Registration and Analysis of Dynamic MRI Image Series



Figure 1: MR images of the lung during expiration and inspiration. Overlayed vector field shows the lung motion between inspiration and expiration (Picture: R. Sandkühler).



Figure 2: Overview of the different developed methods to improve the monitoring process for CF patients (Picture: R. Sandkühler).

PhD Thesis of Robin Sandkühler at CIAN

The aim of this work was the development of new image registration and analysis methods for dynamic MR image series of the lungs.

Cystic fibrosis (CF) is an autosomal-recessive inherited metabolic disorder that affects all organs in the human body. Patients affected with CF suffer particularly from chronic inflammation and obstruction of the airways. Through early detection, continuous monitoring methods, and new treatments, the life expectancy of patients with CF has been increased drastically. Through the development of new MRI sequences and evaluation methods [2], MRI is able to measure physiological changes in the lungs. The process to create physiological maps, i.e., ventilation and perfusion maps, of the lungs using MRI can be split up into three parts: MR-acquisition, image registration, and image analysis.

In this work [1], we present different methods for the image registration part and the image analysis part. We developed a graph-based registration method for 2D dynamic MR image series of the lungs in order to overcome the problem of sliding motion at organ boundaries. Furthermore, we developed a human-inspired learningbased registration method [3]. We also developed a general registration framework called Autograd Image Registration Laboratory (AIRLab) for rapid prototyping registration algorithms.

For the image analysis part, we developed a deep-learning approach based on GRUs that are able to calculate ventilation maps with less than a third of the number of images of the current method. Automatic defect detection in the estimated MRI ventilation and perfusion maps is essential for the clinical routine to automatically evaluate the treatment progression. We developed a weakly supervised method that is able to infer a pixel-wise defect segmentation by using only a continuous global label during training.

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