Automatic lung segmentation in routine imaging is a data diversity problem, not a methodology problem

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Abstract—Automated segmentation of anatomical structures is a crucial step in many medical image analysis tasks. For lung segmentation, a variety of approaches exist, involving sophisticated pipelines trained and validated on a range of different data sets. However, during translation to clinical routine the applicability of these approaches across diseases remains limited. Here, we show that the accuracy and reliability of lung segmentation algorithms on demanding cases primarily does not depend on methodology, but on the diversity of training data. We compare 4 generic deep learning approaches and 2 published lung segmentation algorithms on routine imaging data with more than 6 different disease patterns and 3 published data sets. We show that a basic approach - U-net - performs either better, or competitively with other approaches on both routine data and published data sets, and outperforms published approaches once trained on a diverse data set covering multiple diseases. Training data composition consistently has a bigger impact than algorithm choice on accuracy across test data sets. We carefully analyse the impact of data diversity, and the specifications of annotations on both training and validation sets to provide a reference for algorithms, training data, and annotation. Results on a seemingly well understood task of lung segmentation suggest the critical importance of training data diversity compared to model choice.

Index Terms—pathological lung segmentation, semantic segmentation, routine radiology data

I. INTRODUCTION

The translation of machine-learning approaches developed on specific data sets to the variety of routine clinical data is of increasing importance. As methodology matures across different fields, means to render algorithms robust for the transition from the lab to the clinic become critical. Here, we investigate the impact of model choice and training data diversity in the context of segmentation.

The detection and accurate segmentation of organs is a crucial step for a wide range of medical image processing applications in research and computer-aided diagnosis (CAD) [1]. Segmentation enables the quantitative description of anatomical structures with metrics such as volume, location, or statistics of intensity values, and is paramount for the detection and quantification of pathologies. For machine-learning, segmentation is highly relevant for discarding confounders outside the relevant organ. At the same time, the segmentation algorithm itself can act as a source of bias. For example, a segmentation algorithm can hamper subsequent analysis by systematically excluding dense areas in the lung field [2].

While lung segmentation is regarded as a mostly solved problem in the methodology community, experiments on routine imaging data demonstrate that algorithms performing well on publicly available data sets do not yield accurate and reliable segmentation in routine chest CTs of patients who suffer from severe disease. Thus, the methodological advance does not translate to applicability in the clinical routine. Here, we show that this is primarily an issue of training data diversity, and not of further methodological advances.

Automated lung segmentation algorithms are typically developed and tested on limited data sets, covering a limited spectrum of visual variability by predominantly containing cases without severe pathology [3] or cases with a single class of disease [4]. Such specific cohort datasets are highly relevant in their respective domain, but lead to specialized methods and machine-learning models that struggle to generalize to unseen cohorts when utilized for the task of segmentation. Due to these limitations, in practice, medical image processing studies, especially when dealing with routine data, still rely on semiautomatic segmentations or human inspection of automated organ masks [5, 6]. However, for large-scale data analysis based on thousands of cases, human inspection or any human interaction with single data items, at all, is not an option.

A. Related Work

A diverse range of lung segmentation techniques has been proposed. They can be categorized into rule-based, atlas-based, machine-learning-based and hybrid approaches. Rule-based methods rely on thresholding, edge detection, region-growing, morphological operations, and other “classical” image processing techniques [7, 8, 9, 10]. Atlas-based methods rely on non-rigid image registration between the unlabeled image and one- or more labeled atlases [11, 12, 13]. Machine-learning-based approaches rely on large datasets to learn active shape models [14, 15, 16], locations of landmarks [17], hand-crafted features, or Convolutional Neural Networks (CNN) for end-to-end learning [18]. Hybrid approaches combine various techniques, such as thresholding and texture classification [19, 20, 21], landmarks and shape models [17], and other combinations [22, 23, 24].

The lung appears as a high contrast region in X-ray-based imaging modalities, such as CT, so that thresholding and atlas segmentation methods lead to good results in many
cases [7], [8], [9]. However, disease-associated lung patterns, such as effusion, atelectasis, consolidation, fibrosis, or pneumonia, lead to dense areas in the lung field that impede such approaches. Multi-atlas registration aims to deal with these high-density abnormalities by incorporating additional atlases, shape models, and other post-processing steps [22]. However, such highly complex pipelines are not reproductible without extensive effort, especially if the source code and the underlying set of atlases is not shared. An additional drawback is that these algorithms are usually optimized for chest CT scans, neglecting scans with a larger or smaller field of view. Furthermore, run-time does not scale well when incorporating additional atlases, as registrations tend to be computationally expensive. With respect to these drawbacks, trained machine-learning models have the advantage, in that they can be easily shared without giving access to the training data, they are fast at inference time, and scale well when additional training data are available. Harrison et al. [18] showed that deep-learning-based segmentation outperforms a specialized approach in cases with interstitial lung diseases [18] and provides trained models, inference code, and model specifications for non-commercial use upon request. However, with some exceptions, trained models for lung segmentation are rarely shared publicly, hampering advances in medical imaging research. At the same time, machine-learning methods are limited by the training data available, their number, and the quality of the ground-truth annotations.

Benchmark datasets for training and evaluation are paramount to establish comparability between different methods. However, publicly available datasets with manually annotated organs for development and testing of lung segmentation algorithms are scarce. The VIScERAL Anatomy3 dataset [3] provides a total of 40 segmented lungs (left and right separated) in scans that show the whole body or the whole trunk. The Lung CT Segmentation Challenge 2017 (LCTSC) [4] provides 36 training and 24 test scans with segmented lungs (left and right separated) in scans that show the whole body or the whole trunk. The Lung CT Segmentation Challenge 2017 (LCTSC) [4] provides 36 training and 24 test scans with segmented lungs (left and right separated) in scans that show the whole body or the whole trunk. The Lung CT Segmentation Challenge 2017 (LCTSC) [4] provides 36 training and 24 test scans with segmented lungs (left and right separated) in scans that show the whole body or the whole trunk. The Lung Tissue Research Consortium (LTRC) [2] provides an extensive database of cases collected from the clinical routine (Sec. II-C). We evaluated these segmentation models and our segmentation model trained on these data-sets, and on a diverse routine data-set with more than four different segmentation models on different training data without restriction on disease or disease pattern. We trained four different segmentation models on different training data (public and routine) and evaluated their accuracy on public data-sets, and on a diverse routine data-set with more than six different disease patterns. Furthermore, we compared the performance between two publicly available (trained) lung segmentation models and our segmentation model trained on our diverse data set and submitted results to the LOLA11 challenge for independent evaluation.

II. MATERIALS AND METHODS

Both-, the training dataset and architecture, used for a machine-learning task affect the performance of a trained model. In order to study these effects in the context of lung segmentation, we trained four generic semantic segmentation models (Sec. [II-A] from scratch on three different public training sets (Anatomy3, LTSC, LTRC) and one training set collected from the clinical routine (Sec. [II-C]). We evaluated these
models on public test sets (LTSC, LTRC, and VESSEL12) and routine data, including cases showing severe pathologies. Furthermore, we performed a comparison of models trained on a diverse routine training set to two published automatic lung segmentation systems, which we did not train, but used as provided.

A. Models

We refrained from developing specialized methodology, but utilized generic "vanilla" state-of-the-art deep-learning, semantic segmentation architectures, without modifications, which we trained from scratch. We considered the following four models:

- **U-net**: Ronneberger et al. proposed the U-net for the segmentation of anatomic structures in microscopy images [28]. Since then, the U-net architecture has been used for a wide range of applications and various modified versions have been studied [29]. We utilized the U-net as proposed by Ronneberger et al. with the only adaptation being batch-normalization after each layer.

- **ResU-net**: Residual connections have been proposed to facilitate the learning of deeper networks [31], [32] and are widely used in deep learning architectures. Here, the ResU-net model includes residual connections at every down- and up-sampling block as a second adaptation to the U-net, in addition to batch-normalization.

- **Dilated Residual Network (DRN)**: Yu et al. proposed dilated convolutions for semantic image segmentation [33]. They showed that dilated convolutions can extend the receptive field in higher layers, thereby facilitating context aggregation. Later, they adapted deep residual networks with dilated convolutions (DRN) to perform high-quality semantic segmentations on natural images. Here, we utilized the DRN-D-22 model, as proposed by Yu et al. [34].

- **DeepLab v3+**: Chen et al. proposed a series of semantic segmentation algorithms (DeepLab v1, DeepLab v2, and DeepLab v3(+)), with a particular focus on speed. DeepLab v3 combines
dilated convolutions, multi-scale image representations, and fully-connected conditional random fields as a post-processing step. Deeplab v3+ includes an additional decoder module to refine the segmentation. Here, we utilized the ‘Deeplab v3+’ model as proposed by Chen et al. [34].

B. Implementation Details

We aimed to achieve a maximum of flexibility with respect to the field of view (from partially visible organ to whole-body) and to enable lung segmentation without prior localization of the organ. To this end, we performed segmentation on the slice level (2D). That is, for volumetric scans, each slice was processed individually. We segmented the left and right lung (individually labelled), excluded the trachea and specifically included high density anomalies such as tumor and plural effusions. During training and inference, the images were cropped to the body region using thresholding and morphological operations, and rescaled to a resolution of $256 \times 256$ pixels. Prior to processing, hounsfield units were mapped to the intensity range $[−1024, 600]$ and normalized to the 0-1 range. During training, the images were augmented by random rotation, non-linear deformation and Gaussian noise. We used stratified mini-batches of size 14 holding 7 slices showing the lung and 7 slices which don’t show the lung. For optimization, we used Stochastic Gradient Decent (SGD) with momentum [35].

C. Routine data collection and sampling

We collected representative training and evaluation datasets from the picture archiving and communication system (PACS) of a university hospital radiology department. We included in- and outpatients who underwent a chest CT examination during a period of 2.5 years, with no restriction on age, sex, or indication. However, we applied minimal inclusion criteria with regard to imaging parameters, such as axial-slicing of the reconstruction, number of slices in a series $\geq 100$ and the series description included one of the terms lung, chest, or thorax. If multiple series of a study fulfilled these criteria, the one series with the highest number of slices was used. In total, we collected more than 5300 patients (examined during the 2.5-year period), each represented by a single CT series. From this database, we carefully selected a representative training dataset using three sampling strategies: (1) random sampling of cases (N=57); (2) sampling from image phenotypes [36] (N=71) (the exact methodology for phenotype identification was not in the scope of this work); and (3) manual selection of edge cases with severe pathologies, such as fibrosis (N=28), trauma (N=20), and other pathologies (N=55). In total, we collected 231 cases from routine data for training (hereafter referred to as R231). While the dataset collected from the clinical routine showed a high variability in lung appearance, cases that showed the head or the abdominal area are scarce. To mitigate this bias toward slices that showed the lung, we augmented the number of non-lung slices in R231 by including all slices which did not show the lung from the Anatomy3 dataset.

For testing, we randomly sampled 20 cases from the database that were not part of the training set (hereafter referred to as RRT) and 15 cases with specific anomalies [atelectasis (2), emphysema (2), fibrosis(4), mass (2), pneumothorax (2) and trauma (3)] for testing. Ground-truth labeling was bootstrapped by training of a lung segmentation algorithm (U-net) on the Anatomy3 dataset. The preliminary masks were iteratively corrected in an active-learning fashion. Specifically, the model for the intermediate masks was iteratively retrained after 20-30 new manual corrections were performed with the ITK-Snap software [37]. In total, we performed ground-truth annotation on 266 chest CT scans from 266 individual patients.

D. Evaluation metrics

Automatic segmentations were compared to the ground truth for all test datasets using the following evaluation metrics, as implemented by the Deepmind surface-distance python module[3]. While segmentation was performed on 2D slices, evaluation was performed on the 3D volumes. If not reported differently, the metrics were calculated for the right and left lung separately and then averaged.

1) Dice coefficient (DSC): The Dice coefficient or Dice score is a measure of overlap:

$$D(X, Y) = \frac{2|X \cap Y|}{|X| + |Y|}$$ (1)

where $X$ and $Y$ are two alternative labelings, such as predicted and ground-truth lung masks.

2) Robust Hausdorff distance (HD95): The directed Hausdorff distance is the maximum distance over all distances from points in surface $X_s$ to their closest point in surface $Y_s$. In mathematical terms, the directed robust Hausdorff distance is given as:

$$\bar{H}(X_s, Y_s) = P_{95} \left( \min_{y \in Y_s} d(x, y) \right)$$ (2)

where $P_{95}$ denotes the 95th percentile of the distances. Here, we used the symmetric adaptation:

$$H(X_s, Y_s) = \max \left( \bar{H}(X_s, Y_s), \bar{H}(Y_s, X_s) \right)$$ (3)

3) Mean surface distance (MSD): The mean surface distance is the average distance of all points in surface $X_s$ to their closest corresponding point in surface $Y_s$:

$$\overline{MSD}(X_s, Y_s) = \frac{1}{|X_s|} \sum_{x \in X_s} \min_{y \in Y_s} d(x, y)$$ (4)

Here, we used the symmetric adaptation:

$$MSD(X_s, Y_s) = \max \left( \overline{MSD}(X_s, Y_s), \overline{MSD}(Y_s, X_s) \right)$$ (5)

[3]https://github.com/deepmind/surface-distance
E. Experiments

Study the impact of training data variability: We determined the influence of training data variability (especially public datasets vs. routine) on the generalizability to other public test-datasets, and, specifically, to cases with a variety of pathologies. To this end, we trained the four different models on an equal number of patients (N=36) and slices (N=3393) from each training dataset [Routine Random (RR36), VISCERAL Anatomy3 (VISC36), LTRC (LTRC36), and LCTSC (LCTSC36)] individually. The RR36 dataset is a subset of the 57 randomly sampled cases that we collected for training, and therefore, is also a subset of the full routine dataset R231. Table I gives an overview of the training datasets created. The number of volumes and slices were limited to match the smallest dataset (LCTSC), with 36 volumes and 3393 slices. During this experiment, we considered only slices that showed the lung (during training and testing) to prevent a bias induced by the field of view. For example, images in VISCERAL Anatomy 3 showed either the whole body or the trunk, including the abdomen, while other datasets, such as LTRC, LCTSC, or VESSSEL12 contained only images limited to the chest. Also, trauma patients are scanned with a larger field of view compared to patients in whom only the lung is examined.

| Abbr. | Name               | #Vol. | #Slices | #Slices |
|-------|--------------------|-------|---------|---------|
| RR36  | Routine Random     | 36    | 3393    | 3393    |
| VISC36| VISCERAL Anatomy3  | 36    | 3393    | 3393    |
| LTRC36| LTRC               | 36    | 3393    | 3393    |
| LCTSC36| LCTSC            | 36    | 3393    | 3393    |
| R231  | Routine 231 Cases | 231   | 62224   | 108248  |

The trained P-HNN model does not distinguish between left and right lung. Thus, evaluation metrics were computed on the full lung for masks created by P-HNN. In addition to evaluation on publicly available datasets and methods, we performed an independent evaluation of our lung segmentation model by submitting solutions to the LOLA11 challenge for which 55 CT scans are published but ground-truth masks are available only to the challenge organizers.

Table II gives an overview of the test datasets used. Evaluation on publicly available datasets and methods, we performed an independent evaluation of our lung segmentation model by submitting solutions to the LOLA11 challenge for which 55 CT scans are published but ground-truth masks are available only to the challenge organizers.

Quantitative assessment of the models’ ability to cover tumor areas: Studies on lung segmentation usually use overlap- and surface-metrics to assess the automatically generated lung mask against the ground truth. However, segmentation metrics on the full lung can only marginally quantify the capability of a method to cover pathological areas in the lung as pathologies may be relatively small compared to the lung volume. Carcinomals are an example of high-density areas that are at risk of being excluded by threshold- or registration-based methods, when they are close to the lung border. We utilized the publicly available, previously published Lung1 dataset [38] to quantify the model’s ability to cover tumor areas within the lung. The collection contains scans of 318 non-small-cell lung cancer patients before treatment, with a manual delineation of the tumors. However, no lung masks were available. In this experiment, we evaluated the overlap proportion of tumor volume covered by the lung mask:

\[ TO(T, X) = \frac{|T \cap X|}{|T|} \] (6)

III. Results

Table II gives an overview of the test datasets used. LTRC, LCTSC, and VESS12 are publicly available. RRT is a set of 20 randomly sampled lung CT scans from the routine database. The category ass held two cases from the Lung1 dataset where ground truth masks were created by us and the category normal held four cases with a large field of view from the Visceral Anatomy3 dataset and two cases from the routine database. In total, we collected 191 test cases not used for training.
Fig. 2. Ground-truth annotations in public datasets lack coverage of pathologic areas: Segmentation results for cases in public datasets where the masks generated by our U-net(R231) yielded low Dice scores when compared to the ground truth. Note that public datasets often do not include high-density areas in the segmentations. Tumors in the lung area should be included into the segmentation while the liver should not.

A. Models trained on routine data outperformed models trained on publicly available study data

U-net, ResU-net, and Deeplab v3+ models, when trained on routine data (RR36 models), yielded the best evaluation scores over all test cases. The largest differences in performance were observed on routine test data (RRT), with a U-net trained on Visceral data (VISC36), which yielded an average DSC of 0.84, and, when trained on RR36, 0.92. This advantage of routine data for training is also reflected in the overall results and other evaluation metrics with U-net yielding DSC, HD95, and MSD scores of 0.96±0.08, 9.19±18.15, 1.43±2.26 when trained on RR36 and 0.92 ± 0.14, 13.04 ± 19.04, 2.05 ± 3.08 when trained on VISC36. Table III lists the evaluation results in detail. We report the averaged DSC for the individual test sets and for all test cases combined (All(L), N=191). In addition, we report all test cases combined without the LTRC and LCTSC data considered (All, N=62). The rationale behind this is, that the LTRC test dataset contains 105 volumes and dominates the averaged scores, and the LCTSC dataset contains multiple cases with tumors and effusions that are not included in the ground-truth masks. Thus, an automated segmentation that includes these areas yields a lower score, distorting and misrepresenting the averaged results. Models trained on routine data yielded the highest DSC on all subcategories apart from LCTSC and VESS12. In fact, the models trained on RR36 yielded the lowest performance in terms of DSC on the LCTSC test dataset. However, the lower scores for these models in LCTSC and VESS12 can be attributed to the lack of very-dense pathologies in the ground truth masks, as mentioned above (See qualitative results in Fig. 2).

B. Various deep-learning-based semantic segmentation architectures perform comparably for lung segmentation

We determined that the influence of model architecture is marginal compared to the influence of training data. Considering the models trained on the datasets comprised of 36 scans (RR36, LTRC36, LCTSC36 and VISC36) we observed that the different architectures perform comparably, with the DSC
not varying for more than 0.02 when the same combination of training and test set was applied (Table III). The same conclusion holds when models were trained on the full volumes of the U-net(R231), resnet(R231) and deeplab(R231) achieving the identical DSC of 0.98±0.03 over all test cases. The drr(R231) model yielded a slightly lower DSC over all cases of 0.97±0.06. Detailed results are listed in Table [IV].

C. All training sets generalized well to cases without severe pathologies

Results show, that moderately sized training sets generalizes well to the test cases of the same dataset but also to different datasets without severe pathologies. For example, training the U-net on 36 cases of the LTRC dataset yielded a DSC of 0.99 on the LTRC test set of 105 cases while still generalizing well to the VESS12 dataset (DSC of 0.99) and our selected routine cases with emphysema (DSC of 0.99), mass (DSC of 0.98), or pneumo-thorax (DSC of 0.98). In general, we observed that, independent of training set and architecture, cases without severe pathologies were accurately segmented by the models. Specifically, test cases in the public LTRC and VESS12 datasets received an averaged DSC of at least 0.96 (up to 0.99) depending on architecture and training data. The same conclusion can be drawn for the emphysema, mass, pneumo-thorax and normal test cases for which results vary only little (ΔDSC<0.01) for the different models. Detailed results are listed in Table [III].

D. Generic models trained on routine data outperformed specialized publicly available systems

Compared to P-HNN the U-net(R231) yielded an average DSC of 0.98±0.03 vs. 0.96±0.09 over all 191 test cases. The averaged results without the LTRC and LCTSC datasets yielded DSC, HD95, and MSD scores of 0.98±0.03, 3.14±7.4, 0.62±0.93 vs. 0.94±0.12, 16.8±36.57, 2.59±5.96. Detailed results are given in Table [V] Note that the P-HNN results were calculated on the full lung compared to the left and right
lung for the U-net, giving P-HNN an advantage in achieving better scores. For comparison with the CIP-algorithm, only volumes for which the algorithm did not fail were considered. The CIP-algorithm tends to fail on challenging cases with dense pathologies and on volumes with a large field of view. In total, the CIP algorithm was able to process 160 of the 191 test volumes. Both algorithms yielded comparable DSC when averaged on all test cases. Without LTBC and LCTSC considered, the algorithms yielded average DSC, HD95, and MSD scores of 0.98 ± 0.01, 1.44 ± 1.09, 0.35 ± 0.19 for the U-net(R213) compared to 0.96 ± 0.05, 4.65 ± 6.45, 0.91 ± 1.09 for CIP. Figure 3 shows qualitative results for cases from the routine test sets. In addition to publicly available datasets and our routine data, we created segmentations for the 55 cases of the LOLA11 challenge with the U-net(R231) model.

E. A generic model trained on routine data covers more tumor area than specialized publicly available systems

Table V and Figure 4 show the results for average tumor overlap on the 318 volumes of the Lung1 dataset. U-net(231) covered more tumor volume mean/median (60/69%) compared to P-HNN (50/44%) and CIP (34/13%). Figures 3a and b show qualitative results for tumor cases for U-net(R231) and P-HNN. We found, that 23 cases of the Lung1 dataset had corrupted ground-truth annotation of the tumors (Figure 3c). Figure 3d shows cases with little or no tumor overlap achieved by U-net(R231).

F. Runtime

Batchwise inference of the U-net model requires 12.5ms per slice with a batch size of 20 (4.4 seconds for a volume of 350 slices) on a GeForce GTX 1080Ti GPU with Python 3.6, Pytorch 1.2 and Numpy 1.17.2 and an Intel(R) Xeon(R) W-2125 CPU. Inference on the CPU takes 0.8s per slice or 281 seconds for a volume of 350 slices. In addition, creating the body-mask and cropping the slice takes ∼22ms per slice or 7.7s for the whole volume of 350.

3https://lola11.grand-challenge.org/evaluation/results/
TABLE V
OVERLAP BETWEEN LUNG MASKS AND MANUALLY ANNOTATED TUMOR VOLUME IN THE LUNG1 DATASET. GIVEN ARE MEAN, MEDIAN AND NUMBER OF CASES WITH A SMALLER THAN 5% OVERLAP AND A LARGER THAN 95% OVERLAP.

| Method   | Mean | Median | < 5% | > 95% |
|----------|------|--------|------|-------|
| CIP      | 34%  | 13%    | 113  | 56    |
| P-HNN    | 50%  | 44%    | 48   | 78    |
| U-net(RR36) | 53%  | 54%    | 46   | 79    |
| U-net(R231) | 60%  | 69%    | 37   | 90    |

IV. DISCUSSION

Lung segmentation is a pivotal pre-processing step for many image analysis tasks, such as classification, detection and quantification of lung pathologies. Despite its fundamental importance, publicly available algorithms for pathological lung segmentation are scarce, which impedes research on lung pathologies with medical imaging. This is not only attributed to authors reluctant to make their implementations publicly available, but also to the fact that many algorithms are complex and hard to reproduce. For example, the method with the highest score in the LOLA11 challenge consists of a sophisticated pipeline with multiple processing steps, and relies on a private database of reference atlases [2], rendering it impossible to reproduce the results without access to the data. In contrast to complex processing pipelines, trained machine-learning models are easy to share and use. However, we showed that public datasets do not hold sufficient variability to generalize to a wide spectrum of routine pathologies. This situation is aggravated by the fact that many publicly available datasets don’t include dense pathologies such as tumor or effusions into the lung mask.

The inclusion or exclusion of lung pathologies such as effusions into lung segmentations is a matter of definition and application. While pleural effusions (and pneumothorax) are technically outside the lung, they are assessed as part of lung assessment, and have a substantial impact on lung parenchyma appearance through compression artefacts. Neglecting such abnormalities would hamper automated lung assessment, as they are closely linked to lung function. In addition, lung masks that include pleural effusions greatly alleviate the task of effusion detection and quantification, thus making it possible to remove effusions from the lung segmentation as a post-processing step.

There are a large number of segmentation methods proposed every year, often based on architectural modifications of established models. Isensee et al. showed that such modified design concepts do not improve even very sophisticated models [3]. They achieved state-of-the-art performance on multiple, publicly available segmentation challenges relying only on U-nets. This corresponds to our finding that architectural choice had a subordinate effect on performance, and, given a diverse and large set of training data, a standard semantic segmentation architecture (U-net) can generate high quality lung segmentations.

Volume-based segmentation metrics are valid tools with which assess the segmentation quality on the organ level. However, they are a superficial means by which to assess the quality in pathological lung segmentation. Area-based metrics, such as the Dice score, but also surface-based metrics such as HD95 and MSD, tend to only marginally worsen in the presence of a missed abnormality if the abnormality is small compared to the whole organ. We showed that datasets without lung masks, but with annotated pathologies such as Lung1, can be a means with which to quantify algorithms with respect to the ability to cover abnormal lung areas. We showed that the U-net trained on routine data covered more tumor area than the reference methods.

V. CONCLUSION

We showed that accurate and fast lung segmentation does not require complex methodology and that a proven deep-learning-based segmentation architecture can outperform state-of-the-art methods on diverse (but not necessarily larger) training data are available. By comparing various datasets for training of the models, we illustrated the importance of diverse training data and showed that data from the clinical routine generalize well to unseen cohorts, achieving the second-highest score among all submissions to the LOLA11 challenge. Given these findings, we draw the following conclusions: (1) translating machine-learning approaches from the lab to routine data can require the collection of diverse training data rather than methodological modifications; (2) current, publicly available study datasets do not meet these diversity requirements; and (3) generic, semantic, segmentation algorithms are adequate for the task of lung segmentation. A reliable, universal tool for lung segmentation is fundamentally important to foster research on severe lung diseases and to study routine clinical datasets. Thus, the trained model and inference code are made publicly available under the GPL3 license to serve as an open science tool for research and development and as a publicly available baseline for lung segmentation under https://github.com/JoHof/lungmask.

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