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学位論文題名

Deep Learning-Based Automated Quantitative Analysis and Clinical Application of Synovitis and Joint Space Changes in Rheumatoid Arthritis
(深層学習に基づく関節リウマチの滑膜炎および関節間隙変化の
自動定量解析と臨床応用研究)

1. Background:

Rheumatoid arthritis (RA) is a chronic inflammatory disease marked by synovitis, leading to joint damage such as cartilage destruction, joint space narrowing (JSN), and bone erosion. Synovitis is a key indicator of inflammation and disease activity, making its early detection and quantification vital for RA management.

JSN, a hallmark of RA, is traditionally assessed using the Sharp-van der Heijde (SvdH) scoring method. However, with advancements in RA treatments like biologics and "treat-to-target" strategies reducing radiographic progression, there is a growing need for precise methods to detect early structural changes. High-resolution peripheral quantitative computed tomography (HR-pQCT) provides three-dimensional imaging to accurately measure joint space width (JSW) and monitor subtle changes in inflammatory arthritis.

2. Chapter 1: Fully Automatic Quantification for Hand Synovitis in Rheumatoid Arthritis Using Pixel-Classification-based Segmentation Network in DCE-MRI

Synovitis is a key indicator of RA activity and progression, but traditional methods like manual delineation and RAMRIS scoring are time-consuming and prone to variability.

The study analyzed DCE-MRI data from 28 RA patients. A 1D convolutional neural network (CNN) was used for tissue segmentation (muscle, bone, and synovitis) based on time-intensity curve (TIC) analysis. Preprocessing steps included noise reduction, motion correction, and contrast enhancement. The network was validated through leave-one-out cross-validation.

The model achieved high accuracy, with an average Dice similarity coefficient of 0.73, and performed segmentation in just 1 second per bounding box, significantly reducing manual workload. Strong correlations with manual delineation were observed.

3. Chapter 2: Deep Registration Method for Finger Joint Space Width Changes: A Comparative

Study with HR-pQCT

This study aims to address the limitations of traditional evaluation methods, such as the SvdH scoring system and HR-pQCT, which are either semi-quantitative, time-consuming, or limited by accessibility. The proposed method focuses on providing sensitive, precise, and automated measurements of JSN, a critical feature of RA progression.

The study analyzed data from 58 RA patients across three time points: baseline, 12 months, and 24 months. JSW changes were measured in the MCP2, MCP3, and MCP4 joints. A deep registration algorithm was employed to analyze X-ray images, leveraging its ability to detect subpixel-level changes. The algorithm measured the JSW changes automatically in X-ray images. The outputs were then compared with HR-pQCT parameters (JSW, volume, mean, maximum, minimum, and asymmetry). The correlation between the deep learning measurements and HR-pQCT data was assessed using Spearman's correlation analysis.

The JSW changes measured by the deep learning-based registration method showed correlations with HR-pQCT-measured joint morphology parameters in MCP2 during the month 12 to month 24 interval, with minimum JSW (JSW.min, $r = 0.415$, $p < 0.01$) and asymmetry (JSW.AS, $r = -0.3442$, $p < 0.05$). Among HR-pQCT parameters, JSW.min and JSW.AS showed the most frequent correlations. The deep registration method was able to detect subpixel changes in joint space on X-ray images.

4. Conclusion

In Chapter 1, this method develops a deep registration method using X-ray imaging to quantify JSW changes in RA patients. It demonstrates the potential for fast, reliable, and objective synovitis quantification, addressing the limitations of traditional techniques. Future work will address challenges like differentiating synovitis from nearby structures and external validation for broader clinical applications.

In Chapter 2, this study proposes a fully automatic segmentation and quantification method for synovitis in RA patients using DCE-MRI and deep learning. It offers a promising approach to quantifying JSW changes in RA patients. It addresses the limitations of traditional imaging techniques by providing automated, sensitive, and cost-efficient assessments of JSN. While the study highlights the need for larger datasets and further validation, the method has strong potential for integration into clinical workflows, enabling early detection and improved monitoring of RA progression.

These studies demonstrate promising methods to enhance the precision and automation of RA imaging analysis, supporting early detection and improved disease management.