



Original software publication

MammogramAnnotationTool: Markup tool for breast tissue abnormality annotation

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ABSTRACT

In this work, we present an open-source MATLAB software tool for mammography image annotation. The tool has an easy-to-use graphical user interface enabling simultaneous visualization of both breasts. Annotations can be assigned to six categories for abnormal breast tissue: *malignant mass*, *benign mass*, *malignant calcification*, *benign calcification*, *malignant architectural distortion*, *benign architectural distortion*. Furthermore, characterization details, such as, morphology of the abnormality, can be assigned to each annotation. Optional examination-level breast density assessment can also be specified. This tool has been successfully applied as part of the data collection pipeline in already published deep learning-based segmentation and classification studies.

Code metadata

Current code version
Permanent link to code/repository used for this code version
Permanent link to Reproducible Capsule
Legal Code License
Code versioning system used
Software code languages, tools, and services used
Compilation requirements, operating environments & dependencies
Link to developer documentation/manual
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v1.3
<https://github.com/SoftwareImpacts/SIMPAC-2023-465>
MIT License
git
MATLAB (MathWorks, Natick, MA, United States)
MATLAB R2023a, Image Processing Toolbox
https://github.com/MIPT-Oulu/MammogramAnnotationTool_public/blob/Rev1.3.0/README.md
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1. Introduction

Breast cancer is the most common cancer among female population [1]. The survival rate for breast cancer is high when it is found in its early stages (e.g. [2]). Mammography is a widely used imaging modality for breast cancer screening to search for tumors in symptomless women for early detection of breast cancer.

Mammography images are typically evaluated by two experienced radiologists to find suspicious changes in breast tissue. Due to the complex and varying nature of the breast tissue (e.g., tissue superimposition), interpretation can be challenging. Radiographic appearance of a breast depends on amount of fat, stroma, and gland, where fat appears as radiolucent and the other two mentioned as radiopaque [3].

Radiographically, cancerous cases can be identified by inspecting a mass density, specific shape and border characteristics of mass, existence of microcalcifications and architectural distortions. In addition, asymmetries between the left and right breast in mammography images are assessed [4]. Changes in the breast tissue, in comparison to normal parenchymal patterns, can be subtle and small. These submillimeter-size changes encountered in mammography result in a demand for high resolution.

In a screening setting, images are commonly acquired from four *standard views*, i.e., right and left side both for craniocaudal (CC) and mediolateral oblique (MLO) views. The images are stored in Digital Imaging and Communications in Medicine (DICOM) format which is an international standard for medical images and related information (ISO

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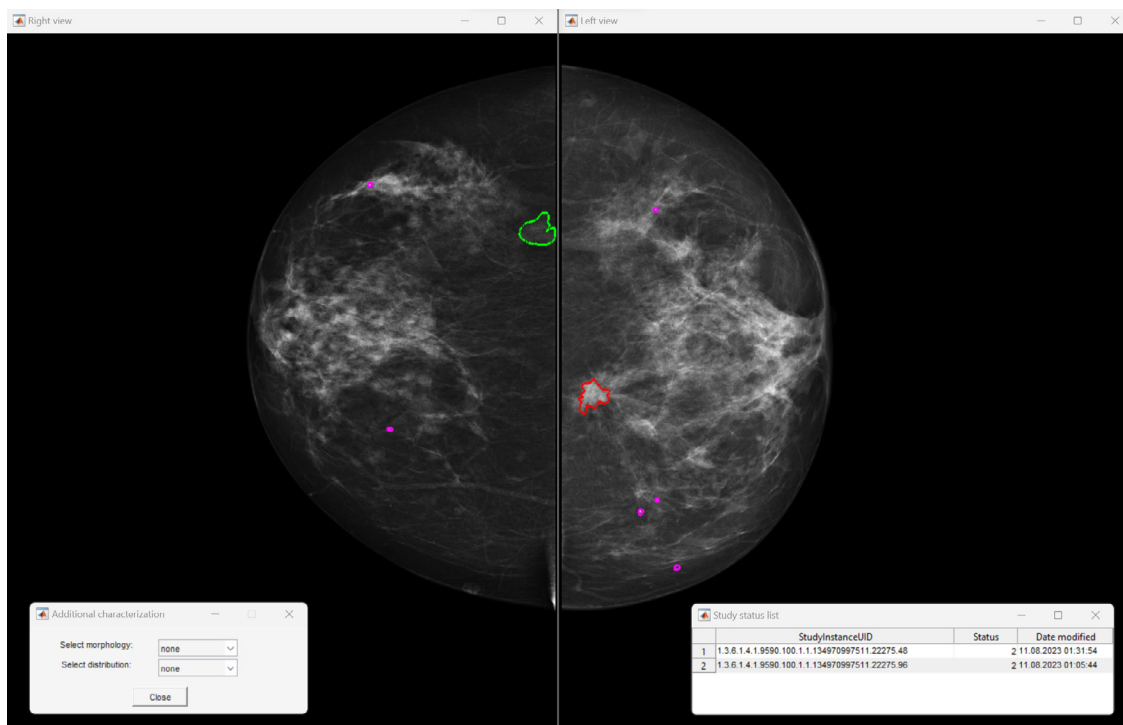


Fig. 1. Annotation tool graphical user interface (GUI) components. Right and left mammographic views are shown with markup for several abnormalities. Pop-up dialog for additional characterization can be seen on the bottom left side in the figure and the auxiliary study listing on the bottom right.

Source: Mammograms courtesy of Breast Research Group, INESC Porto, Portugal.

12052:2017). It comprises detailed information about image acquisition parameters, such as, imaging protocol, image processing, radiation dose, and imaging device and software version.

Several general-purpose software platforms and packages exist for processing medical images: 3D Slicer,² [5] Insight Toolkit,³ [6] Medical Imaging Interaction Toolkit,⁴ [7] and Fiji⁵ [8] to name a few. However, these software platforms and packages have also several features and functionalities which might not be relevant for the task at hand and would require customization. Therefore a dedicated software may be more preferable. There exists only a few dedicated software for mammography annotation [9,10]. For example, Zheng et al. have developed an online tool written in Java for annotating mammograms [9]. This tool was applied to provide an annotated case library for educational purposes. Dembrower et al. have implemented an in-house MATLAB-based annotation tool for mammography images as a part of their data collection of 1,182,733 screening examinations. However, it is not openly available [10].

Our current work describes a mammogram annotation tool to facilitate pixel-wise annotation of breast abnormalities observable via breast imaging. The MammogramAnnotationTool was designed and developed together with radiologists to be easy to use and so that it supports necessary image processing features. Furthermore, the tool enables structured outputs to ensure a common representation format for the defined reference standard. The tool is based on MATLAB (MathWorks, Natick, MA, United States), a commonly used environment for scientific computing with libraries also for the construction of user interfaces. The tool has been used as a part of a data collection pipeline in studies related to deep learning-based breast mass segmentation and screening mammography examination classification [11,12]. The experiments reported in these studies were performed in a supervised learning fashion, typically requiring accurately annotated examples verified by an experienced radiologist or a group of radiologists.

2. Software description

MammogramAnnotationTool provides means for reviewing and performing free-form markup for mammography screening examinations having the four standard views. Keyboard and mouse shortcuts for annotations, panning, zooming, windowing, and study selection are offered for user-friendly and efficient use. The user can switch between examinations with a couple of different ways, e.g., using arrow keys or via list of all examinations specified by a Comma-Separated Values (CSV) file which is requested in the data requirements (see https://github.com/MIPT-Oulu/MammogramAnnotationTool_public/blob/Rev1.3.0/README.md). In more detail, the main functionalities included in the software are:

- It enables viewing screening mammography examinations with exactly four standard views.
- It enables the user to input breast density assessment and stores the information as CSV files.
- It enables three groups of free-form pixel-wise contours to be drawn to annotate malignant and benign masses, malignant and benign calcifications, and malignant and benign architectural distortions with the possibility to assign additional characterizations based on Breast Imaging Reporting and Database System (BIRADS) [13].
- It automatically produces pixel-wise masks for each annotated view and the previously mentioned breast abnormalities and stores them as 8-bit Portable Network Graphics (PNG) files.
- It automatically produces view-wise image-level labels (see for example [12]) based on the pixel-wise annotation masks defined as binary labels indicating malignancy (labeled as 1) or the absence of it (labeled as 0) and benignity (labeled as 1) or the absence of it (labeled as 0), which are currently combined view-wise and stored as CSV files and specifically aimed at allowing the replication of the experiments reported by Wu et al. [14].
- It automatically creates a data structure (binary MATLAB MAT-file) to save progress containing all data related to examination

² <https://www.slicer.org/>

³ <https://itk.org/>

⁴ <https://www.mitk.org/>

⁵ <https://fiji.sc/>

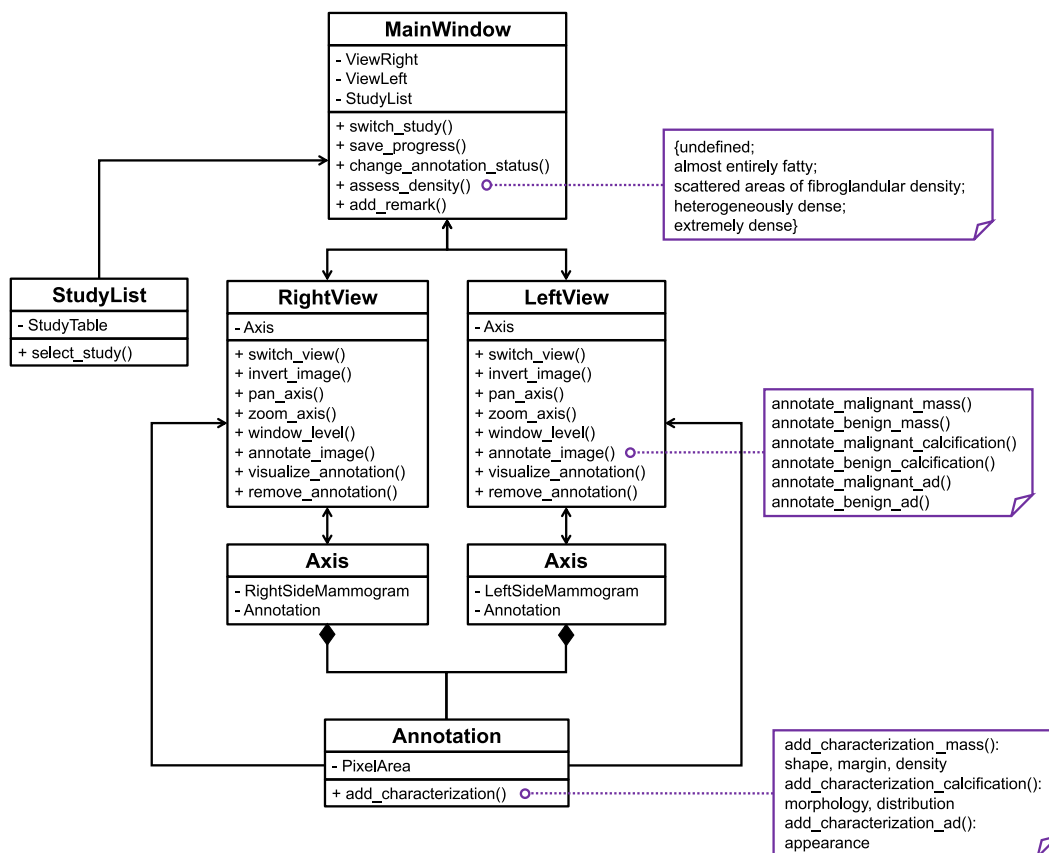


Fig. 2. Conceptual illustration of the annotation tool software components. Associations are represented by solid connectors with arrows. Filled diamond connector cap represents composition.

annotations, also the more intricate abnormality related binary labels.

The conceptual illustration of the main software components and their associations are presented in Fig. 2 in a form of a class diagram-like graphical notation.

As one particularly useful feature, our software provides a values of interest look up table (VOI LUT) conversion function for mammography data ported from Pydicom [15] to MATLAB script. To highlight, the VOI LUT conversion is an essential post-processing step for mammography images. It specifies a potentially non-linear conversion for the pixel values transforming them into meaningful values for viewing purposes, thus making the reading more efficient.

3. Impact

The developed annotation tool is specifically designed for screening mammography examination annotation with four standard views. An important requirement for a tool in this context is for it to be interactive. The software allows for markup of benign and malignant findings showing simultaneously right and left mammograms (Fig. 1), their detailed characterization, and potential removal. The GUI windows for the views can be placed based on user preferences, on two screens or side-by-side on one screen. The possibility for side-by-side viewing is very important, as radiologists often compare breast images to each other to detect discrepancies in the tissue structure.

So far, this annotation tool has been used in our studies related to deep learning-based mass segmentation and classification of mammography images [11,12]. In these studies, the tool has been utilized for approximately 3,000 malignant suspect examinations with 12,000 images of a Finnish screening mammography dataset, covering several mammography imaging device versions, namely Senograph Essential

and Senograph Essential DS, GE Healthcare, Chicago, Illinois, United States, with Standard Operating Procedure (SOP) Class Unique Identifier (UID) 1.2.840.10008.5.1.4.1.1.1.2. Additional testing has been conducted utilizing examinations from the Portuguese IN-breast dataset [16], and we expect that our software can be used for versatile data. The encountered dimensions for mammograms for presentation were 5928-by-4728, 4740-by-3540, 3062-by-2394, 2294-by-1914, 3328-by-2560 and 4084-by-3328.

The MammogramAnnotationTool development repository can be found on GitHub (https://github.com/MIPT-Oulu/MammogramAnnotationTool_public/). User contributions and development ideas are very welcome.

4. Limitations and future work

The software is currently limited to be used with mammography screening examinations with exactly four standard views, requiring the user to prepare their desired dataset for annotation according to this specification. No safety precautions have been taken, other than saving the progress up to the previously annotated examination, to account for situation where one or more of the expected views are missing. Another limitation concerns removing annotations. In case of overlapping annotations, all annotations sharing the specified coordinates will be removed.

In addition to producing annotated data prior to experimental phase, the tool could also be utilized in an active learning fashion (see for example [17]). Specifically, the tool could be included within a machine learning pipeline to facilitate answering interactive queries and provide labels to new data instances selected by the active learning algorithm. This could potentially reduce the annotation cost in terms of annotated examinations.

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CRediT authorship contribution statement

Antti Isosalo: Conceptualization, Methodology, Software, Resources, Writing – original draft, Visualization. **Satu I. Inkinen:** Conceptualization, Methodology, Software, Resources, Writing – original draft, Supervision, Project administration, Funding acquisition. **Helinä Heino:** Methodology, Software, Writing – review & editing. **Topi Turunen:** Conceptualization, Software, Writing – review & editing. **Miika T. Nieminen:** Conceptualization, Resources, Writing – review & editing, Supervision, Project administration, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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