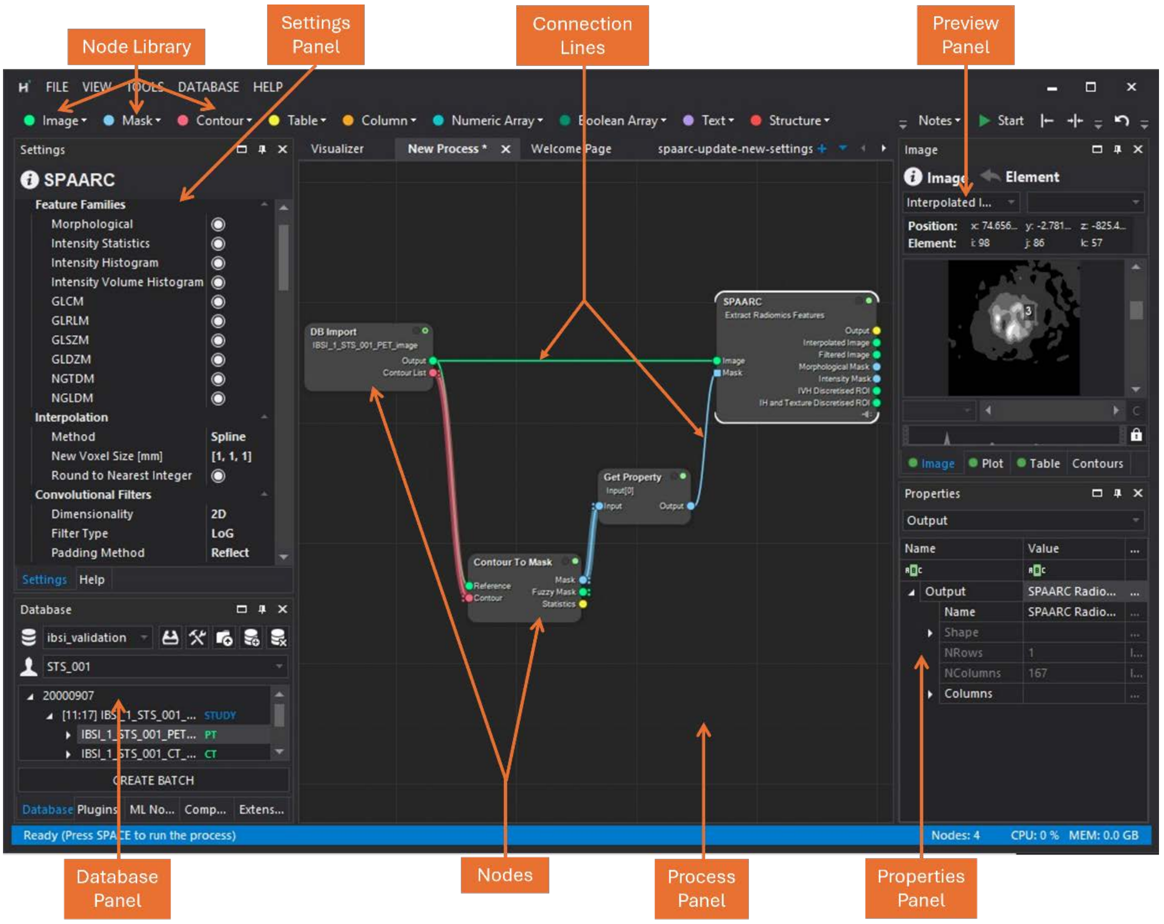
[1] https://spaarc-radiomics.io



Settings

SPAARC

Feature Families
Morphological ○
Intensity Statistics ○
Intensity Histogram ○
Intensity Volume Histogram ○
GLCM ○
GLRLM ○
GLSZM ○
GLDZM ○
NGTDM ○
NGLDM ○

Interpolation
Method **Spline**
New Voxel Size [mm] **[1, 1, 1]**
Round to Nearest Integer ○

Convolutional Filters
Dimensionality **2D**
Filter Type **LoG**
Padding Method **Reflect**

Database
ibsi_validation
STS_001
20000907
[11:17] IBSI_1_STS_001_... STUDY
IBSI_1_STS_001_PET... PT
IBSI_1_STS_001_CT_... CT
CREATE BATCH

Position: x: 74.656... y: -2.781... z: -825.4...
Element: i: 98 j: 86 k: 57

Properties
Output

Name	Value
Output	SPAARC Radio...
Name	SPAARC Radio...
Shape	
NRows	1
NColumns	167
Columns	

Ready (Press SPACE to run the process)
Nodes: 4 CPU: 0 % MEM: 0.0 GB

Fig. 1. Hero Imaging Workspace highlighting the 5 Primary panels; the Database, Process, Settings, Preview, and Properties panels. The Process panel also contains a sample radiomics workflow with Nodes and Connection Lines.

MATERIALS AND METHODS

Hero Imaging Platform

Hero Imaging platform offers an intuitive visual programming interface which simplifies advanced medical imaging workflows. The Hero Imaging workspace (shown in Fig. 1) comprises five primary panels: the Database, Process, Settings, Preview, and Properties panels. Within the Database panel, medical image databases in DICOM or NIfTI file formats are stored and retrieved. These databases are organized by patients and studies, which enables support for batch processing. Scans can be imported from the database panel into the process panel as nodes through a simple drag-and-drop interface. Additional nodes can be incorporated into the process panel from the node library or by utilizing right-click functionality within the process window. The settings panel allows for the adjustment of parameters associated with a selected node, while the preview panel facilitates the visualization of outputs, including images, plots, tables, or contours generated by the selected node. Furthermore, the properties panel provides detailed information regarding the output produced by any selected node.

Node input and output connections are color-coded for clarity: green, blue, red, and yellow signify that a node of type image, mask, contour, and table, respectively, can be connected. A white colour indicates that multiple node types can be connected. The shapes of the connections also convey information: circles represent mandatory inputs, while squares denote optional ones. Two small dots signify that a list can be connected, and outlines indicate that multiple inputs can be connected. Nodes are connected by dragging from the output of one node to the input of another and can be disconnected by double-clicking on the connection lines. Moreover, each node features a status button located in the top right corner, providing information about the node's execution when hovered upon. A green status button indicates a successful execution, while yellow denotes an encountered error during execution. A red status button signifies that the node cannot be executed.

Hero Imaging SPAARC Node

SPAARC is a multiplatform software that incorporates a comprehensive set of 165 standardized radiomic features and 7 convolutional filters, adhering to the guidelines established by the IBSI [3, 4]. SPAARC offers implementations in both MATLAB[2] (The Mathworks, Natick, USA) and Python[3] programming environment. However, SPAARC$_{\text{Hero}}$ is specifically developed in Python, as Hero Imaging platform provides robust support for creating custom nodes to execute Python libraries, with full debugging capabilities.

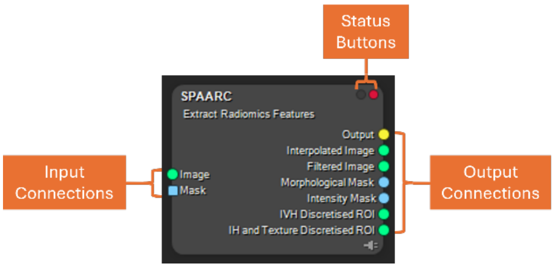


Fig. 2. SPAARC$_{\text{Hero}}$ node highlighting the input connections, output connections and status button.

As shown in Fig. 2 the SPAARC$_{\text{Hero}}$ node consists of 2 inputs and a max of 7 output connections. It accepts, as input, a medical image and a binary annotation mask from Hero nodes of type image and mask, respectively. The SPAARC$_{\text{Hero}}$ node returns the computed radiomic features as Hero connection type table. The interpolated image, filtered image, and discretized region of interest images are returned as Hero connection type image. While morphological and intensity masks are returned as Hero connection type mask.

Configuration of SPAARC$_{\text{Hero}}$ follows the IBSI configuration standard and can be adjusted in the settings panel, which is divided into sub-menus described as follows:

- Feature Families: settings for selecting families of radiomic features to extract.
- Convolutional Filtering: settings for specifying the type of convolutional filtering to apply.
- Interpolation: settings for translating image intensities from the original image grid to an interpolation grid.
- Convolutional filters: settings for configuring the properties of the IBSI-standardized convolutional filters.
- Re-segmentation: settings for defining exclusion criteria for voxels from a previously segmented ROI.
- Discretization: settings for quantizing image intensities within the ROI.
- Texture Analysis: settings for texture-based feature families.

The IBSI manuals include full detailed description of the configuration settings and functions within the Radiomic feature extraction pipeline to which SPAARC adhere [11, 12].

IBSI Validation Dataset and Configuration

To validate the developed SPAARC$_{\text{Hero}}$, we employed the IBSI validation dataset [4]. This dataset comprises a group of 51 patients diagnosed with soft-tissue sarcoma who underwent multimodality imaging, including co-registered computerized tomography (CT), fluorine 18 fluorodeoxyglucose (F18-FDG) positron emission tomography (PET), and T1-weighted (T1w) magnetic resonance imaging (MRI) scans. Each image in the dataset was accompanied by a segmentation of the gross tumor volume, utilized as the region of interest (ROI). For each imaging modality, nine specific Test cases were defined for image processing and convolutional filters. More details about the test cases and configurations can be found in the Benchmarking Phase 3: validation section of the IBSI 2 manual [11].

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[2] https://www.mathworks.com

[3] https://www.python.org

RESULTS

An illustrative radiomic analysis workflow with SPAARC$_{\text{Hero}}$ is depicted in the process panel of Fig. 1. A total of 486 features were extracted, comprising 18 features extracted through 9 different configurations, across 3 image modalities. These features were extracted using SPAARC$_{\text{Hero}}$ as well as two other IBSI-compliant frameworks: (a) the MATLAB version of SPAARC (SPAARC$_{\text{MATLAB}}$) and MIRP, and exported to comma separated values file format (CSV) for further statistical analysis. Figure 3, shows the intraclass correlation coefficient (ICC) estimates and their 95% confidence intervals. The ICC was calculated using the Pingouin statistical package[4] version 0.5.4, based on a single rater, absolute-agreement, two-way random-effects model. The reproducibility of each feature was categorized as follows [4]: poor (lower bound less than 0.50), moderate (between 0.50 and 0.75), good (between 0.75 and 0.90), and excellent (greater than 0.90). Among the 486 features, 462 (95.06%) demonstrated good to excellent reproducibility (ICC 95% CI lower bound, >0.75). Only twelve features (2.47% of 486) were poorly reproducible (ICC 95% CI lower bound, <0.50). These features were primarily associated with Laplacian of Gaussian and, separable and non-separable wavelet filters. Specifically, coefficient of variation and quartile coefficient of dispersion features represented the majority, accounting for 4 and 7 out of the 12 poorly reproducible features, respectively.

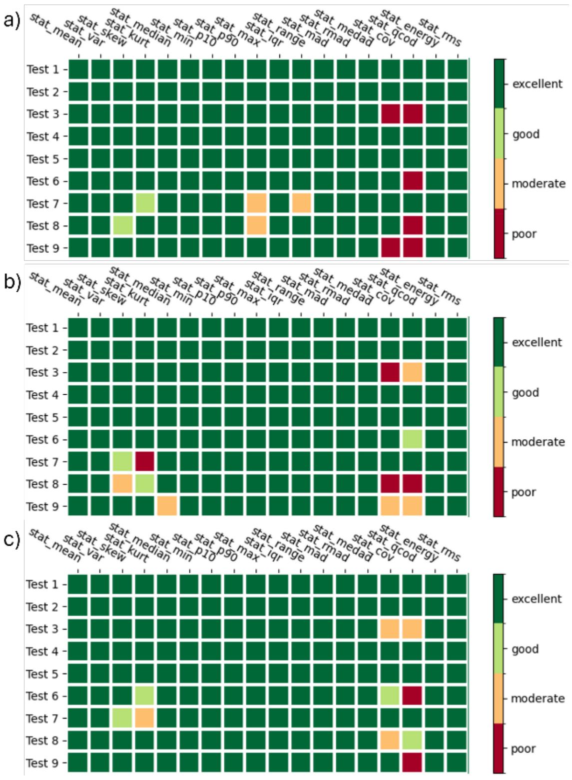

Fig. 3. Reproducibility of features extracted by SPAARC$_{\text{Hero}}$, SPAARC$_{\text{MATLAB}}$ and MIRP from the IBSI validation dataset a) CT, b) T1w MRI and C) F18-FDG PET.

DISCUSSION

The integration of IBSI-compliant radiomic image analysis in the Hero Imaging platform improves the usability of SPAARC for researchers and clinicians battling cancer. The findings from our validation experiment complement the reported IBSI validation results [4], where similar features were found to be poorly reproducible. SPAARC's adherence to IBSI's standardized methodological details mitigate discrepancies in extracted features, thus enhancing reproducibility in radiomics studies. Moving forward, we aim to assess SPAARC Hero for its potential in the diagnosis, prognosis, and monitoring of cancer and other diseases.

Acknowledgments

The integration of radiomic analysis in the Hero Imaging platform is funded by the Cardiff University Engineering and Physical Sciences Research Council (EPSRC) Impact Acceleration Account (IAA), programme code EP/X525522/1.

Conflicts of Interest

Patrik Brynolfsson, PhD is an employee of Hero Imaging and developer of the Hero Imaging platform.

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[4] https://pingouin-stats.org/

REFERENCES

[1] J. J. Birchman, S. L. Tanimoto, A. H. Rowberg, H.-S. C. M.d, and Y. Kim, ‘Applying a visual language for image processing as a graphical teaching tool in medical imaging’, in *Medical Imaging VI: Image Capture, Formatting, and Display*, SPIE, May 1992, pp. 379–390. doi.org/10.1117/12.59516

[2] M. E. Mayerhoefer et al., ‘Introduction to Radiomics’, *J. Nucl. Med.*, vol. 61, no. 4, pp. 488–495, Apr. 2020. doi.org/10.2967/jnumed.118.222893

[3] A. Zwanenburg *et al*., ‘The Image Biomarker Standardization Initiative: Standardized Quantitative Radiomics for High-Throughput Image-based Phenotyping’, *Radiology*, vol. 295, no. 2, pp. 328–338, May 2020.
doi.org/10.1148/radiol.2020191145

[4] P. Whybra *et al*., ‘The Image Biomarker Standardization Initiative: Standardized Convolutional Filters for Reproducible Radiomics and Enhanced Clinical Insights’, *Radiology*, vol. 310, no. 2, p. e231319, Feb. 2024.
doi.org/10.1148/radiol.231319

[5] C. Nioche *et al*., ‘LIFEx: A Freeware for Radiomic Feature Calculation in Multimodality Imaging to Accelerate Advances in the Characterization of Tumor Heterogeneity’, *Cancer Research*, vol. 78, no. 16, pp. 4786–4789, Aug. 2018.
doi.org/10.1158/0008-5472.CAN-18-0125

[6] J. J. M. Van Griethuysen *et al*., ‘Computational Radiomics System to Decode the Radiographic Phenotype’, *Cancer Research*, vol. 77, no. 21, pp. e104–e107, Nov. 2017.
doi.org/10.1158/0008-5472.CAN-17-0339.

[7] A. Zwanenburg *et al*., ‘Assessing robustness of radiomic features by image perturbation’, *Sci. Rep.*, vol. 9, no. 1, p. 614, Jan. 2019.
doi.org/10.1038/s41598-018-36938-4

[8] P. Whybra,'Standardisation and optimisation of radiomic techniques for the identification of robust imaging biomarkers in oncology', PhD Thesis, Cardiff University, 2021.

[9] P. Whybra, C. Parkinson, K. Foley, J. Staffurth, and E. Spezi, ‘Assessing radiomic feature robustness to interpolation in 18F-FDG PET imaging’, *Sci. Rep.*, vol. 9, no. 1, p. 9649, Jul. 2019.
doi.org/10.1038/s41598-019-46030-0

[10] C. Piazzese, K. Foley, P. Whybra, C. Hurt, T. Crosby, and E. Spezi, ‘Discovery of stable and prognostic CT-based radiomic features independent of contrast administration and dimensionality in oesophageal cancer’, *PLoS ONE*, vol. 14, no. 11, p. e0225550, Nov. 2019.
doi.org/10.1371/journal.pone.0225550

[11] A. Depeursinge *et al*., ‘Standardised convolutional filtering for radiomics’, Feb. 07, 2024, *arXiv*, 7 Feb. 2024. doi.org/10.48550/arXiv.2006.05470

[12] A. Zwanenburg, S. Leger, M. Vallières, and S. Löck, ‘Image biomarker standardisation initiative’, *Radiology*, vol. 295, no. 2, pp. 328–338, May 2020. doi.org/10.48550/arXiv.1612.07003

Cynhadledd Ymchwil
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Cardiff Engineering
Research Conference

E. Spezi and M. Bray (eds.) 2024. *Proceedings of the Cardiff University School of Engineering Research Conference 2024.*
Cardiff: Cardiff University Press.
doi.org/10.18573/conf3

Cardiff University School of Engineering Research Conference 2024 was held from 12 to 14 June 2024 at Cardiff University.

The work presented in these proceedings has been peer reviewed and approved by the conference organisers and associated scientific committee to ensure high academic standards have been met.

Cardiff University Press | Gwasg Prifysgol Caerdydd

First published 2024

Cardiff University Press
Cardiff University, Trevithick Library
First Floor, Trevithick Building, Newport Road
Cardiff CF24 3AA

cardiffuniversitypress.org

Editorial design and layout by
Academic Visual Communication

ISBN: 978-1-9116-5351-6 (PDF)