Efficient population-based big MR data analysis: a lung segmentation and volumetry example

Tatyana Ivanovska[1,3], Andreas Pomschar[2], Roberto Lorbeer[2], Wolfgang Kunz[2], Holger Schulz[4], Holger Hetterich[2], Henry Völzke[3], Fabian Bamberg[5], Anette Peters[2,4], and Florentin Wörgötter[1]

[1] Georg-August University, Göttingen, Germany
`tiva@phys.uni-goettingen.de`
[2] Hospital of the Ludwig-Maximilians-University, Munich, Germany
[3] Ernst-Moritz-Arndt University, Greifswald, Germany
[4] German Research Centre for Environmental Health, Munich, Germany
[5] University of Tuebingen, Tübingen, Germany

Abstract. In this paper, we discuss magnetic resonance (MR) lung imaging and the related image processing tasks from two on-going epidemiological studies conducted in Germany.
A modularized system for efficient lung segmentation is proposed and applied for test lung datasets from both studies. The efficiency of the framework is demonstrated by comparison of automatically computed results to the manually created ground truth masks. The presented pipeline allows one to obtain highly accurate segmentation results even for MR data with lower quality.

Keywords: MRI, Lung, Segmentation and Volumetry, Epidemiology

1 Introduction

Population-based studies with a clinical-epidemiological focus use imaging techniques, similar to clinical practice [20]. Magnetic resonance imaging (MRI) is a non-invasive, non-ionizing method. This technique offers high spatial, as well as high temporal resolution to image not only the anatomical structures but also functional processes.

MRI is applied in multiple population-based studies, such as the Study of Health in Pomerania [15,21], National Cohort [22], Cooperative Health Research In The Augsburg Region (KORA) [13], the Rotterdam study [7], the Norwegian Aging study [12]. The acquired huge amounts of imaging data are then analyzed by many different research groups in multiple projects.

Automatic segmentation is an essential step in medical image analysis, medical visualization [2], and computer-aided diagnosis. Manual segmentation of large volumes of MR data is extremely time consuming and thus cost intensive, while also demonstrating a high inter- and intra-observer variability. Automatized segmentation and visualization techniques of medical data on the other hand promise to mitigate these limitations. They are actively developed and applied [1, 14, 16]. Although a significant number of segmentation strategies for different organs from MR data have been proposed, there is a lack of a general strategy, which would allow for application of a modularized approach to similar segmentation tasks [17] for different studies, as well as the comparison of used imaging protocols from the quantitative image analysis perspective.

In this work, we focus on MR-based lung imaging, which is used for assessing lung volumes, boundaries, detection of nodules, infiltrates, and masses [8], from two epidemiological studies, namely, the Study of Health in Pomerania (SHIP [21]) and Cooperative Health Research In The Augsburg Region (KORA) [6].

The paper is organized as follows. In Section 2, the imaging protocols from both studies as well as the manually acquired ground truth data are presented and discussed. The possible segmentation strategies in the frame of a generalizable framework are presented in Section 3. The segmentation results are discussed in Section 4. The Section 5 concludes the paper.

2 Materials

Here, three aspects of data are presented, namely, general information about the studies, data acquisition protocols, as well as the ground truth masks.

2.1 General Study Information

SHIP is a population-based study, which investigates common risk factors, subclinical disorders and manifest diseases. It applies highly innovative non-invasive imaging methods in a population of northeast Germany [21]. The data was acquired from participants aged 20-79 years. SHIP is the first population based cohort worldwide which includes whole-body MRI [5, 15]. The MR data from 3332 subjects are available for analysis.

KORA [6] is population-based study of adult residents (25-74 years old) in a well-defined small area in southern Germany where rural and urban residents could be well-defined by community size. In the MRI-Substudy 400 participants aged 38-72 years old were randomly recruited, among them 103 pre-diabetic subjects, 54 diabetic subjects, and 243 participants without diabetes.

2.2 Lung MR Data

All MRI studies in SHIP are performed on a 1.5-T MR scanner(Magnetom Avanto; Siemens Medical Systems, Erlangen, Germany) [5]. Each participant undergoes standardized whole body MRI including an axial T1-weighted VIBE (volume-interpolated breath hold examination) sequence (typical parameters: repetition time (TR) 31 ms, echo time (TE) 11 ms, flip angle 8°, voxel size $1.8 \times 1.8 \times 3$ mm) and an axial T2-weighted HASTE (half-Fourier single-shot turbo spinecho) sequence (TR 5500 ms, TE 220 ms, flip angle 150°, voxel size $2.3 \times 1.8 \times 5$ mm) for chest imaging. To avoid motion artifacts 21 s of breath hold are needed for the VIBE sequence. The HASTE sequence is taken in two steps and then the parts are composed together with the navigator control. In total, 40 s are needed for the HASTE sequence. Because of the small slice thickness (3 mm) and bigger spatial resolution when compared to the HASTE sequences, the VIBE sequence is preferable for the task of automatic lung segmentation and volumetry.

In MRI-KORA, lung imaging was acquired as a part of the Multi-echo Dixon sequence on a 3-T MR scanner (Magnetom Skyra, Siemens Medical Systems, Erlangen, Germany). A three-dimensional parallel-accelerated opposed- and in-phase volumetric interpolated breath-hold examination (VIBE) prototype was used to image the thoracal region. To avoid motion artifacts 15 s of breath hold are required for acquisition. The parameters of the acquisition are as follows, TR 4.1 ms, TE 2.496ms, flip angle 9°, view matrix 256 × 256, slice thickness 3 mm [6]. For automatic processing, the in-phase sequence was selected.

The example slices from both studies are shown in Figure 1. One can observe the intensity inhomogeneity and partial volume effects due to a lower spatial resolution in the KORA example (right), when compared to the SHIP example (left).

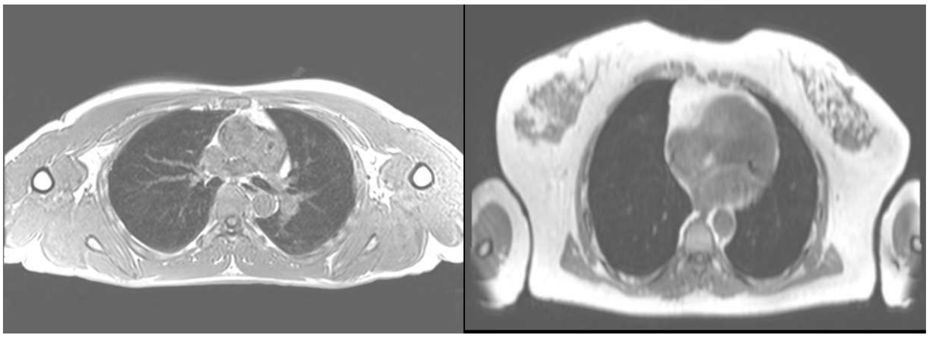

Fig. 1. Example slices from SHIP (left) and KORA (right) data.

In both studies subjects were placed in the supine position, and the acquisition was performed in the middle inspiration phase. Therefore, the MRI defined lung volumes are not directly comparable to spirometry-based volumes.

The spatial resolution of SHIP data is $512 \times 512 \times 88$. The spatial resolution of KORA data is $288 \times 160 \times 288$.

2.3 Ground truth masks

In both studies a limited number of randomly selected datasets (10 for SHIP and 17 for KORA) were evaluated manually by four independent experts, namely, radiologists and pulmonologists with more than 3 years of experience. Two readers evaluated each test set. For the evaluation, the experts manually segmented the lung volume excluding the tracheal part and including the hilus region .

The cutoff was defined, as the region where the main bronchi enter the lung parenchyma.

3 Segmentation Strategy

The task of lung segmentation from MR images usually consists of 3D lung region detection, separation of the lungs from the large airways, and exclusion or inclusion of the pulmonary vessel regions. The depiction of smaller structures such as lung borders and fissures was not possible due to resolution limitation in the used MR protocols.

3.1 Related Work

Recently, some approaches for lung segmentation from MRI have been presented in the literature [8,10,11,19]. There are basically two groups of methods, namely, intensity-based and atlas or model-based ones.

According to Tustison et al. [19], the atlas-based technique provides slightly more accurate results, when the correspondent atlas library is built for a specific cohorts, compared to the classical intensity-based approaches.

However, the intensity-based approaches are preferable, when only a limited number of ground truth masks are available, which would not be sufficient for accurate model generation. Moreover, the classical methods are rather fast and produce highly accurate results for lung volumetry. For instance, Kohlmann et. al [11] presented an automated segmentation procedure, which utilizes 3D region growing scheme and morphological operations [16]. Ivanovska et al. [10] proposed a coarse-to-fine intensity-based approach, where the airways are first extracted from the rest of image, thereafter the lung regions are refined by extracting the tracheal parts and separating the lungs. Further segmentation methods are assessed in a review by Ivanovska et al. [8].

3.2 Proposed pipeline

The approach of Ivanovska et al. [10] was applied to SHIP data and consisted of the following modules (cf. Figure 2): extraction of lungs, extraction of trachea, separation of lungs, and final lung smoothing.

However, the KORA datasets exhibit stronger intensity inhomogeneities and have lower spatial resolution when compared to SHIP data (cf. Figure 1). Therefore, we extended this pipeline by adding several new modules to the framework. The general pipeline structure remains the same though.

First: The intensity inhomogeneity correction module is applied prior to any processing. To our experience, the N4ITK algorithm [18] produces acceptable results and with only limited computation requirements.

Second: To avoid processing of unnecessary regions, we propose to pre-extract a coarse region of interest that contains airways.

Third: Due to a lower spatial resolution, the trachea extraction module often failed to detect the tracheal boundaries correctly, especially in the region of the mediastinum. Hence, we updated the module by adding the 3D Vesselness filter [4] to ensure the proper trachea selection and excluded 2D Watershed [16] from processing.

The updated modularized lung segmentation framework, which is applied both to SHIP and KORA data, is presented in Figure 2.

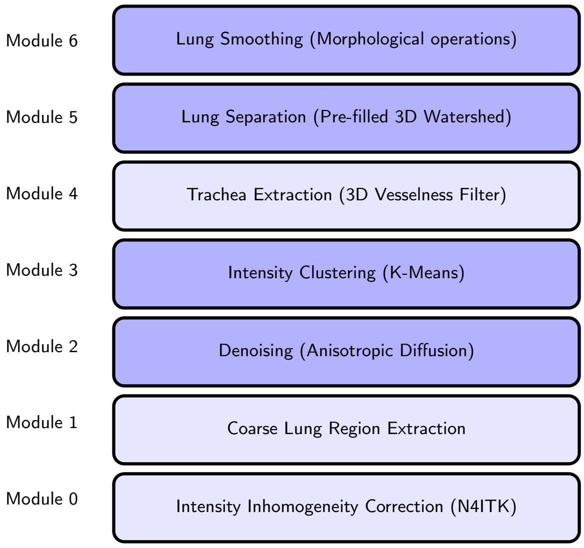

Fig. 2. Lung Segmentation Framework: Main modules of the approach by Ivanovska et al. [10] shown in dark blue and the newly introduced or updated modules for KORA data are shown in light blue.

In Figure 3, segmentation results of KORA data as demonstrated in an overlaid manner.

4 Results and Discussion

Here, we present the results and discuss data, segmentation pipelines, and extension perspectives.

4.1 Qualitative comparison of SHIP and KORA lung data

Lung imaging is one of the important components of the SHIP-MRT program [5, 15], and thus the MRI imaging protocol uses two specialized sequences (high-resolution VIBE and coarser HASTE).

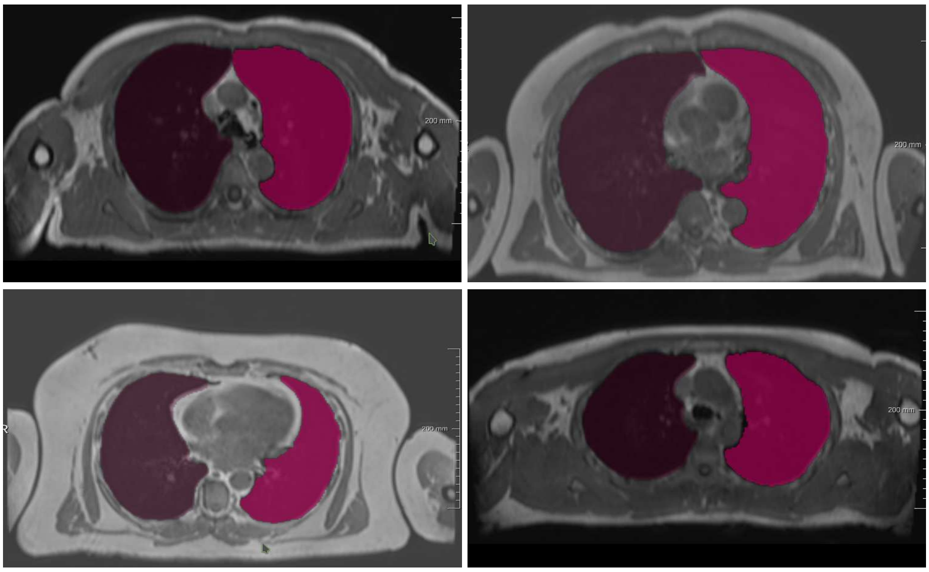

Fig. 3. Example results from KORA data.

The KORA Study is mainly focused on cardiovascular examinations, with only a ”byproduct“, which is acquired together with the abdominal organs [6]. This is reflected in two limiting factors:

- The lung region is not acquired completely in some datasets (cf. Figure 4).
- The spatial resolution is lower than in the specialized sequence used in SHIP (cf. Figure 1).

Additionally, the acquisition time of the Dixon sequence in KORA is only 15 seconds, while the high resolution VIBE-sequence in SHIP takes 21 seconds. This allows for reduction of the total MRI measurement time and the corresponding study expenses.

Although the KORA data contain some artifacts that represent a challenge for automated image processing, the proposed framework allows us to successfully tackle this problem.

4.2 Quantitative comparison of automated segmentation results

The proposed pipeline is applied both to SHIP and KORA test sets, and the parameter settings are fixed for both groups of datasets. We use DICE coefficients [3] to evaluate the performance of the pipeline. The inter-observer variability for each pair of experts is evaluated in the same manner. The values (mean± standard deviation) are presented in Table 1. One can observe that the proposed pipeline produces high quality results, and the differences between the

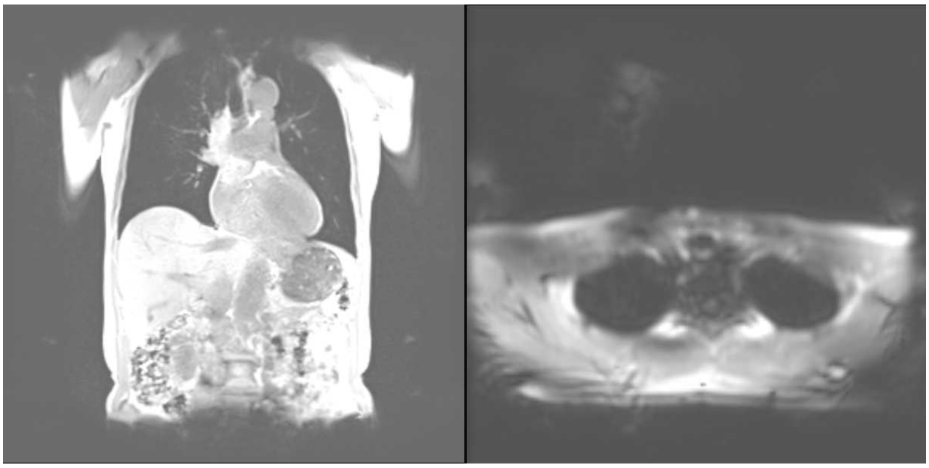

Fig. 4. Coronal (left) and axial (right) example slices, demonstrating the artifacts on the lung tops in KORA data.

automated method and manual readings are quantitatively very similar to the differences between two experts, namely, DICE coefficient is ≥ 0.95.

To demonstrate the efficiency of the framework, we applied the algorithm presented by Ivanovska et al. [10] both to SHIP and KORA test sets and compared the results to one expert groundtruth. The results are 0.915 ± 0.047 and 0.9589 ± 0.00699 for KORA and SHIP data, respectively. One can observe that the average DICE coefficient for KORA data are about $3 - 4\%$ higher for the proposed framework than for the original algorithm from [10] (95% vs. 92%), whereas the results for SHIP are slightly lower, namely, 95.2% versus 96%.

Data	Auto vs. R1	Auto vs. R2	R1 vs. R2
KORA	0.95 ± 0.01	0.946 ± 0.012	0.957 ± 0.014
SHIP	0.951 ± 0.009	0.9522 ± 0.0056	0.955 ± 0.0077

Table 1. Dice coefficient for segmentation results produced by the proposed pipeline (Auto) and the manual results from two experts (R1 and R2) are compared to each other both for SHIP and KORA data.

4.3 Possible framework extensions

Several future extensions and improvements to this framework seem possible. First, one could add the analysis of the tracheal part that is excluded from the processing after extraction (Module 4 in Figure 2). The precondition for such an analysis is that the scanning includes the tracheal region of interest. Here, one could study the tracheal dimensions and search narrowed areas as an indication for tracheal stenosis [9].

Second, statistical and visual analytics studies on the lung volumes and shapes, and the differences between diabetic, pre-diabetic, and healthy subjects could be conducted, and the results from the SHIP cohort would be used for comparison. An example 3D view of the lungs is shown in Figure 5.

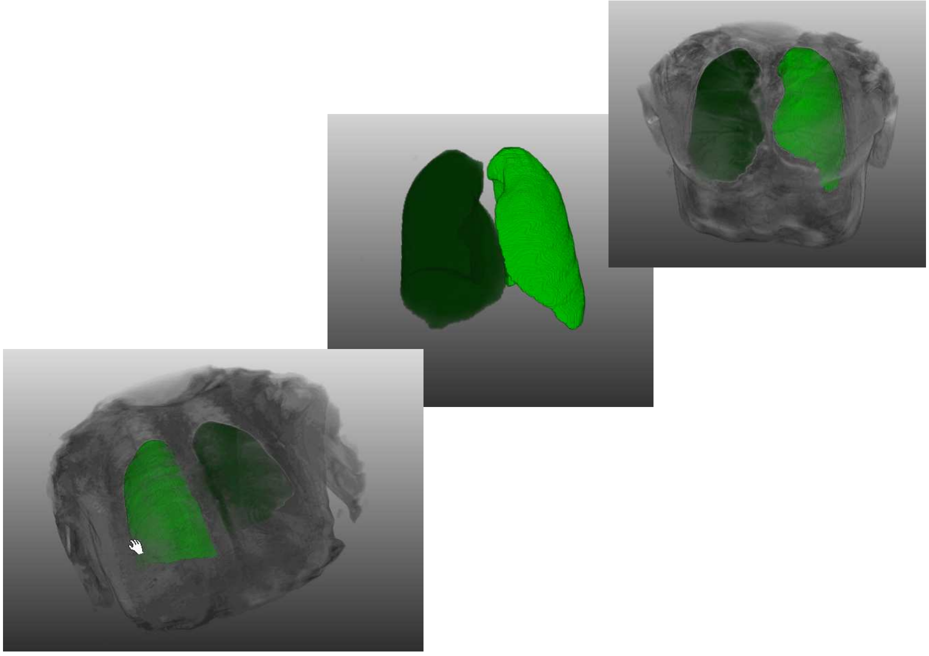

Fig. 5. An example of segmented lungs are shown in a 3D view.

Third, one could analyze the definition of the "middle inspiration" phase among different subjects and scanning protocols.

5 Conclusions and Future Work

In this paper, an efficient and extendable framework for lung segmentation from native MRI was proposed and applied to the data with different protocols from two epidemiological studies. We have shown the efficiency of the segmentation pipeline even for more challenging data.

For future work, we plan to run a statistical analysis of the processed full data sets (400 subjects for KORA and 3332 subjects for SHIP) as well as application of the framework to MR data from further epidemiological studies.

Acknowledgements

The contributions to data collection made by field workers, radiologists, technicians, interviewers, and computer assistants are gratefully acknowledged.

Sources of Funding The KORA study was initiated and financed by the Helmholtz Zentrum München âĂŞ German Research Center for Environmental Health, which is funded by the German Federal Ministry of Education and Research (BMBF) and by the State of Bavaria. Furthermore, KORA research was supported within the Munich Center of Health Sciences (MC-Health), Ludwig-Maximilians-University, as part of LMUinnovativ. The KORA-MRI sub-study received funding by the German Research Foundation (DFG, Deutsche Forschungsgemeinschaft). The KORA-MRI sub-study was supported by an unrestricted research grant from Siemens Healthcare.

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