

Convolutional Neural Networks with Template-Based Data Augmentation for Functional Lung Imaging Segmentation

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Rationale and Objectives: We propose an automated segmentation pipeline based on deep learning for ventilation-based quantification which improves on our previously reported methodology in terms of computational efficiency while maintaining accuracy and robustness. The large data requirements for the proposed framework is made possible by a novel template-based data augmentation strategy.

Materials and Methods: A novel deep learning approach based on convolutional neural network models (i.e., U-net) were generated using a custom multilabel Dice metric loss function and a novel template-based data augmentation strategy. Development and processing utilized *ANTsR-Net*—a growing open-source repository of well-known deep learning architectures first introduced here which interfaces with the Advanced Normalization Tools (ANTs) package and the R statistical project. Training (including template generation and data augmentation) employed XXX images. Evaluation was performed on the remaining YYY images through comparison with a previously reported automated segmentation algorithm based on Gaussian mixture modelling with Markov Random field (MRF) spatial priors.

Results:

Conclusions: The proposed deep learning framework yielded comparable results as the MRF-based algorithm. Such an approach reduces computational time without sacrificing accuracy.

Key Words: Advanced Normalization Tools, ANTsRNet, hyperpolarized gas imaging, neural networks, U-net

INTRODUCTION

Probing lung function under a variety of conditions and/or pathologies has been significantly facilitated by the use of hyperpolarized gas imaging and corresponding quantitative image analysis methodologies. Such developments have provided direction and opportunity for current and future research trends [1]. Computational techniques targeting these imaging technologies permit spatial quantification of localized ventilation with potential for increased reproducibility, resolution, and robustness over traditional spirometry and radiological readings [2, 3].

One of the most frequently used image-based biomarkers for the study of pulmonary development and disease is based on the quantification of regions of limited ventilation, also known as *ventilation defects* [4]. These features have been shown to be particularly salient in a clinical context. For example, ventilation defect volume to total lung volume ratio has been shown to outperform other image-based features in discriminating asthmatics vs. non-asthmatics [5]. Ventilation defects have also demonstrated discriminative capabilities in chronic obstructive pulmonary disease (COPD) [6]. These findings, along with related research, has motivated the development of multiple automated (and semi-automated) segmentation algorithms which have been proposed in the literature (e.g., [7–11]) and are currently used in a variety of clinical research investigations (e.g., [12]).

Despite the enormous methodological progress with existing quantification strategies, recent developments in machine learning (specifically “deep learning” [13]) have generated new possibilities for quantification with improved capabilities in terms of accuracy, robustness, and computational efficiency. The outgrowth of research, in conjunction with advances in computational hardware, has resulted in significant developments in various image research areas including classification, segmentation, and object localization and has led to co-optation by the medical imaging analysis community [14].

In this work, we develop and evaluate a convolutional neural network segmentation framework, based on the U-net architecture [15], for functional lung imaging using hyperpolarized gas. As part of this framework we include a deep learning analog to earlier work from our group targeting segmentation of proton lung MRI [16]. This is motivated by common use case scenarios in which proton images are used for quantifying corresponding ventilation images (i.e., masking regions of interest a

la [7–9]).

One of the practical constraints to adopting deep learning techniques is the large data requirements for the training process oftentimes necessitating ad hoc strategies for simulating additional data from available data—a process termed *data augmentation* [17]. While common approaches to data augmentation include the application of randomized simulated linear (e.g., translation, rotation and affine) or elastic transformations and intensity adjustments (e.g., brightness and contrast), we propose an approach tailored to commonly encountered medical imaging scenarios. In the proposed approach, an optimal shape-based template is constructed from a subset of the available data. Subsequent pairwise image registration between all training data and the resulting template permits a “pseudo-geodesic” transformation of each image to every other image thus potentially converting a data set of size N to an augmented data set of size N^2 . In this way, transformations are constrained to the shape space representing the population of interest.

To enhance relevance to the research community, we showcase this work in conjunction with the introduction of *ANTsRNet*—a growing open-source repository of well-known deep learning architectures which interfaces with the Advanced Normalization Tools (ANTs) package [18] and its R package (i.e., ANTsR) [18]. This permits the public distribution of all code, data, and models for external reproducibility which can be found on the GitHub repository corresponding to this manuscript [19]. This allows other researchers to apply the developed models and software to their data and/or use the models to initialize their own model development tailored to their studies.

In the work described below, we first provide the acquisition protocols for both the helium and ventilation images followed by a discussion of the analysis methodologies for the proposed segmentation framework. This is contextualized with a brief overview of existing quantification methods (including that previously proposed by our group and used for the evaluative comparison). We also summarize the key contributions of this work viz., the template-based data augmentation and the current feature set of ANTsRNet.

MATERIALS AND METHODS

Image acquisition

Both proton and ventilation mages used for this study were taken from current and previous studies from our group. Ventilation images comprised both Helium-3 and Xenon-129 acquisitions as our current segmentation processing does not distinguish between ventilation gas acquisition protocols and we expected similar agnosticism for the proposed approach.

Ventilation. Hyperpolarized MR image acquisition was performed under an Institutional Review Board (IRB)-approved protocol with written informed consent obtained from each subject. In addition, all imaging was performed under an Food and Drug Administration (FDA)-approved physician's Investigational New Drug application (IND 57866) for hyperpolarized gas. MRI data were acquired on a 1.5 T whole-body MRI scanner (Siemens Sonata, Siemens Medical Solutions, Malvern, PA) with broadband capabilities and a flexible ${}^3\text{He}$ chest radiofrequency coil (RF; IGC Medical Advances, Milwaukee, WI; or Clinical MR Solutions, Brookfield, WI). During a 10–20-second breath-hold following the inhalation of hyperpolarized gas, a set of 19–28 contiguous axial sections were collected. Parameters of the fast low angle shot sequence were as follows: repetition time msec / echo time msec, 7/3; flip angle 10° ; matrix, 80×128 ; field of view, 26×42 cm; section thickness, 10 mm; and intersection gap, none. Total acquisition time varies between 5–8 seconds depending on the size of the subjects.

Proton. A three-dimensional (3D) proton gradient-echo sequence (repetition time [TR]:1.80 ms, echo time [TE] 0.78 ms, flip angle 10° , bandwidth per pixel 1090 Hz/Pixel, partial Fourier: phase direction 6/8, slice direction 6/8) was used to acquire multiple images sets from multiple subjects at varying inflation levels. Acquisition time was 4 sec per image set. All imaging studies were performed under a physician's Investigational New Drug application for hyperpolarized gas imaging using a protocol approved by Institutional Review Board of our institute. All subjects provided written informed consent and the data were deidentified prior to analysis.

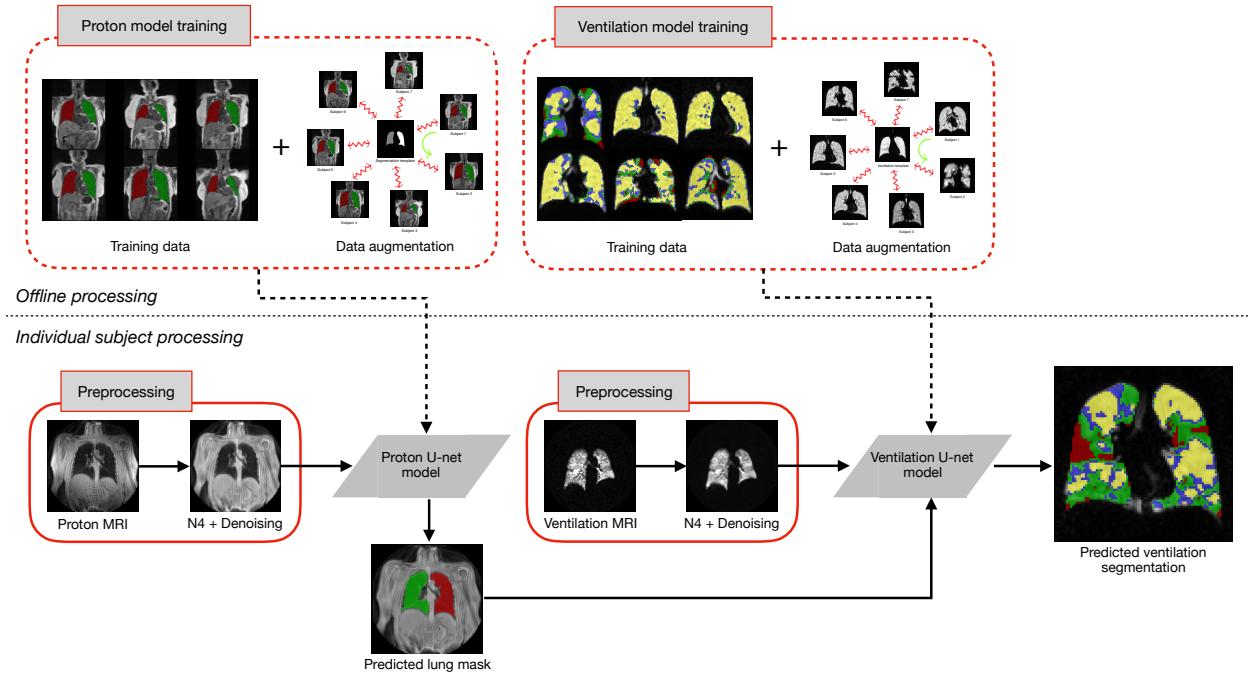


Figure 1: Illustration of the proposed workflow. Training the U-net models for both proton and ventilation imaging includes template-based data augmentation. This offline training is computationally intensive but is only performed once. Subsequent individual subject preprocessing includes MR denoising and bias correction. The proton mask determined from the proton U-net model is included as a separate “channel” for ventilation image processing.

Image processing and analysis

We first review our previous contributions to the segmentation of proton and hyperpolarized gas MR images [7, 16] as we use these previously described techniques for evaluative comparison. We then describe the deep learning analogs (including preprocessing) extending earlier work and discuss the proposed contributions which include:

- convolution neural networks for structural/functional lung segmentation,
- template-based data augmentation, and
- open-source availability.

An overview of the resulting framework is provided in Figure 1. The most computationally intensive portion is the offline processing for model training for both structural and functional imaging. However, once that is complete, individual processing consists of a couple of preprocessing steps followed

by application of the models which has minimal computational requirements.

Previous approaches for lung and ventilation-based segmentation

Automated ventilation-based segmentation, described in [7], employs a Gaussian mixture model using a Markov random field (MRF) spatial prior which is optimized via the expectation-maximization algorithm which has been used in a number of clinical studies (e.g., [20, 21]). Briefly, the intensity histogram profile is modeled using Gaussians with means and standard deviations designed to model the intensities of the individual ventilation classes (e.g., ventilation defect, hypo-ventilation, and normal ventilation). At each iteration the resulting estimated labels are then refined based on MRF spatial modeling to smooth out the effects of noise. The parameters of the class-specific Gaussians are then re-estimated. This iterative process continues until convergence. We also iterate this segmentation with application of N4 bias correction [22]. Unlike other segmentation methods which rely solely on intensity distributions while discarding spatial information, (e.g., K-means variants [8, 10], histogram rescaling and thresholding [9]), our technique employs both spatial and intensity information for probabilistic classification.

Because of our dual structural/functional acquisition protocol [23], we also previously formulated a joint label fusion (JLF) approach for segmenting the left and right lungs in proton MRI as well as estimating the lobar volumes. An atlas set consisting of a cohort of both the proton MRI and the corresponding lung segmentation is spatially normalized to an unlabeled image. A weighted consensus from the normalized images and segmentations is used to determine each voxel label. Although the method yields high quality results which are fully automated, one of the drawbacks is the time and computational resources required to perform the image registration for each member of the atlas set and the subsequent voxelwise label estimation.

Preprocessing

Because of the low-frequency imaging artifacts introduced by confounds such as radiofrequency coil inhomogeneity, we perform a retrospective bias correction on both sets of images using the N4 algorithm [24]. These are included in our previously proposed ventilation [7] and structural [16] seg-

mentation frameworks. Since the initial release of these pipelines we have also adopted an adaptive, patch-based denoising algorithm specific to MR [25] which we have reimplemented in the ANTs toolkit. The dual effects of these data cleaning techniques on both the proton images and ventilation images are shown in Figure 2.

U-net architecture for structural/functional lung segmentation

Deep learning, a term denoting neural network architectures with multiple hidden layers, has gained prominence in recent years. In the field of image analysis and computer vision, deep learning with convolution neural networks (CNNs) has been particularly prominent due, in large part, to the annual ImageNet Large Scale Visual Recognition Challenge [26]. Specifically, one of the participating groups in the 2012 ImageNet challenge was the earliest adopter of CNNs. The resulting architecture, colloquially known as “AlexNet” [27], surpassed any approach that had been proposed previously and laid the groundwork for future CNN-based architectures for image classification such as VGG [28] and GoogLeNet [29]. The recent successes of CNNs are historically rooted in the pioneering work of LeCun et al. [30] and Fukushima [31] and others which drew inspiration from earlier work on the complex arrangement of cells within the feline visual cortex [32]. CNNs are characterized by common components i.e., convolution, pooling, and activation functions which can be put together in various arrangements to perform such tasks as image classification and voxelwise segmentation.

The U-net architecture was introduced in [15] which extended the fully convolutional neural network (FCN) approach introduced by Long, Shelhamer, and Darrel [33]. U-net augments the “encoding path” (see left side of Figure 3) common to such architectures as VGG and FCN with a symmetric decoding path where the corresponding encoding/decoding layers are linked via skip paths for enhanced feature detection. The nomenclature reflects the descending/ascending aspect of its architecture. Each series in both encoding and decoding branches is characterized by two convolutional layers sandwiching an optional dropout layer. This latter modification from the original is meant to provide additional regularization for over-fitting prevention [34]. Output consists of a segmentation probability image for each label from which a segmentation map can be inferred.

We used U-net to build separate models for segmenting both structural and functional lung images.

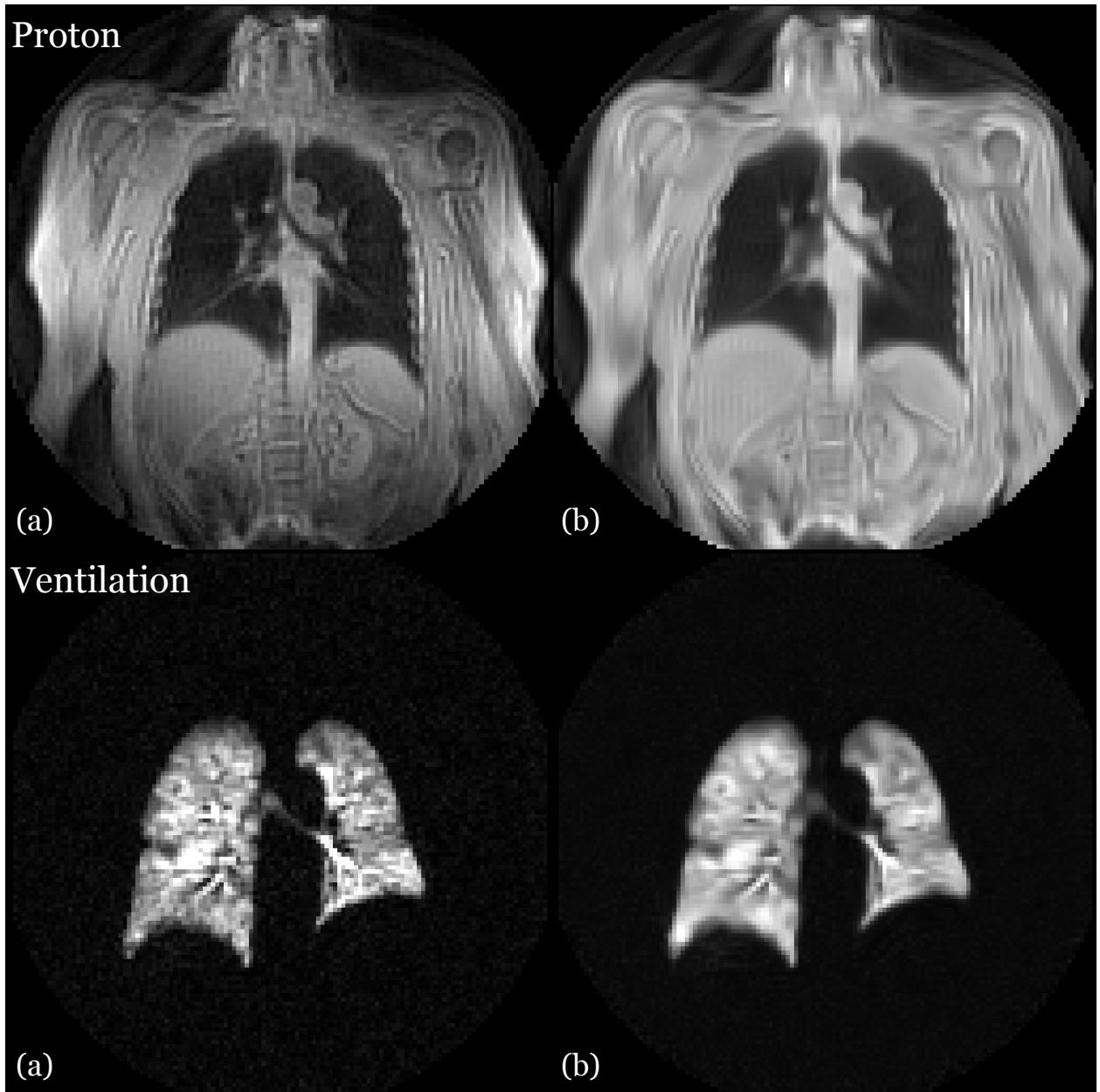


Figure 2: Side-by-side image comparison showing the effects of preprocessing on the proton (top) and ventilation (bottom) MRI. (a) Uncorrected image showing MR field inhomogeneity and noise. (b) Corresponding corrected image in which the bias and noise effects have been ameliorated.

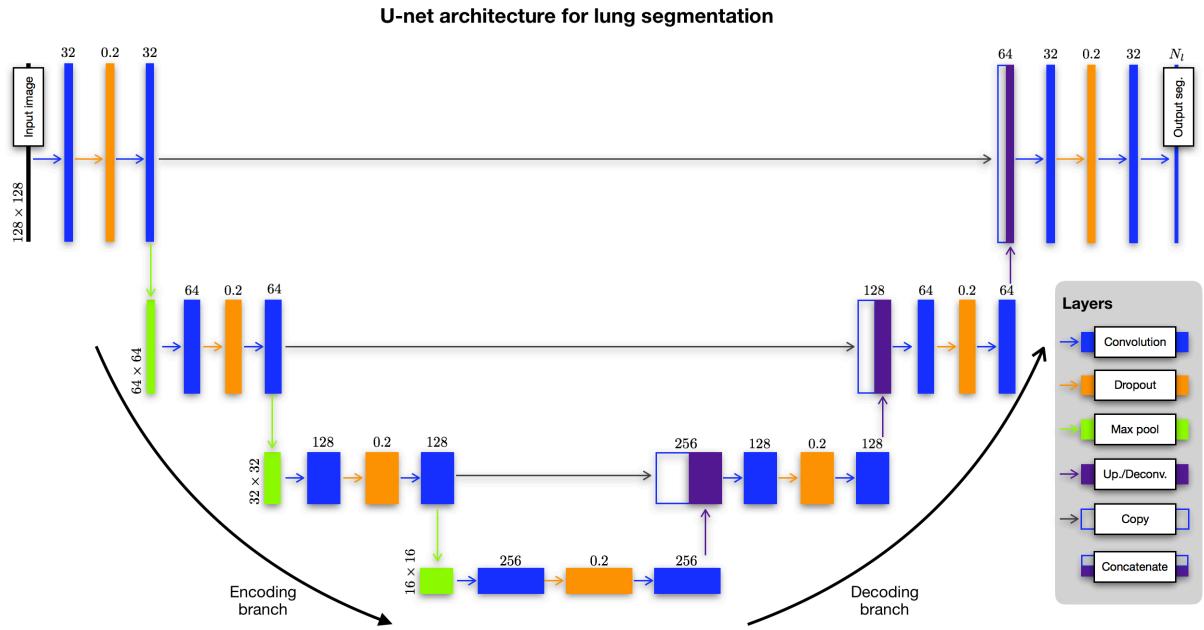


Figure 3: The modified U-net architecture for both structural and functional lung segmentation. Network layers are represented as boxes with arrows designating connections between layers. The main parameter value for each layer is provided above the corresponding box. Input 2-D images are typically of size 128×128 voxels or are resampled accordingly. Each layer of the descending (or “encoding”) branch of the network is characterized by two convolutional layers. Modification of the original architecture includes an intermediate dropout layer for regularization (dropout rate = 0.2). A max pooling operation produces the feature map for the next series. The ascending (or “decoding”) branch is similarly characterized. A convolutional transpose operation is used to upsample the feature map following a convolution → dropout → convolution layer series until the final convolutional operation which yields the segmentation probability maps.

For cases where dual acquisition provides both images, we use the structural images to provide a mask for segmentation of the ventilation image. We used an open-source implementation written by our group and provided with the ANTsRNet R package [35] which is described in greater detail below. We also implemented a multi-label dice coefficient loss function along with specific batch generators for generating batch image data on the fly. Specific parameters for the architectural components are as follows:

- Convolution layers
 - kernel size: 2×2
 - activation: rectified linear units (ReLU) [36]
 - number of filters: doubled at every layer starting with $N = 32$
- Dropout layers

- rate: 0.2
- Max pooling layers
 - size: 2×2
 - stride length: 2×2
- Upsampling/ transposed convolution (i.e., deconvolution) layers
 - kernel size: 5×5
 - stride length: 2×2
 - activation: rectified linear units (ReLU) [36]

Template-based data augmentation

In order to generate data cohorts of sufficient size necessary for deep learning approaches, we have designed of a template-based data augmentation strategy. The need for large training data sets is a well-known limitation associated with deep learning algorithms. Whereas the architectures developed for such tasks as the ImageNet competition have access to millions of annotated images, such data access is not always available and such is typically the case in medical imaging. In order to achieve data set sizes necessary for learning functional models, various data augmentation strategies have been employed [17]. These include application of intensity transformations, such as brightening and enhanced contrast. They might also include spatial transformations such as arbitrary rotations, translations, and even simulated elastic deformations. Such transformations might not be ideal if they do not represent shape variation within the range within the population under study.

We propose a template-based approach whereby image data sampled from the population is used to construct a representative template that is optimal in terms of shape and/or intensity [37]. In addition to the representative template, this template-building process yields the transformations to/from each individual image to the template space. This permits a propagation of the training data to the space of each individual image. In the simplest case, the training data is used to construct the template and then each individual training data is propagated to the space of every other individual training data. In this way, a training data set of size N can be expanded to a data set of size N^2 (cf Figure 1). A more complicated use case could build a template from M data sets (where $M > N$). Transformations between the training data and the template could then be used to propagate

the training data to the spaces of the individual members of the template-generating data for an augmented data set size of $M \times N$.

ANTsRNet

In addition to the contributions previously described, we also introduce ANTsRNet [35] to the research community which not only contains the software to perform the operations specific to structural and functional lung image segmentation but also performs a host of other deep learning tasks wrapped in a thoroughly documented and well-written R package. The recent interest in deep learning techniques and the associated successes with respect to a variety of applications has motivated adoption of such techniques. Basic image operations such as classification, object identification, and segmentation (as well as more focused techniques) have significant potential for facilitating basic medical research. ANTsRNet is built using the Keras neural network library (available through R) and is highly integrated with the ANTsR package, the R interface of the ANTs toolkit. Consistent with our other software offerings, ongoing development is currently carried out on GitHub using a well-commented coding style, thorough documentation, and self-contained working examples.

It should be noted that various implementations of different deep learning architectures exist and are largely available to the public. However, we feel that ANTsRNet fills an unmet need. Based on our own search, many publicly available implementations, while functional, are not developed with large-scale distribution and application as end goals. There is little, if any, coding consistency between the various implementations leading to non-standardized APIs and difficulties in code navigation for debugging and/or didactic reasons. In addition, the vast majority employ the Python language which is understandable given its widespread usage by data scientists. However, this work makes these powerful new developments available through a major platform heavily used by statisticians and data scientists. In addition, the R-based interface to the ANTs toolkit allows for preprocessing and data augmentation strategies specific to medical imaging.

Several architectures have been implemented for both 2-D and 3-D images spanning the broad application areas of image classification, object detection, and image segmentation (cf. Table 1). It should be noted that most reporting in the literature has dealt exclusively with 2-D implementations. This is

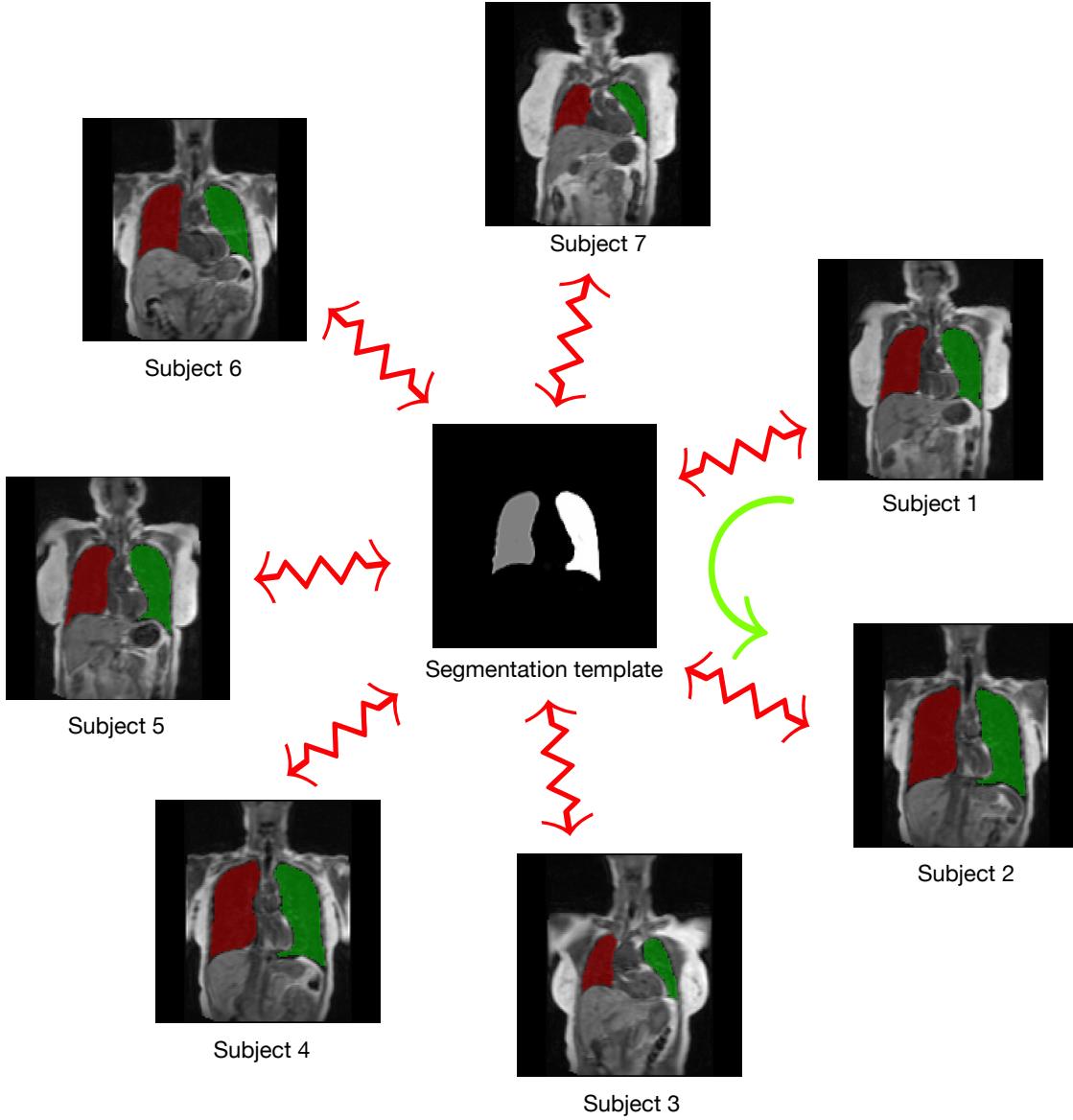


Figure 4: We introduce a novel data augmentation strategy for medical images using ANTs-based template construction. Shown here is the 2-D U-net example where we create a template from the training data segmentation images where the foreground designates the left and right lungs. This avoids the lack of internal correspondence while generating plausible global shape variations when mapping between individual training data. We used 60+ images to create such a template permitting $60^2 = 3600$ possible deformable shapes which can be further augmented by more conventional strategies (e.g., brightness transformations, translations, etc.).

understandable due to memory and computational speed constraints limiting practical 3-D application on current hardware. However, given the importance that 3-D data has for medical imaging and the rapid progress in hardware, we feel it worth the investment in implementing corresponding 3-D architectures. Each architecture is accompanied by one or more self-contained examples for testing and illustrative purposes. In addition, we have made novel data augmentation strategies available to the user and illustrated them with Keras-specific batch generators.

RESULTS

DISCUSSION

Significant progress has been made from earlier quantification approaches in which human labelers manually identified areas of poor ventilation or applied simple thresholding techniques. More sophisticated automated and semi-automated techniques have advanced our ability to investigate the use of hyperpolarized gas imaging as quantitative image-based biomarkers. Deep learning techniques can further enhance these methodologies by potentially increasing accuracy, generalizability, and computational efficiency. In this work, we provided a deep learning framework for segmentation of structural and functional lung MRI for quantification of ventilation. This framework is based on the U-net architecture and implemented using the Keras API available through the R statistical project. It demonstrated

There are several limitations to the proposed framework. The most obvious is that it does not leverage the full 3-D nature of the image data collected. The trained models were based on 2-D coronal slices and therefore subsequent prediction is limited to those views. Even though good results were achieved in this study, even better results might be achieved by training 3-D models. However, even though the software is available for such model generation (e.g., ANTsRNet), model optimization requires significant hardware resources which were not available for this study. Also, evaluative comparison was made using manually-refined segmentations which is certainly useful but additional evaluations using various clinical measures would also be helpful in determining the relative utility of various segmentation approaches. For example, how does the performance of the various methods

Table 1: Current ANTsRNet capabilities comprising architectures for applications in image segmentation, image classification, and object localization. Self-contained examples with data are also provided to demonstrate usage for each of the architectures. Although the majority of neural network architectures are originally described for 2-D images, we generalized the work to 3-D implementations where possible.

ANTsRNet		
Image Segmentation		
U-net [?]	(2-D)	Extends fully convolutional neural networks by including an upsampling decoding path with skip connections linking corresponding encoding/decoding layers.
V-net [?]	(3-D)	3-D extension of U-net which incorporates a customized Dice loss function.
Image Classification		
AlexNet [?]	(2-D, 3-D)	Convolutional neural network that precipitated renewed interest in neural networks.
VGG16/VGG19 [?]	(2-D, 3-D)	Also known as 'OxfordNet'. VGG architectures are much deeper than AlexNet. Two popular styles are implemented.
GoogLeNet [?]	(2-D)	A 22-layer network formed from <i>inception blocks</i> meant to reduce the number of parameters relative to other architectures.
ResNet [?]	(2-D, 3-D)	Characterized by specialized <i>residualized blocks</i> (and skip connections).
ResNeXt [?]	(2-D, 3-D)	A variant of ResNet distinguished by a hyper-parameter called <i>cardinality</i> defining the number of independent paths.
DenseNet [?]	(2-D, 3-D)	Based on the observation that performance is typically enhanced with shorter connections between the layers and the input.
Object Localization		
SSD300/SSD512 [?]	(2-D, 3-D)	The Multibox Single-Shot Detection (SSD) algorithm for determining bounding boxes around objects of interest.
SSD7 [?]	(2-D, 3-D)	Lightweight SSD variant which increases speed by slightly sacrificing accuracy. Training size requirements are smaller.

translate into utility as an imaging biomarker for lung function?

Future research will certainly look into these issues as potential improvements to the existing framework. As a surrogate for full 3-D models, we are looking into developing additional 2-D U-net models

for the axial and sagittal views. Since slice-by-slice processing is computationally efficient in the deep learning paradigm, we can process 3-D images along the three canonical axes and combined the results for increased accuracy. More broadly, it would be of potential interest to investigate the use of image classification techniques (e.g., VGG [28]) for classifying lung disease phenotype directly from the images.

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