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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 van der Heijde modification of the Sharp (VdH-S) 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 analyzes hand DCE-MRI data from 28 RA patients (six males, mean age 53.7 years). A 1D convolutional neural network (CNN) is used for tissue segmentation (muscle, bone, and synovitis) based on time-intensity curve (TIC) analysis. Preprocessing steps include noise reduction, motion correction, and contrast enhancement. The network is validated through leave-one-out cross-validation.

The model achieves high accuracy, with an average Dice similarity coefficient of 0.73, and performs segmentation in just 1 second per bounding box, significantly reducing manual workload. Strong correlations with manual delineation are 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 VdH-S 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 analyzes data from 58 RA patients (mean age 58 ± 10 years; 37 females) across three time points: baseline, 12 months, and 24 months. JSW changes are measured in the MCP2, MCP3, and MCP4 joints. A deep registration algorithm is employed to analyze X-ray images, leveraging its ability to detect sub-pixel-level changes. The algorithm measures JSW changes automatically in X-ray images. The outputs are then compared with HR-pQCT parameters (JSW volume, mean, maximum, minimum, and asymmetry). The correlation between the deep learning measurements and HR-pQCT data is assessed using Spearman's correlation analysis.

The JSW changes measured by the deep learning-based registration method show correlations with HR-pQCT-measured joint morphology parameters in MCP2 during the month 12 to month 24 interval, with minimum JSW (JSW.min, $r = 0.415$, $p < .01$) and asymmetry (JSW.AS, $r = -0.3442$, $p < .05$). Among HR-pQCT parameters, JSW.min and JSW.AS show the most frequent correlations. Between the baseline-to-12-month and baseline-to-24-month intervals, JSW changes measured via deep registration on X-rays significantly correlate with MCP2 ($r = 0.3269$, $p < .05$), MCP3 ($r = 0.2968$, $p < .05$), and MCP4 ($r = 0.478$, $p < .01$). The deep registration method can detect sub-pixel 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 limitations of traditional techniques. Future work will focus on addressing challenges like differentiating synovitis from nearby structures and external validation for broader clinical application.

In Chapter 2, this study validates a deep learning method for quantitatively measuring JSW changes in finger joints of RA patients using X-rays and compares its performance with morphological parameters related to JSW changes measured by the HR-pQCT. It addresses the limitations of traditional imaging techniques by providing automated, sensitive, and cost-efficient assessments of JSN. This method effectively quantifies subtle JSW changes in RA patients using X-ray images, demonstrating its feasibility and clinical utility.

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