TrueLung: an automated pipeline for computation and analysis of functional perfusion and ventilation lung MRI with matrix pencil decomposition

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ABSTRACT

Purpose: To introduce and evaluate TrueLung, a fast and automated pipeline for analysis of free-breathing and contrast-agent free pulmonary functional magnetic resonance imaging (MRI).

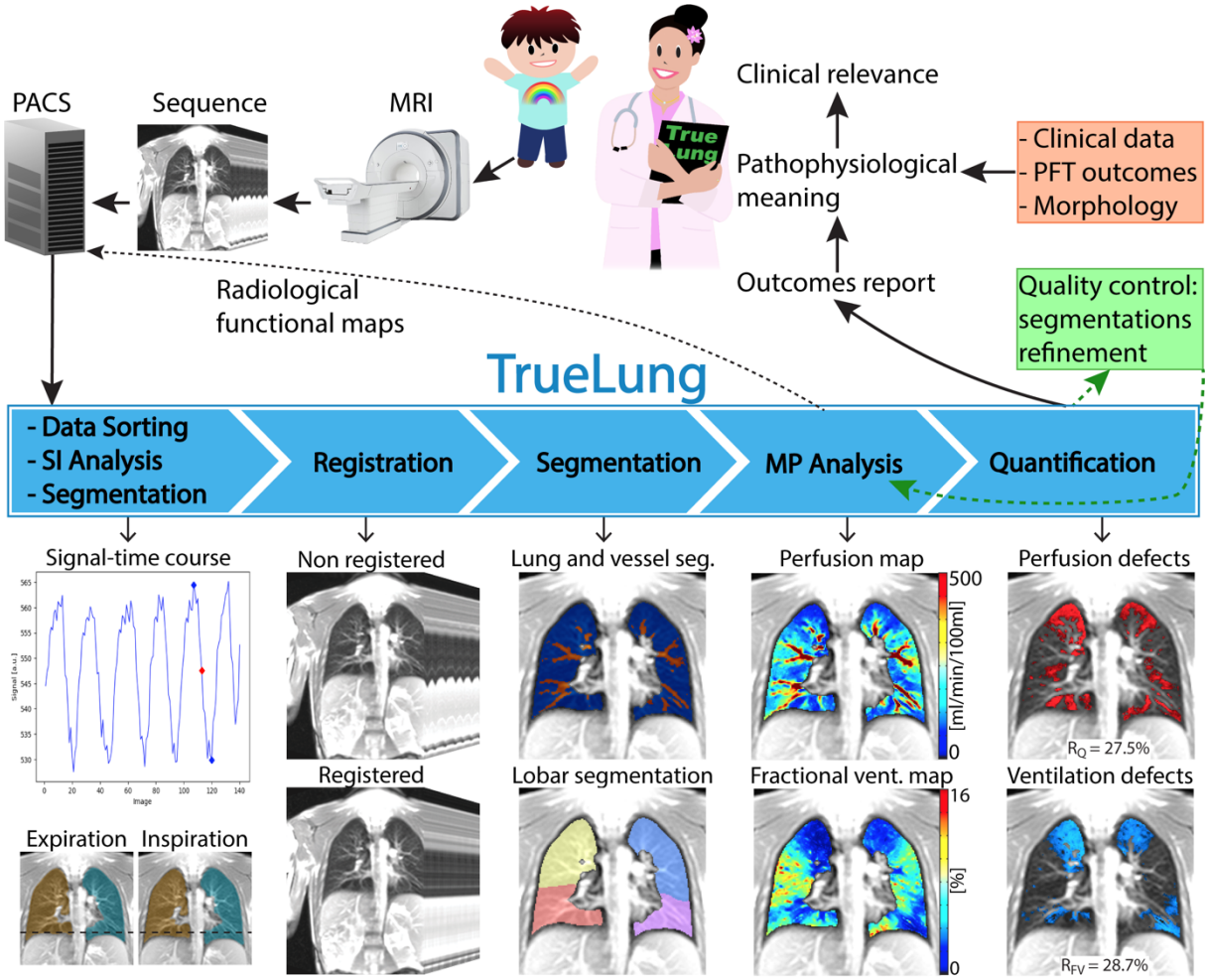
Materials and Methods: Two-dimensional time-resolved ultra-fast balanced steady-state free precession MR acquisitions are transferred to TrueLung, which includes image quality checks, image registration, and computation of perfusion and ventilation maps with matrix pencil decomposition. Neural network whole-lung and lobar segmentations together with specific algorithms allow quantification of impaired relative perfusion (R_Q) and fractional ventilation (R_{FV}). TrueLung delivers functional maps and quantitative pulmonary outcomes, which are also summarized into documents for clinicians.

We evaluated the pipeline using images from 75 cystic fibrosis children obtained at 1.5T. An observer assessed whole-lung and lobar segmentations and manually refined them when necessary. The impact of the segmentation refinement on R_Q and R_{FV} was quantified.

Results: Functional imaging was performed at 7.9±1.8 (mean±SD) coronal slice positions per patient, in 6min 20s. The whole pipeline required 20min calculation per patient. TrueLung automatically delivered the functional maps of all the subjects for radiological assessment. Quality controlling the maps and segmentations lasted 1min 12s per patient. The automated segmentations and quantification of whole-lung defects were satisfying in 88% of patients and the lobar quantification in 73%. The segmentations refinements required on average 16s per patient for the whole-lung masks and 2min 10s for the lobar masks.

The relative differences in R_{FV} and R_Q between fully-automated and manually refined data were on average 0.7% (1.2%) and 2.0% (2.9%) for whole-lung quantification [median, (third quartile)], and 1.7% (3.9%) and 1.2% (3.8%) on lobar level, indicating the refinements could be potentially omitted in several patients.

Conclusions: TrueLung quickly delivers objective results in a standardized way for functional lung maps and quantitative outcomes for radiological and pneumological assessment with minimal manual input required. TrueLung can be used for clinical research in cystic fibrosis and might be broadly applied in clinical routine for various lung diseases.



Teaser figure. *The end-to-end workflow and TrueLung.*

Schematic of the whole workflow, the TrueLung pipeline and its processing steps: data sorting, signal intensity analysis and segmentation of expiratory/inspiratory images, image registration, segmentation of the whole-lung, lung lobes, and vessels, MP analysis and generation of functional maps, quantitative defect calculation of R_{FV} and R_Q, generation of and reports and quality controlling. The functional maps after the MP analysis can be sent back to PACS for radiological examination. The quality control includes verification of the segmentation masks and the manual refinement, when necessary. Manually refined datasets are re-processed with the MP analysis and quantification modules. The pipeline can be run on a normal workstation equipped with a CUDA compatible GPU.