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Advancing Perfusion MRI with Deep Learning: From Reproducibility to Radiogenomics

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Perfusion MRI has emerged as a valuable technique for characterizing brain tumor physiology, but its broader clinical impact has been constrained by issues of reproducibility, variability in acquisition, and small dataset limitations. Over the past several years, a sequence of studies has progressively addressed these barriers, outlining a clear trajectory of methodological innovation in neuro-oncologic imaging.

The initial step applied recurrent neural networks to DSC-MRI time-series, representing the first radiologic study to capture temporal dynamics for IDH mutation prediction. This pioneering work demonstrated the feasibility of sequence modeling but was restricted by limited sample sizes. Subsequent efforts focused on reproducibility: a DCE-to-DSC framework stabilized arterial input function estimation, uncertainty-aware learning improved robustness against noise and variability, and super-resolution with denoising enhanced spatiotemporal fidelity of perfusion MRI parameters. A perfusion-specific super-resolution model further extended these benefits while maintaining clinical efficiency.

The field then advanced toward representation learning. Unsupervised approaches such as vector-quantized variational autoencoders enabled extraction of latent perfusion features and tumor-region clustering, providing more reproducible analysis independent of predefined input functions.

A major milestone was the introduction of spatiotemporal tumor habitat analysis. Using multiparametric MRI (diffusion and perfusion) acquired longitudinally, voxel-wise clustering defined three habitats—hypervascular cellular, hypovascular cellular, and nonviable tissue. Temporal changes in these habitats correlated with time-to-progression and recurrence sites, with post-treatment expansion of hypovascular cellular regions strongly linked to early progression. Building on this, a tumor habitat score was developed to stratify patients by survival risk and differentiate recurrence from treatment effects, establishing a new paradigm for imaging-based biomarkers.

Most recently, these advances have converged in a graph-based radiogenomic framework, where perfusion-derived latent features are aggregated into super-voxels, structural guidance is incorporated, and hierarchical graph deep learning integrates spatiotemporal information for genetic mutation prediction.

In summary, perfusion MRI research has advanced from early sequence modeling, through reproducibility-driven innovations, to unsupervised learning, habitat analysis, and graph-based radiogenomics. This evolution demonstrates how methodological innovation can transform perfusion MRI into a reproducible, biologically meaningful, and clinically actionable imaging biomarker for precision neuro-oncology.

Keywords: *Perfusion MRI, Deep learning, Reproducibility, Tumor habitat analysis, Radiogenomics*