

## INTERNATIONAL SYMPOSIUM ON RADIOLOGY, NUCLEAR MEDICINE, AND DIAGNOSTIC IMAGING



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### MuscleJ2: An Automated Bioinformatics Tool for Standardized Histological Analysis of Muscle Biopsies

Histological analysis of skeletal muscle is essential for understanding its structure and function in various physiological and pathological contexts, including neuromuscular disorders. While several software tools have been developed for automated muscle analysis, most are limited in scope, not standardized across laboratories, or rely on fragmented workflows. To address these limitations, we developed MuscleJ/J2, a new comprehensive and fully automated bioinformatics tool for the quantitative analysis of entire mammal muscle biopsy sections.

Building on the ImageJ platform, MuscleJ2 integrates advanced image processing to quantify a wide range of histological parameters, including fibrosis, vascularization, cell phenotypes, peri-myonuclear regions, and individual capillaries, within a single standardized pipeline. It automatically generates detailed, reproducible reports on muscle status, suitable for both research and clinical applications.

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MuscleJ2 is designed to be shared across laboratories and integrated into national patient registries, thereby enabling multicenter studies and facilitating patient selection and follow-up in clinical trials, particularly in the rapidly evolving field of gene and cell therapies for neuromuscular diseases. Importantly, we are currently establishing correlations between histological data generated by MuscleJ2 and non-invasive imaging approaches, such as MRI and ultrasound, to better understand how macroscopic imaging features reflect underlying cellular alterations. This integrative approach aims to improve diagnostic precision, enable standardized monitoring of disease progression, and enhance the evaluation of therapeutic efficacy across clinical trials.

### Biography

Dr Alicia Mayeuf-Louchart is a dedicated researcher specializing in developmental biology and metabolic diseases. She earned her Master's in Reproduction and Development (2009) from Université Paris Diderot and completed her PhD at Sorbonne University under Prof. Margaret Buckingham at the Institut Pasteur. Her doctoral research focused on molecular genetics and cell fate determination in embryonic development. After her PhD, she joined INSERM in Lille for postdoctoral studies on nuclear receptors and circadian rhythms in metabolic regulation. Her work advanced understanding of glycogen metabolism in brown adipose tissue. In 2020, she became a full researcher at INSERM, and by 2024, the Group Leader of the Lille-Neuroendocrinology team. As a Principal Investigator, she leads research on metabolism and biological rhythms in stem cells.